



A DOPHOENIX

APPL PARTS

IMIS
Internal Misc. Paper
LET.
Misc. Incoming Letter

371P
PCT Papers in a 371 Application

A...
Amendment Including Elections

ABST
Abstract

ADS
Application Data Sheet

AF/D
Affidavit or Exhibit Received

APPENDIX
Appendix

ARTIFACT
Artifact

BIB
Bib Data Sheet

CLM
Claim

COMPUTER
Computer Program Listing

CRFL
All CRF Papers for Backfile

DIST
Terminal Disclaimer Filed

DRW
Drawings

FOR
Foreign Reference

FRPR
Foreign Priority Papers

IDS
IDS Including 1449

NPL
Non-Patent Literature

OATH
Oath or Declaration

PET.
Petition

RETMAIL
Mail Returned by USPS

SEQLIST
Sequence Listing

SPEC
Specification

SPEC NO
Specification Not in English

TRNA
Transmittal New Application

CTNF
Count Non-Final

CTRS
Count Restriction

EXIN
Examiner Interview

M903
DO/EO Acceptance

M905
DO/EO Missing Requirement

NFDR
Formal Drawing Required

NOA
Notice of Allowance

PETDEC
Petition Decision

OUTGOING

CTMS
Misc. Office Action

1449
Signed 1449

892

ABN
Abandonment

APDEC
Board of Appeals Decision

APEA
Examiner Answer

CTAV
Count Advisory Action

CTEQ
Count Ex parte Quayle

CTFR
Count Final Rejection

INCOMING

AP.B
Appeal Brief

C.AD
Change of Address

N/AP
Notice of Appeal

PA..
Change in Power of Attorney

REM
Applicant Remarks in Amendment

XT/
Extension of Time filed separate

Internal

SRNT
Examiner Search Notes

CLMPTO
PTO Prepared Complete Claim Set

ECBOX
Evidence Copy Box Identification

WCLM
Claim Worksheet

WFEE
Fee Worksheet

File Wrapper

FWCLM
File Wrapper Claim

IIFW
File Wrapper Issue Information

SRFW
File Wrapper Search Info

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
17831	ENU01625	AN161C30:45	67-86	483-504	NAP		g2462677	141	48	0.00004	27	39	(Z99568) hypothetical protein. [Schizosaccharomyces pombe]
17832	ENU01626	80..4101	69-89	490-512	NAP		g2909624		152	1.00E-36	44	33	(AL021942) hypothetical protein Rv0565c [Mycobacterium tuberculosis]
17833	ENU01627	AN161C7014: 3929..4417	54-75	481-500	NAP		g13533008	148	35	0.3			hypothetical 53.5 KD protein in GCD14-POS18 intergenic region; hypothetical protein YJL123c - yeast (Saccharomyces cerevisiae); (Z49398) ORF YJL123c [Saccharomyces cerevisiae]
17834	ENU01628	AN161S4363: 554..66	37-65	462-483	NAP		g1352891	422	153	5.00E-37	44	40	putative glycosyltransferase HOC1 precursor; probable membrane protein YJR075w - yeast (Saccharomyces cerevisiae); (Z49575) ORF YJR075w [Saccharomyces cerevisiae]; (L47993) ORF YJR075w [Saccharomyces cerevisiae]; (U62942) Hoc1p [Saccharomyces cerevisiae] (AL021748) hypothetical [Schizosaccharomyces pombe] (AF072850) cytochrome p450 CYP4C19 [Lytechinus anamesis] (AL023287) probable helicase [Schizosaccharomyces pombe] (AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f; coded for by C. elegans cDNA cm18g...
17835	ENU01629	AN161C2320: 1370..1858	22-47	444-468	NAP		g2842511	966	177	5.00E-44	50	36	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region; (AE000443) orf, hypothetical protein [Escherichia coli]"
17836	ENU01630	AN161C347:2	39-60	468-487	NAP		g3452329	194	93	1.00E-18	39	93	(Z98530) ribosomal protein [Schizosaccharomyces pombe]
17837	ENU01631	134..2624	23-56	453-473	NAP		g3116120	136	79	2.00E-14	27	15	
17838	ENU01632	422..4929	41-72	457-492	NAP		g2773203	598	215	1.00E-55	61	30	
17839	ENU01633	162..656	66-86	492-518	NAP		g2851420	253	79	2.00E-14	33	16	
17840	ENU01634	5:8243..7747	52-71	478-506	NAP		g2330823	319	95	2.00E-24	65	65	

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
17841	ENU01635	...		65-84	497-521	NAP		g2132957		75	3.00E-13	30	31	probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (AL023589) spliceosome-associated protein [Schizosaccharomyces pombe] lymphocyte specific helicase - mouse ; (U25691) lymphocyte specific helicase [Mus musculus] (Z98601) diphosphomevalonate decarboxylase [Schizosaccharomyces pombe] (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe] (Z92774) fadD3 [Mycobacterium tuberculosis] (Y17393) prefoldin subunit 2 [Mus musculus] (L47106) kinesin [Neurospora crassa] (AF015825) unknown [Bacillus subtilis] ; (Z99110) yjIB [Bacillus subtilis] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe] fruit protein PKIWI501 ; hypothetical protein - kiwi fruit ; (L27810) PKIWI501 [Actinidia delictosa] (D64003) hypothetical protein [Synecocystis sp.] "omega-6 fatty acid desaturase, endoplasmic reticulum (delta-12 desaturase) ; (L26296) delta-12 desaturase [Arabidopsis thaliana] " "(AB018078) oligo-1,4 - 1,4-glucantransferase / amylo-1,6-glucosidase [Saccharomyces cerevisiae] "
17842	ENU01636	ANI61C4567:		48-74	486-505	NAP		g3135996	589	120	8.00E-27	41	32	
17843	ENU01637	ANI61S483:3		27-50	466-485	NAP		g2137490	465	185	2.00E-46	54	27	
17844	ENU01638	ANI61C2329:		27-47	457-488	NAP		g2330786	969	152	2.00E-36	47	40	
17845	ENU01639	ANI61C5098:		56-75	498-517	NAP		g3738207	339	147	5.00E-35	43	50	
17846	ENU01640	ANI61C2362:		28-48	470-490	NAP		g1877292	206	52	9.00E-12	30	32	
17847	ENU01641	ANI61C7547:		44-72	473-507	NAP		g3212116	127	63	0.000000	30	91	
17848	ENU01642	ANI61C6627:		54-71	499-518	NAP		g1947184	579	122	4.00E-41	81	14	
17849	ENU01643	ANI61C1152:		23-54	466-489	NAP		g2612899	147	52	5.00E-10	35	95	
17850	ENU01644	ANI61C7562:		23-46	462-490	NAP		g3192023	187	101	5.00E-21	36	33	
17851	ENU01645	ANI61C2007:		22-49	474-493	NAP		g1170600	140	36	0.14	30	91	
17852	ENU01646	ANI61C4822:		66-93	506-537	NAP		g1001214	443	156	1.00E-37	45	33	
17853	ENU01647	ANI61S344:1		33-54	475-505	NAP		g1169598	954	370	e-102	98	44	
17854	ENU01648	ANI61C5920:		62-81	505-536	NAP		g3986291	544	152	9.00E-41	57	9	

Seq num	Seq id	Primer Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17855	ENNU01649	AN161C9533: 64-83	2666..2148	514-540	NAP	g4185903	922	202	3.00E-62	83	27		(AJ132432) fimbrin [Gibberella pulicaris]
17856	ENNU01650	AN161C4266: 42-67	770..1289	500-519	NAP	g118774	1172	177	5.00E-44	60	21		DNA ligase (polydeoxyribonucleotide synthase (ATP)); DNA ligase (ATP) (EC 6.5.1.1) - fission yeast (Schizosaccharomyces pombe); (X05107) DNA ligase [Schizosaccharomyces pombe]
17857	ENNU01651	AN161C8612: 72-90	1145..625	528-550	NAP	g2131348	383	56	1.00E-16	39	26		hypothetical protein YDL156w - yeast (Saccharomyces cerevisiae); (X97751) D1536 [Saccharomyces cerevisiae]; (Z74204) ORF YDL156w [Saccharomyces cerevisiae]
17858	ENNU01652	AN161C6664: 68-87	1400..876	531-550	NAP	g4538926	357	124	5.00E-28	43	23		(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]
17859	ENNU01653	AN161C7770: 41-65	2237..1710	505-526	NAP	g2494301	1373	271	3.00E-72	78	39		eukaryotic translation initiation factor 2 gamma subunit (EIF-2-gamma); (U37354) initiation factor eIF-2 gamma subunit [Schizosaccharomyces pombe]
17860	ENNU01654	AN161C4206: 49-68	2519..1992	508-534	NAP	g3560221	328	143	8.00E-34	43	50		(AL031523) hypothetical protein [Schizosaccharomyces pombe]
17861	ENNU01655	AN161C3455: 22-55	1377..1908	490-511	NAP	g585222	485	182	2.00E-45	60	90		glutathione peroxidase homolog YBR244W; probable glutathione peroxidase (EC 1.11.1.9) - yeast (Saccharomyces cerevisiae); (Z36113) ORF YBR244w [Saccharomyces cerevisiae]
17862	ENNU01656	AN161C3754: 56-75	5352..5883	525-545	NAP	g586542	855	149	1.00E-35	41	29		general amino acid permease ACP2; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae); (X75891) YBR1007 [Saccharomyces cerevisiae]; (Z36001) ORF YBR132c [Saccharomyces cerevisiae]; YBR1007 gene [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17863	ENU01657	AN161C7497: 932..400	22-41	492-512	NAP		g729611	807	189	9.00E-48			vanadate resistance protein GOG5/VRG4/VAN2 ; vanadate resistance protein VAN2 - yeast (Saccharomyces cerevisiae) ; (L33915)
17864	ENU01658	AN161C9506: 865..743	61-82	531-551	NAP		g3093417	512	173	6.00E-43	49	58	vanadate resistant protein [Saccharomyces cerevisiae] ; (U15599) Van2p [Saccharomyces cerevisiae] ; (Z72747) ORF YGL225w [Saccharomyces cerevisiae] ; VRG4 gene [Saccharomyces cerevisiae] (AF036546) protein kinase CK2 beta subunit [Candida albicans] hypothetical 27.4 KD protein in HYR1 3'region ; hypothetical protein YIR042c - yeast (Saccharomyces cerevisiae) ; (Z46902) unknown [Saccharomyces cerevisiae].
17865	ENU01659	AN161C9637: 5288..5822	25-46	498-517	NAP		g731928	393	163	7.00E-40	46	73	
17866	ENU01660	AN161C8632: 1385..855	50-78	525-544	NAP		g585381	1296	257	4.00E-84	94	68	lactam utilization protein LAMB ; lactam utilization protein lamb - Emmericella nidulans ; (M77283) lamb [Emmericella nidulans] (AL031545) putative coatmer delta subunit [Schizosaccharomyces pombe] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:ID14061) [Arabidopsis thaliana] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa] RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae) ; (Z72998) ORF YGR213c [Saccharomyces cerevisiae] ; (X84736) RTA1 [Saccharomyces cerevisiae]
17867	ENU01661	AN161C1444: 1040..1577	66-85	542-561	NAP		g3581908	589	122	5.00E-49	70	67	
17868	ENU01662	AN161C2252: 70..606	22-52	490-517	NAP		g1351714	103	47	0.00008	22	32	
17869	ENU01663	AN161C2212: 2027..2565	29-51	506-525	NAP		g3549879	768	124	5.00E-28	49	30	
17870	ENU01664	AN161C1102: 7..562..22	45-64	522-543	NAP		g3600039	183	95	4.00E-19	30	23	
17871	ENU01665	AN161C9234: 1247..707	52-71	531-550	NAP		g2970667	215	56	8.00E-15	41	46	
17872	ENU01666	AN161C3224: 374..4922	53-73	538-559	NAP		g1710802	199	75	3.00E-13	33	56	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17873	ENU01667	AN161C8425: 1..551	22-46	498-530	NAP		g466190	551	213	5.00E-55	54	80	ribosomal large subunit pseudouridine synthase B (pseudouridylylate synthase) (uracil hydrolyase) ; hypothetical protein X13 - Bacillus subtilis ; (L09228) ORFX13 [Bacillus subtilis] ; (Z99116) similar to hypothetical proteins [Bacillus subtilis] (X82490) unnamed protein product [Fusarium oxysporum] (AL023590) Glutathione S-transferase [Schizosaccharomyces pombe] histidine biosynthesis bifunctional amidotransferase / cyclase ; amidotransferase HIS7 (EC 2.4.2.-) / cyclase HIS7 - yeast (Saccharomyces cerevisiae) ; (Z36117) ORF YBR248c [Saccharomyces cerevisiae]
17874	ENU01668	AN161C461: 58..1409	54-74	539-563	NAP		g2274947	177	79	2.00E-14	28	61	hypothetical 57.2 KD protein in MET8-HPC2 intergenic region ; hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae) ; (Z36083) ORF YBR214w [Saccharomyces cerevisiae]
17875	ENU01669	AN161C2346: 2599..2045	57-87	550-569	NAP		g3136036	189	68	1.00E-14	33	58	myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe] (Y11113) endoglucanase IV [Hypocrea jecorina]
17876	ENU01670	AN161C6107: 5339..4783	62-94	555-576	NAP		g585255	588	231	2.00E-60	70	29	probable membrane protein YPL224c - yeast (Saccharomyces cerevisiae) ; (Z73580) ORF YPL224c [Saccharomyces cerevisiae]
17877	ENU01671	AN161C3450: 677..120	72-96	566-587	NAP		g586334	307	77	8.00E-14	37	35	probable oxidoreductase YJR096w ; aldehyde reductase homolog YJR096w - yeast (Saccharomyces cerevisiae) ; (Z49596) ORF YJR096w [Saccharomyces cerevisiae] (U88308) C32E8.5 gene product [Caenorhabditis elegans] (AF053318) CCR4-associated factor 1 [Homo sapiens]
17878	ENU01672	AN161C1133: 8:560..3	68-87	563-583	NAP		g2500938	380	127	7.00E-31	46	32	
17879	ENU01673	AN161C7642: 157..716	62-81	560-579	NAP		g2315274	220	87	7.00E-17	38	52	
17880	ENU01674	AN161C3041: 202..762	22-46	521-540	NAP		g2133005	317	71	8.00E-19	38	36	
17881	ENU01675	AN161C8628: 2821..2259	41-60	536-561	NAP		g1176340	313	94	9.00E-21	36	57	
17882	ENU01676	AN161C6429: 7156..7718	35-56	523-555	NAP		g1825727	407	138	3.00E-32	43	60	
17883	ENU01677	AN161C7861: 82..644	22-49	522-542	NAP		g4106061	534	169	1.00E-41	58	51	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17884	ENU01678	AN161C1228:	45-64	541-569	NAP		g1706503	2105	135	3.00E-31	41	12	DNA polymerase alpha (DNA polymerase I); DNA-directed DNA polymerase I; DNA-directed DNA polymerase (EC 2.7.7.7) - yeast (Saccharomyces cerevisiae) ; (Z50161) DNA Polymerase I [Saccharomyces cerevisiae] ; (Z71378) ORF YNL102w [Saccharomyces cerevisiae] (U73857) betaine-aldehyde dehydrogenase [Escherichia coli] verprolin ; verprolin - yeast (Saccharomyces cerevisiae) ; (U19028) Vrp1p [Saccharomyces cerevisiae] ; MDP2 gene [Saccharomyces cerevisiae]
17885	ENU01679	AN161C9640:	55-78	558-579	NAP		g1657510	1307	201	3.00E-51	52	37	glucose transporter (sugar carrier) ; glucose transport protein STP1 - Arabidopsis thaliana ; (X55350) glucose transporter [Arabidopsis thaliana]
17886	ENU01680	AN161C7173:	48-68	559-578	NAP		g2507155	179	59	0.000000	34	19	probable monooxygenase MTCY31.20 ; (Z73101) hypothetical protein Rv0892 [Mycobacterium tuberculosis] lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
17887	ENU01681	AN161C7819:	72-91	586-605	NAP		g134976	359	45	0.0004			tropomyosin ; tropomyosin - yeast (Schizosaccharomyces pombe) ; (L04126) tropomyosin [Schizosaccharomyces pombe] ; tropomyosin [Schizosaccharomyces pombe]
17888	ENU01682	AN161C652.5:	52-71	562-586	NAP		g1731385	334	96	2.00E-19	37	33	lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348) lysophospholipase [Penicillium chrysogenum]
17889	ENU01683	AN161C5538:	22-41	537-558	NAP		g125886	475	77	1.00E-23	38	47	
17890	ENU01684	AN161C1189:	36-63	554-574	NAP		g401205	288	86	2.00E-16	41	97	
17891	ENU01685	AN161C8980:	22-48	542-561	NAP		g730338	1174	262	2.00E-69	67	30	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17892	ENU01686	ANI61C5264:	60-79	577-599	NAP		g1666269	328	149	2.00E-35	41	74	(Z82021) cytochrome P450 [Agaricus bisporus]
17893	ENU01687	ANI61C1059	25-55	543-566	NAP		g1253399	724	214	3.00E-55			serine/threonine-protein kinase KIN28 ; probable protein kinase KIN28 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (X04423) protein kinase [Saccharomyces cerevisiae] ; (X95644) ORF 2330 [Saccharomyces cerevisiae] ; (Z74156) ORF YDL108w [Saccharomyces cerevisiae] ; protein kinase [Saccharomyces cerevisiae]
17894	ENU01688	ANI61C2075:	22-46	539-563	NAP		g1170905	777	157	6.00E-38	61	50	24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
17895	ENU01689	ANI61C2888:	24-44	537-567	NAP		g2498527	234	97	9.00E-20	36	21	dimethylglycine dehydrogenase precursor (MEGL YDH) ; dimethylglycine dehydrogenase - rat ; (X55995) dimethylglycine dehydrogenase [Rattus norvegicus] (Z98533) rho gdp dissociation inhibitor. [Schizosaccharomyces pombe]
17896	ENU01690	ANI61C8417:	58-78	585-606	NAP		g2330853	351	119	2.00E-26	45	74	hypothetical protein (AL022600) [Schizosaccharomyces pombe]
17897	ENU01691	ANI61C8659:	70-98	602-619	NAP		g3080529	223	101	6.00E-21	37	64	hypothetical 143.6 KD protein C26A3.09C in chromosome I ; (Z69240) hypothetical protein [Schizosaccharomyces pombe]
17898	ENU01692	ANI61C8489:	23-42	551-573	NAP		g1723237	148	62	2.00E-12	31	12	"OVCA1=candidate tumor suppressor [human, fetal brain, Peptide, 443 aa]"
17899	ENU01693	ANI61C754:	7	26-46	553-576	NAP	g1438796	1015	245	1.00E-64	61	43	

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17900	ENNU01694	AN161C6597:	68-87	600-619	NAP		g132744	474	146	3.00E-38			"60S ribosomal protein L17 ; ribosomal protein L23.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (X01694) ribosomal protein L17 [Saccharomyces cerevisiae] ; (X79489) L23 B x-137 [Saccharomyces cerevisiae] ; (Z35848) ORF YBL087c [Saccharomyces cerevisiae] ; (U18916) Rpl17bp: Ribosomal protein, large subunit [Saccharomyces cerevisiae] ; (U15653) ribosomal protein L17B [Saccharomyces cerevisiae] "
17901	ENNU01695	AN161C6603:	36-55	571-590	NAP		g3426129	717	152	2.00E-36	47	13	"(AL031307) leptomycin B resistance protein, ABC transporter [Schizosaccharomyces pombe] " hypothetical 118.4 KD protein in WRS1-PKH2 intergenic region ; hypothetical protein YOL098c - yeast (Saccharomyces cerevisiae) ; (Z48149) similarity with D. melanogaster insulinase [Saccharomyces cerevisiae] ; (Z74840) ORF YOL098c [Saccharomyces cerevisiae] (AC005623) alien-like protein [Arabidopsis thaliana] (AB011003) UDP-N-acetylglucosamine pyrophosphorylase [Candida albicans] probable 1-acyl-SN-glycerol-3-phosphate acyltransferase (1-AGP acyltransferase) (1-AGPAT) (lysophosphatidic acid acyltransferase) (LPAAT) ; probable sn2-acylglyceride fatty acyltransferase (EC 2.3.1.-) - yeast (Saccharomyces cerevisiae) ; (L13282) acyltransferase [Saccharomyces cerevisiae] ; (Z74100) ORF YDL052c [Saccharomyces cerevisiae]
17902	ENNU01696	AN161C2370:	63-82	598-617	NAP		g3915530	223	76	1.00E-13	25	17	
17903	ENNU01697	AN161C2471:	55-74	589-610	NAP		g3885329	560	210	7.00E-54	47	46	
17904	ENNU01698	AN161C7526:	23-42	557-579	NAP		g3413964	458	161	5.00E-39	55	36	
17905	ENNU01699	AN161C8576:	23-44	560-579	NAP		g464422	491	176	1.00E-43			

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17906	ENU01700	ANI61C1038	22-55	556-578	NAP		g585972	461	161	5.00E-39	48	58	SCO2 protein precursor ; SCO1 protein homolog SCO2 - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0308 [Saccharomyces cerevisiae] ; (Z35893) ORF YBR024w [Saccharomyces cerevisiae] ; ORF YBR0308 [Saccharomyces cerevisiae]
17907	ENU01701	ANI61C9637	72-91	604-629	NAP		g118109	560	214	3.00E-55			[Saccharomyces cerevisiae] peptidyl-prolyl cis-trans isomerase (PPIASE) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
17908	ENU01702	ANI61C8628	22-44	563-582	NAP		g2088561	165	84	9.00E-16	31	60	(U95053) glutamate-cysteine ligase regulatory subunit [Mus musculus] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] (D87078) similar to D.melanogaster puntillo protein (S22026) ; similar to human KIAA0099 protein(D43951) [Homo sapiens]
17909	ENU01703	ANI61C5399	71-92	603-632	NAP		g2808725		48	0.00004			cyanamide hydratase (urea hydro-lyase) ; cyanamide hydratase (EC 4.2.1.69) - fungus (Myrothecium verrucaria) ; (M59078) cyanamide hydratase [Myrothecium verrucaria] (AL022070) mago-nashi homolog [Schizosaccharomyces pombe]
17910	ENU01704	ANI61C4146	22-48	561-583	NAP		g1944416	617	134	5.00E-31	40	21	(AL033389) putative allantoinase permease [Schizosaccharomyces pombe]
17911	ENU01705	ANI61C8125	22-53	560-584	NAP		g117800	730	211	4.00E-54	60	73	60S ribosomal protein L15 ; (Y15321) putative ribosomal protein L15 [Aspergillus niger]
17912	ENU01706	ANI61C9584	22-53	553-586	NAP		g2950474	340	96	2.00E-19	57	97	(U24698) norsolorinic acid reductase [Aspergillus parasiticus]
17913	ENU01707	ANI61C5212	72-97	611-638	NAP		g3850093	294	86	2.00E-16	33	36	
17914	ENU01708	ANI61C1119	68-90	617-636	NAP		g3122672	798	155	5.00E-54	91	77	
17915	ENU01709	ANI61C1135	29-49	576-598	NAP		g1200177	916	85	3.00E-32	42	47	

Database Information

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17916	ENU01710	ANI61C1038	22-54	571-591	NAP		g1730665	121	61	0.000000	24	90	hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae]
		0:3175..3787								01			aspartic proteinase 3 precursor (YAP3IN 1) ; aspergillopepsin I (EC 3.4.23.18) YAP3 precursor - yeast (Saccharomyces cerevisiae) ; (U53877) Yap3p: aspartic proteinase [Saccharomyces cerevisiae] ; (X89514) Aspartyl protease [Saccharomyces cerevisiae] ; (Z73292) ORF YLR120c [Saccharomyces cerevisiae] (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] succinate dehydrogenase (ubiquinone) iron-sulfur protein precursor (IP) ; (AF042062) succinate dehydrogenase iron-sulphur protein [Mycosphaerella graminicola]
17918	ENU01712	ANI61C4637	56-76	611-630	NAP		g2276352	429	173	1.00E-42	47	49	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17919	ENU01713	ANI61C9863	22-44	571-596	NAP		g3334166	904	276	8.00E-74	81	57	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
		1144..528											putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17920	ENU01714	ANI61C9609	26-47	582-602	NAP		g1351714	695	115	3.00E-26	36	40	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17921	ENU01715	ANI61C9609	26-47	582-602	NAP		g1351714	695	115	3.00E-26	36	40	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17922	ENU01716	ANI61C6570	24-52	582-601	NAP		g2388943	659	204	5.00E-52	53	52	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
		625..5											putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17923	ENU01717	ANI61C9806	25-44	584-606	NAP		g3810864	422	66	2.00E-18	36	53	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
		193..816											putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17924	ENNU01718	ANI61C3200:	47-66	597-630	NAP		g2498268	143	61	0.000000	36	36	copper transport protein CTR3 (copper transporter 3) ; probable membrane protein YLR411w - yeast (Saccharomyces cerevisiae) ; (U20162) Ctr3p [Saccharomyces cerevisiae] ; (U81482) copper transporter 3 [Saccharomyces cerevisiae] probable eukaryotic translation initiation factor 3 beta subunit (EIF-3 beta) ; (Z70691) eukaryotic translation initiation factor 3 beta subunit [Schizosaccharomyces pombe] (AL022117) putative o-methyltransferase [Schizosaccharomyces pombe] (Z99162) farnesyltransferase beta subunit [Schizosaccharomyces pombe] (AL031545) hypothetical ryandoline receptor domain containing protein [Schizosaccharomyces pombe] signal recognition particle 54 K D protein homolog ; signal recognition particle 54K protein homolog - Aspergillus niger ; (L38317) srpA gene product [Aspergillus niger] ; srpA gene [Aspergillus niger] (AF030296) ubiquitin conjugating enzyme UBC1 [Glomerella cingulata] (AF012091) cystein rich protein [Metarhizium anisopliae] "endo-1,4-beta-xylinase 2 precursor (xylinase 2) (1,4-beta-D-xylin xylanohydrolase 2) ; endo-1,4-beta-xylinase (EC 3.2.1.8) 2 precursor - Emericella nidulans ; (Z49893) xylinase [Emericella nidulans] " hypothetical protein YOL151w - yeast (Saccharomyces cerevisiae) ; (Z48239) orf2 [Saccharomyces cerevisiae] ; (Z74893) ORF YOL151w [Saccharomyces cerevisiae]
17925	ENNU01719	ANI61C5549:	60-81	622-644	NAP		g1723536	633	110	4.00E-39	42	25	
17926	ENNU01720	ANI61C1131	35-55	600-619	NAP		g2959364	299	136	1.00E-31	41	70	
17927	ENNU01721	ANI61C4472:	58-79	611-642	NAP		g2408017	229	78	7.00E-22	41	39	
17928	ENNU01722	ANI61C9766:	48-73	613-632	NAP		g3581910	562	155	2.00E-37	45	48	
17929	ENNU01723	ANI61C1069	22-47	588-607	NAP		g3334345	2295	333	6.00E-91	92	39	
17930	ENNU01724	ANI61C1043	63-82	632-652	NAP		g3323498	654	132	1.00E-51	94	80	
17931	ENNU01725	ANI61C3265:	67-88	639-658	NAP		g2352898	780	116	1.00E-49	52	50	
17932	ENNU01726	ANI61C1074	46-65	617-639	NAP		g1722902	1116	250	5.00E-98	96	88	
17933	ENNU01727	ANI61C7309:	63-82	626-657	NAP		g2132023	300	93	3.00E-20	33	55	

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Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
17941	ENU01735	AN161C1069	49-68	634-653	NAP		g2132301	219	62	0.000000	30	84	hypothetical protein YPR143w - yeast (Saccharomyces cerevisiae) ; (U40829)
		1:1390..744								004			Note that there is an overlapping ORF on the other strand (27648-27085)
17942	ENU01736	AN161C1646: 650..4	72-91	641-676	NAP		g3581866	298	137	6.00E-32	40	76	[Saccharomyces cerevisiae] (AL031541) putative dehydrogenase [Streptomyces coelicolor]
17943	ENU01737	AN161C1050 5:10224..10876	23-55	611-633	NAP		g1083640	186	85	6.00E-16	26	39	cytochrome P450III - rat ; (X79991) cytochrome P450III [Rattus norvegicus] ; (D38381) P450 6beta-2 [Rattus norvegicus] ; cytochrome P450 [Rattus norvegicus]
17944	ENU01738	AN161C1116 0:1150..1803	55-77	646-666	NAP		g3219917	212	64	4.00E-18	28	84	hypothetical 27.4 KD protein C30D10.14 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
17945	ENU01739	AN161C8325: 773..1431	22-45	612-638	NAP		g2131352	336	101	5.00E-21	48	87	hypothetical protein YDL166c - yeast (Saccharomyces cerevisiae) ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74214) ORF YDL166c [Saccharomyces cerevisiae]
17946	ENU01740	AN161C7771: 2257..2894	30-50	629-646	NAP		g2493387	2647	458	e-128	98	43	probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
17947	ENU01741	AN161C8376: 39..700	57-75	657-676	NAP		g1352268	911	325	1.00E-88	77	60	Deoxyhypusine synthase ; (U22400) deoxyhypusine synthase [Neurospora crassa]
17948	ENU01742	AN161C744:7 3..735	32-54	632-651	NAP		g1723438	219	74	8.00E-13	43	19	hypothetical 52.3 KD protein C56F8.06C in chromosome I precursor ; (Z69728) unknown
17949	ENU01743	AN161C9987: 115..777	23-43	624-643	NAP		g2462674	356	122	2.00E-27	32	57	[Schizosaccharomyces pombe] (Z95395) hypothetical protein [Schizosaccharomyces pombe]
17950	ENU01744	AN161C2574: 4710..4048	22-54	620-642	NAP		g3702646	276	104	6.00E-22	34	36	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
17951	ENU01745	AN161C3010: 256..920	49-69	651-670	NAP		g2131405	462	150	7.00E-36	51	51	hypothetical protein YDR267c - yeast (Saccharomyces cerevisiae) ; (U51030) Ydr267cp [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17952	ENU01746	ANI61C9890:	49-68	652-673	NAP		g549768	133	55	0.000000	5		hypothetical 61.1 KD protein in YPT52-DBP7 intergenic region ; hypothetical protein YKR016w - yeast (Saccharomyces cerevisiae) ; (Z28241) ORF YKR016w [Saccharomyces cerevisiae]
17953	ENU01747	ANI61C4162:	23-46	627-647	NAP		g3913152	919	336	1.00E-91	70	66	"alpha-L-arabinofuranosidase precursor (arabinoxylan arabinofuranohydrolase) ; (Z78010) (1,4)-beta-D-arabinoxylan arabinofuranohydrolase [Aspergillus tubingensis]"
17954	ENU01748	ANI61C8530:	43-63	647-668	NAP		g2492755	704	113	5.00E-50	54	72	sorbitol utilization protein SOU2 ; (AF002134) Sou2p [Candida albicans]
17955	ENU01749	ANI61C7365:	37-56	629-664	NAP		g2330856	841	75	5.00E-17	32	18	(Z98533) putative ma-directed ma polymerase [Schizosaccharomyces pombe]
17956	ENU01750	ANI61C3463:	67-86	674-699	NAP		g2131494	346	91	8.00E-18	35	38	hypothetical protein YDR440w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr440wp; CAI: 0.13 [Saccharomyces cerevisiae]
17957	ENU01751	ANI61C8563:	22-44	632-656	NAP		g626251	280	47	1.00E-11			citrate transport protein - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2039-ORF [Saccharomyces cerevisiae] ; (Z36160) ORF YBR291c [Saccharomyces cerevisiae] ; ORF YBR2039 [Saccharomyces cerevisiae] (Z99292) hypothetical protein [Schizosaccharomyces pombe]
17958	ENU01752	ANI61C319.4	24-51	637-659	NAP		g2414577	431	88	1.00E-34	40	69	[Schizosaccharomyces pombe] (L47321) glycoprotein 150 [Murine herpesvirus 68] ; (Y09060) serine threonine rich glycoprotein [murine herpesvirus 68] ; (U97553) glycoprotein 150 [murine herpesvirus 68]
17960	ENU01754	ANI61C737.1	25-48	648-667	NAP		g266564	1297	343	e-124	96	41	M-phase inducer phosphatase ; protein-tyrosine-phosphatase (EC 3.1.3.48) nimT - Emerticella nidulans ; (X64601) NIMT/CDC25 [Emerticella nidulans] (AL023776) hypothetical protein [Schizosaccharomyces pombe]
17961	ENU01755	ANI61C8708:	32-59	656-675	NAP		g3184056	76	46	0.0002			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17962	ENU01756	AN150C6889	47-66	665-690	NAP		g2132389		233	1.00E-60	57	73	"phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X92441) YOR50-12 [Saccharomyces cerevisiae] ; (Z75130) ORF YOR222w [Saccharomyces cerevisiae]"
		_1:1734..1049											
17963	ENU01757	AN161C70:24	22-45	645-667	NAP		g2496730	369	169	2.00E-41	40	55	hypothetical protein Y4OU precursor ; (AE000089) Y4OU [Rhizobium sp. NGR234]
		89..1802											
17964	ENU01758	AN161C7798:	28-47	656-675	NAP		g2132397	344	134	5.00E-31	44	42	POSS protein - yeast (Saccharomyces cerevisiae) ; (Z73544) ORF YPL188w [Saccharomyces cerevisiae]
		790..101											
17965	ENU01759	AN161C8193:	22-48	642-673	NAP		g1351368	360	100	2.00E-35			RNA polymerase II holoenzyme cyclin-like subunit ; cyclin homolog UME3 - yeast (Saccharomyces cerevisiae) ; (U20635) Ssn8p [Saccharomyces cerevisiae] ; (U20221) RNA polymerase II holoenzyme cyclin-like subunit [Saccharomyces cerevisiae] ; (U16248) cyclin [Saccharomyces cerevisiae] ; (Z71301) ORF YNL025c [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
		3049..2356											
17966	ENU01760	AN161C5471:	22-41	657-676	NAP		g1703215	283	129	2.00E-29	29	36	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
		2354..1658											
17967	ENU01761	AN161C9593:	22-49	655-677	NAP		g731806	707	270	5.00E-72	56	20	"probable calcium-transporting ATPase 7 ; probable membrane protein YIL048w - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 1151, CAl: 0.17, similar to S30768 S30768 probable ATPase - yeast (saccharomyces cerevisiae) [Saccharomyces cerevisiae]"
		1..698											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17968	ENU01762	ANI61C1070	60-79	696-715	NAP		g1730823	610	136	2.00E-31	38	36	probable mannosyltransferase ALG9 ; probable membrane protein YNL219c - yeast (Saccharomyces cerevisiae) ; (Z71495) ORF YNL219c
		6:8487..9184											[Saccharomyces cerevisiae] ; (X96417) putative mannosyltransferase [Saccharomyces cerevisiae]
17969	ENU01763	ANI61C7105	22-44	652-680	NAP		g586542	859	95	1.00E-41	46	36	general amino acid permease AGP2 ; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae) ; (X75891) YBR1007 [Saccharomyces cerevisiae] ; (Z36001) ORF YBR132c [Saccharomyces cerevisiae] ; YBR1007 gene [Saccharomyces cerevisiae] (U70619) heroin esterase [Rhodococcus sp.]
17970	ENU01764	ANI61C3637	28-63	669-688	NAP		g2088525	352	83	4.00E-18	37	64	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (AL035226) major facilitator superfamily protein [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe]
17971	ENU01765	ANI61C1020	53-76	695-714	NAP		g125935	137	65	5.00E-10	32	19	hypothetical 26.1 KD protein in POP4-SHM1 intergenic region ; hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae) ; (X70529) ORF YBR1729 [Saccharomyces cerevisiae] ; (Z36130) ORF YBR261c [Saccharomyces cerevisiae]
17972	ENU01766	ANI61C4189	35-54	674-697	NAP		g4160574	519	63	2.00E-18	33	40	unknown ; (AF046024) UBA3 [Homo sapiens] ; (AB012190) Nedd8-activating enzyme hUba3 [Homo sapiens] (AL035396) SRG1-like protein [Arabidopsis thaliana] (AF069492) SONA [Emmericella nidulans]
17973	ENU01767	ANI61C8086	56-76	701-720	NAP		g3135989	619	183	1.00E-45	39	40	
17974	ENU01768	ANI61C7151	24-45	670-689	NAP		g586379	359	120	6.00E-36	40	98	
		490..1197											
17975	ENU01769	ANI61C8423	39-59	686-705	NAP		g4507765	660	204	5.00E-52	46	53	
		208..916											
17976	ENU01770	ANI61C2775	71-91	715-737	NAP		g4454019	45	0.00007				
17977	ENU01771	ANI61C9647	36-55	681-704	NAP		g3202044	1440	496	e-140	98	65	
		1724..1014											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17978	ENU01772	ANI61C7619:	70-89	711-738	NAP		g729968	889	301	3.00E-81	60	53	"saccharopine dehydrogenase [NADP+, L-glutamate forming]; saccharopine dehydrogenase (NADP+, L-glutamate-forming) (EC 1.5.1.10) - yeast (Saccharomyces cerevisiae); (X77363) saccharopine dehydrogenase (NADP+, L-glutamate forming) [Saccharomyces cerevisiae]; (Z71665) ORF YNR050c [Saccharomyces cerevisiae]"
17979	ENU01773	ANI61C1147	57-79	706-726	NAP		g2624697	823	266	5.00E-76	76	53	Pectin Lyase A
17980	ENU01774	ANI61C8541:	54-76	704-723	NAP		g1709941	298	106	2.00E-22	27	35	proline-specific permease; proline transport protein - yeast (Saccharomyces cerevisiae); (X95720) O6345 [Saccharomyces cerevisiae]; (Z75256) ORF YOR348c [Saccharomyces cerevisiae] (AL023518) hypothetical protein [Schizosaccharomyces pombe] "hypothetical 23.7 KD protein C13G6.14 in chromosome I; hypothetical protein SPAC13G6.14 - fission yeast (Schizosaccharomyces pombe); hypothetical protein SPAC24B11.03 - fission yeast (Schizosaccharomyces pombe); (Z54308) hypothetical protein [Schizosaccharomyces pombe]; (Z67757) unknown [Schizosaccharomyces pombe]; (AF125215) diadenosine 5', 5'''-P1, P6-hexaphosphate hydrolase [Schizosaccharomyces pombe]"
17981	ENU01775	ANI61C6911:	35-56	687-707	NAP		g3130055	90	41	0.000000	28	64	RAS-2 protein; (D16137) NC-ras-2 protein [Neurospora crassa]
17982	ENU01776	ANI61C578:8	22-41	678-697	NAP		g1175461	212	75	5.00E-13			
17983	ENU01777	ANI61C1120	22-41	680-699	NAP		g2500078	676	151	2.00E-55	68	94	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17984	ENU01778	ANI61C1029	22-51	680-699	NAP		g1730800	334	120	1.00E-37	37	85	hypothetical 28.8 KD protein in PSD1-SK01 intergenic region ; hypothetical protein YNL168c - yeast (Saccharomyces cerevisiae) ; (X92517) N1696 [Saccharomyces cerevisiae] ; (Z71444) ORF YNL168c [Saccharomyces cerevisiae] (D64052) cytochrome P450 like_TBP [Nicotiana tabacum] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		4:9723..9004											
17985	ENU01779	ANI61C1253:	68-87	728-748	NAP		g1545805	653	102	9.00E-27	66	44	
		7171..6449											
17986	ENU01780	ANI61C4046:	58-83	706-741	NAP		g3560142	680	132	3.00E-30	34	38	
		3414..2689											
17987	ENU01781	ANI61C6939:	61-80	729-748	NAP		g2493965	729	218	5.00E-70	64	15	
		556..1285											
17988	ENU01782	ANI61C6754:	25-45	693-712	NAP		g1351711	3300	181	9.00E-72	59	18	
		3042..3771											
17989	ENU01783	ANI61C177:2	43-62	713-732	NAP		g2635242	234	93	2.00E-18	31	61	
		2..753											
17990	ENU01784	ANI61C6621:	25-44	696-715	NAP		g2982954	658	139	1.00E-32	42	44	
		2002..2734											
17991	ENU01785	ANI61C1038	24-43	689-714	NAP		g3257130	388	109	2.00E-23	35	57	
		8:6660..7392											
17992	ENU01786	ANI61C380:1	26-49	698-717	NAP		g2808634	545	150	1.00E-35	46	20	
		856..2589											
17993	ENU01787	ANI61C124:7	27-47	700-719	NAP		g3914244		70	2.00E-15			
		..741											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17994	ENU01788	ANI61C3719:	67-90	741-761	NAP		g1352938	479	188	4.00E-47	43	61	hypothetical 39.7 KD protein in HOM6-PMT4 intergenic region ; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae) ; (Z49642) ORF YJR142w [Saccharomyces cerevisiae]
17995	ENU01789	ANI61C846:2	22-49	700-719	NAP		g1351369	850	275	3.00E-73	60	41	meiotic mRNA stability protein kinase UME5 ; (U20222) Stb10p [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
17996	ENU01790	ANI61C8292:	22-57	699-720	NAP		g118066	495	186	1.00E-46	41	45	cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
17997	ENU01791	ANI61C2524:	60-80	738-759	NAP		g2493572	414	175	2.00E-43	41	45	putative CDP-diacylglycerol--serine O-phosphatidyltransferase (phosphatidylserine synthase) ; (Z86109) unknown [Saccharomyces pastorianus]
17998	ENU01792	ANI61C1071	32-51	713-737	NAP		g2842695	79	58	0.000000	23	17	hypothetical 150.9 KD protein C6G9_04 in chromosome I ; (Z81317) hypothetical protein [Schizosaccharomyces pombe]
17999	ENU01793	ANI61C3292:	63-83	749-769	NAP		g2330659	222	59	2.00E-14	29	16	(Z98595) putative snf2 family helicase [Schizosaccharomyces pombe]
18000	ENU01794	ANI61S1000:	52-71	738-759	NAP		g117619	76	3.00E-13	30	37	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18001	ENU01795	AN161C5352:	57-83	748-768	NAP		g3123159	493	202	1.00E-51	45	60	hypothetical 40.4 KD TRP-ASP repeats containing protein C14B1.4 in chromosome III ; (Z37139) similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; cDNA EST CEMSE07F comes from this gene; cDNA EST EMBL:T00918 comes from this gene; cDNA EST EMBL:D70900 comes from this gene; cD...
18002	ENU01796	AN161C6476:	68-89	750-781	NAP		g2804298	680	92	6.00E-31	37	39	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous] (AC000133) ORF [Emeritella nidulans]
18003	ENU01797	AN161C1116	61-80	749-775	NAP		g1870210	1452	481	e-135	98	53	(AL031174) beta-transducin [Schizosaccharomyces pombe]
18004	ENU01798	AN161C1060	65-87	758-779	NAP		g3393019	791	194	5.00E-81	60	53	putative seryl-TRNA synthetase YHR011W (serine--TRNA ligase) (SERRS) ; serine--TRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10400) Yhr011wp [Saccharomyces cerevisiae]
18005	ENU01799	AN161C8864:	58-77	751-772	NAP		g731635	551	189	2.00E-47	44	53	"(AL031532) yeast gtr2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe]"
18006	ENU01800	AN150C2350	23-58	720-744	NAP		g3560242		251	2.00E-67	55	75	putative flavin-containing monamine oxidase MTV014.14 ; (AL021646) hypothetical protein Rv3170 [Mycobacterium tuberculosis] (AF097728) pyruvate carboxylase [Aspergillus terreus]
18007	ENU01801	AN161C1420:	22-47	724-743	NAP		g3913051	244	76	3.00E-13	30	55	RAS-related protein RAB-11B ; GTP-binding protein Rab11b - mouse ; (L26528) Rab11b [Mus musculus]
18008	ENU01802	AN161C6541:	22-44	723-744	NAP		g3806120	3163	392	e-108	89	19	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
18009	ENU01803	AN161C1003	22-56	726-750	NAP		g1172815	699	251	6.00E-74	78	91	
18010	ENU01804	AN150C6358	47-73	756-775	NAP		g1437475		151	3.00E-42	40	80	

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18011	ENU01805	ANI61C8273:	72-91	771-803	NAP		g1346665	128	53	0.000002	35	33	"N-terminal acetyltransferase 2 (amino-terminal, alpha-amino, acetyltransferase 2) ; protein N-acetyltransferase (EC 2.3.1.-) NAT2 - yeast (Saccharomyces cerevisiae) ; (X85807) ORF G6630 [Saccharomyces cerevisiae] ; (Z72932) ORF YGR147c [Saccharomyces cerevisiae] "
		4655..3882											probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (Y17243) cytochrome P450 [Gibberella fujikuroi] (AL021839) myb family DNA binding protein [Schizosaccharomyces pombe] phosphoribosylaminoimidazole carboxylase (AIR carboxylase) (AIRC) ; (U70673) phosphoribosylaminoimidazole carboxylase [Filiobasidiella neoformans] hypothetical 36.2 KD protein in HAM1-PEM2 intergenic region ; hypothetical protein YJR070c - yeast (Saccharomyces cerevisiae) ; (Z49570) ORF YJR070c [Saccharomyces cerevisiae] ; (L47993) ORF YJR070c [Saccharomyces cerevisiae] unknown ; (D87432) Similar to Schistosoma mansoni amino acid permease (L25068). [Homo sapiens] (D17548) protein-tyrosine phosphatase [Saccharomyces cerevisiae] (X98493) ACC oxidase [Nicotiana tabacum] (X63998) aminopeptidase yscII [Saccharomyces cerevisiae] (AL023796) cyclin C homologue [Schizosaccharomyces pombe]
18012	ENU01806	ANI61C3339:	54-73	756-786	NAP		g2132957	768	271	5.00E-72	53	49	
		3593..2819											
18013	ENU01807	ANI61C3910:	51-70	765-784	NAP		g4127832	220	106	2.00E-22	32	46	
		207..982											
18014	ENU01808	ANI61C1094	43-62	743-778	NAP		g2894269	225	68	8.00E-11	44	29	
		2:150..216											
18015	ENU01809	ANI61C9734:	54-73	758-790	NAP		g2500019	1081	123	5.00E-29	48	39	
		2103..1324											
18016	ENU01810	ANI61C9817:	35-54	748-773	NAP		g1352887	525	157	7.00E-43	51	70	
		902..122											
18017	ENU01811	ANI61C8177:	35-54	755-774	NAP		g4507053	223	85	5.00E-16	34	45	
		14..795											
18018	ENU01812	ANI61C7083:	38-58	762-781	NAP		g459243	155	86	3.00E-16	33	29	
		90..875											
18019	ENU01813	ANI61C1049	37-57	758-780	NAP		g2826769		83	2.00E-15			
		4:4220..5005											
18020	ENU01814	ANI61C1857:	39-58	765-783	NAP		g3368	2245	207	8.00E-53	41	28	
		2322..2414											
18021	ENU01815	ANI61C5906:	27-46	753-772	NAP		g3192038	395	129	3.00E-29	32	74	
		1318..531											

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18022	ENU01816	ANI61C9151:	22-53	751-769	NAP	g2500768	963	190	5.00E-66	61	66	Septin homolog SPN2 ; (U29888)
		4849..4060										septin homolog [Schizosaccharomyces pombe]
18023	ENU01817	ANI61C9777:	58-78	782-805	NAP	g2665711		82	1.00E-19			(AF035413) AgaG [Agrobacterium tumefaciens]
18024	ENU01818	ANI61C9875:	52-71	783-806	NAP	g1705594	1074	327	6.00E-89	67	47	peroxisome assembly protein CAR1 (peroxin-2) ; car1 protein - Podospora anserina ; (X87329) peroxisome assembly factor [Podospora anserina]
		79..875										hypothetical protein YLR189c - yeast (Saccharomyces cerevisiae) ; (U17246)
18025	ENU01819	ANI61C6977:	22-46	759-778	NAP	g1077411	721	240	8.00E-67	56	20	Ylr189cp [Saccharomyces cerevisiae] (AJ009657) Mu3 subunit of clathrin-associated protein complex AP-3 [Drosophila melanogaster]
		1666..868										"asparaginyl"-TRNA synthetase, mitochondrial precursor (asparagine--TRNA ligase) (ASNRS) ; hypothetical protein YCR024c - yeast (Saccharomyces cerevisiae) ; (X59720)
18026	ENU01820	ANI61C1134:	22-43	759-778	NAP	g3341417		62	2.00E-20			YCR024c, len:492 [Saccharomyces cerevisiae] "
		3715..2917										cerevisiae] "
18027	ENU01821	ANI61C1485:	25-44	761-782	NAP	g135160	639	165	3.00E-40	40	51	(AL034352) putative GTP-binding protein [Schizosaccharomyces pombe] (AF095899) PDI related protein A [Aspergillus niger]
		1557..2356										mitochondrial import receptor subunit TOM40 (MOM38 protein) (translocase of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa]
18028	ENU01822	ANI61C5728:	24-46	773-792	NAP	g3925768	675	115	9.00E-34	46	70	actin interacting protein 2 ; AIP2 protein - yeast (Saccharomyces cerevisiae) ; (U35667) Aip2p [Saccharomyces cerevisiae] ; (Z67750)
18029	ENU01823	ANI61C8692:	56-75	793-824	NAP	g3873259	1526	257	5.00E-68	58	56	putative protein [Saccharomyces cerevisiae] ; (Z74226) ORF YDL178w [Saccharomyces cerevisiae]
		967..157										
18030	ENU01824	ANI61C7436:	58-77	807-827	NAP	g127218	924	257	5.00E-68	57	66	
		2475..3286										
18031	ENU01825	ANI61C3438:	22-45	772-791	NAP	g1168396	833	298	2.00E-80	58	50	
		1120..309										

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18032	ENU01826	ANI61C1214:	24-52	780-799	NAP		g130806	249	56	0.000000	35	22	pre-mRNA processing RNA helicase PRP5 ; pre-mRNA processing protein PRP5 - yeast (Saccharomyces cerevisiae) ; (M33191) PRP5 [Saccharomyces cerevisiae] ; (Z36106) ORF YBR237w [Saccharomyces cerevisiae]
18033	ENU01827	ANI61C5721:	22-51	769-799	NAP		g2498971	369	56	4.00E-28	36	54	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans] putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans] (AC006223) hypothetical protein [Arabidopsis thaliana] putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] "(AL034382) putative spindle pole body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]"
18034	ENU01828	ANI61C5721:	22-51	769-799	NAP		g2498971	369	56	4.00E-28	36	54	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans] (AC006223) hypothetical protein [Arabidopsis thaliana] putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] "(AL034382) putative spindle pole body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]"
18035	ENU01829	ANI61C9612:	22-53	767-799	NAP		g4263703	221	101	2.00E-23	33	53	putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] "(AL034382) putative spindle pole body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]"
18036	ENU01830	ANI61C1628:	31-53	793-816	NAP		g1710663	2331	428	e-119	72	23	putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] "(AL034382) putative spindle pole body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]"
18037	ENU01831	ANI61C7971:	22-51	783-813	NAP		g3947884	625	146	2.00E-34	48	70	putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] "(AL034382) putative spindle pole body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]"
18038	ENU01832	ANI61C1061:	52-70	810-845	NAP		g4588080	616	175	3.00E-43	35	56	(AF095286) guanine deaminase GDA [Homo sapiens]
18039	ENU01833	ANI61C5959:	51-70	827-849	NAP		g115699	1548	226	2.00E-90	58	57	"catalase (PXP-9) ; catalase (EC 1.11.1.6), peroxisomal - yeast (Candida tropicalis) ; (X13978) catalase (AA 1 - 485) [Candida tropicalis] ; (X06660) catalase (AA 1 - 485) [Candida tropicalis] ; peroxisomal catalase [Candida tropicalis]"
18040	ENU01834	ANI61C9843:	55-74	837-856	NAP		g2414656	694	234	7.00E-61	47	54	(Z99261) putative aminotransferase [Schizosaccharomyces pombe]

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18041	ENU01835	ANI61C1438:	24-45	807-826	NAP	g2127591	137	57	0.000000	29	81		N-acetylphosphinothricin-tripetide-deacetylase - Streptomyces viridochromogenes; (X65195) N-acetylphosphinothricin-tripetide-deacetylase [Streptomyces viridochromogenes]
		1368..522								02			
18042	ENU01836	ANI61C1600:	24-43	811-831	NAP	g2293194	289	89	2.00E-32				(AF008220) yfR [Bacillus subtilis]; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
		1195..346											(AF102147) putative dimethyladenosine transferase [Homo sapiens]
18043	ENU01837	ANI61C6951:	26-45	816-835	NAP	g4050050	648	159	8.00E-72	54	82		(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
		582..1433											sporulation protein SPS19 (sporulation-specific protein SPX19); sporulation protein SPS19 - yeast (Saccharomyces cerevisiae); (X78898) NI362 [Saccharomyces cerevisiae]; (Z71479) ORF YNL202w [Saccharomyces cerevisiae]
18044	ENU01838	ANI61C9308:	32-55	817-842	NAP	g3395556	676	66	2.00E-32	51	59		
		2353..1501											
18045	ENU01839	ANI61C7122:	57-77	845-867	NAP	g730864	506	152	3.00E-38	53	71		
		49..878											
18046	ENU01840	ANI61C1011	68-87	860-879	NAP	g2494910	1455	255	3.00E-67	47	33		hypothetical 91.7 KD TRP-ASP repeats containing protein in NUP116-FAR3 intergenic region; probable membrane protein YMR049c - yeast (Saccharomyces cerevisiae); (Z49703) unknown [Saccharomyces cerevisiae] (Z75526) Weak similarity to Staphylococcus autolysin gene (TR-G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis elegans] (AC004850) vacuolar assembly protein VPS41 homolog (SS3) [Homo sapiens] mutS (E. coli) homolog 3; (U61981) hMSH3 [Homo sapiens] (U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
		9:2048..1195											
18047	ENU01841	ANI61C122:	1 47-69	840-859	NAP	g3874039	295	90	2.00E-17	42	27		
		400..546											
18048	ENU01842	ANI61C8569:	40-65	834-853	NAP	g4309891	317	124	7.00E-28	37	33		
		66..921											
18049	ENU01843	ANI61C2388:	49-69	843-863	NAP	g4505249	1372	278	4.00E-74	48	25		
		1763..2619											
18050	ENU01844	ANI61C3304:	22-45	814-836	NAP	g517205	305	149	3.00E-35	33	47		
		3423..2567											

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18051	ENU01845	AN161C924:4	70-92	867-890	NAP		g3810847	341	161	8.00E-39	39	37	(AL032684) zinc finger protein [Schizosaccharomyces pombe]
18052	ENU01846	AN161C8857: 9..911	29-48	824-854	NAP		g2492894	1809	331	5.00E-90	56	13	adenylate cyclase (ATP pyrophosphate-lyase) (adenyl cyclase); adenylate cyclase (EC 4.6.1.1) - Podospora anserina; (L43413) adenyl cyclase [Podospora anserina]
18053	ENU01847	AN161C4219: 925..57	44-68	850-869	NAP		g2132252	703	74	1.00E-12	28	40	hypothetical protein YPL263c - yeast (Saccharomyces cerevisiae); (Z73619) ORF YPL263c [Saccharomyces cerevisiae]
18054	ENU01848	AN161C5719: 921..50	49-79	856-878	NAP		g1717749	522	153	1.00E-45	41	32	"potassium transport protein; (Z69369) SPAC3F10.02c, potassium transport gene, len: 841, co nfiict with PIR:S50225 potassium transport protein homolog at position 4549 causes frameshift near N-terminus [Schizosaccharomyces pombe]"
18055	ENU01849	AN161C6777: 874..1	50-69	854-881	NAP		g1175428	583	229	3.00E-59	41	89	(Z54140) conserved hypothetical protein [Schizosaccharomyces pombe] (AL022598) UDP-galactose transporter homologue [Schizosaccharomyces pombe]
18056	ENU01850	AN161C8505: 2230..1356	59-79	870-891	NAP		g3080508	510	168	4.00E-41	45	68	(AL023592) zinc finger protein [Schizosaccharomyces pombe]
18057	ENU01851	AN161C8544: 103..977	72-93	880-904	NAP		g3136060	281	145	5.00E-34	34	59	[Schizosaccharomyces pombe]
18058	ENU01852	AN161C7094: 1117..236	42-61	863-882	NAP		g113382	323	50	0.00002	36	58	alcohol dehydrogenase III; alcohol dehydrogenase (EC 1.1.1.1) III - Emericella nidulans; (X02764) alcohol dehydrogenase 3 [Emmericella nidulans] (U94348) acetyl-coenzyme A synthetase [Pyrobaculum aerophilum] (U38783) orf of unknown function; Method: conceptual translation supplied by author
18059	ENU01853	AN161C5249: 176..1059	26-45	848-867	NAP		g4100125	317	89	3.00E-34	40	37	[Schizosaccharomyces pombe]
18060	ENU01854	AN161C1107 8:47..931	33-57	856-875	NAP		g1145409	110	76	3.00E-13	26	42	(Z69254) alpha-galactosidase [Hypoocrea jecorina]
18061	ENU01855	AN161C1082 1:1936..1052	43-62	857-885	NAP		g1580818	1121	439	e-122	67	39	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
18062	ENU01856	AN161C1077 5:2172..1288	42-62	865-884	NAP		g3850084	543	86	2.00E-35	44	72	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18063	ENU01857	ANI61C5563:	25-45	846-868	NAP		g3873847	153	89	3.00E-17	35	29	(Z82256) cDNA EST EMBL:D67325 comes from this gene; cDNA EST EMBL:C13315 comes from this gene; cDNA EST EMBL:D37596 comes from this gene; cDNA EST EMBL:D69512 comes from this gene; cDNA EST EMBL:C11315 comes from this gene; cDN...
		970..85											
18064	ENU01858	ANI61C9914:	59-78	883-902	NAP		g1723213	499	146	2.00E-34	40	54	hypothetical 51.5 KD protein C3H8.02 in chromosome I ; (Z69086) unknown
		1844..2729											[Schizosaccharomyces pombe]
18065	ENU01859	ANI61C4664:	24-43	854-874	NAP		g3080538	623	182	2.00E-45	48	61	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
		653..1545											[Schizosaccharomyces pombe]
18066	ENU01860	ANI61C1025	22-53	855-875	NAP		g3915186	197	103	2.00E-21	39	57	ubiquitin-conjugating enzyme E2-21 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (peroxin-4) ; (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]
		5:1471..2366											(Z99295) pre-mrna splicing factor [Schizosaccharomyces pombe]
18067	ENU01861	ANI61C7946:	52-74	888-907	NAP		g2414602	434	85	8.00E-16	37	56	(X98931) heat shock protein 70 [Emmericella nidulans]
		2004..1107											myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
18068	ENU01862	ANI61C1054	34-56	873-892	NAP		g2764949	1252	334	3.00E-96	97	43	(L48797) toxin pump [Cochliobolus carbonum]
		8:1613..720											(AF010145) hexose transporter [Aspergillus parasiticus]
18069	ENU01863	ANI61C5778:	39-58	871-901	NAP		g2500938	988	238	4.00E-62	41	52	hypothetical 40.7 KD protein in OPDE 3'region (ORF2) ; hypothetical protein 2 - Pseudomonas aeruginosa ; (Z14064) ORF2 [Pseudomonas aeruginosa]
		1808..2712											hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe]
18070	ENU01864	ANI61C2559:	67-86	905-930	NAP		g1063421		99	4.00E-20			
		227..1131											
18071	ENU01865	ANI61C257:1	22-53	861-886	NAP		g2306977	1117	124	1.00E-41	56	42	
		317..410											
18072	ENU01866	ANI61C5632:	22-47	868-887	NAP		g732227	502	80	4.00E-32	42	79	
		31..938											
18073	ENU01867	ANI61C1078	54-73	900-919	NAP		g1351673	521	174	7.00E-43	42	66	
		4:1116..209											

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18074	ENU01868	AN161C1004	67-86	921-940	NAP		g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase [Schizosaccharomyces pombe]
18075	ENU01869	AN161C562:8	71-91	925-944	NAP		g134297	482	155	4.00E-47	40	70	SCJ1 protein; SCJ1 protein - yeast (Saccharomyces cerevisiae); (X58679) SCJ1 [Saccharomyces cerevisiae]; (Z49809) unknown [Saccharomyces cerevisiae]; heat shock protein [Saccharomyces cerevisiae]
18076	ENU01870	AN161C1004	67-86	921-940	NAP		g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase [Schizosaccharomyces pombe]
18077	ENU01871	AN161C924:2	72-91	911-946	NAP		g1706692	1046	206	1.00E-52	52	61	C-24(28) sterol reductase; probable transport protein ERG4 - yeast (Saccharomyces cerevisiae); (Z72534) ORF YGL012w [Saccharomyces cerevisiae]
18078	ENU01872	AN161C7696: 18..936	39-59	896-915	NAP		g2598593		39	0.034			(Y15369) MtN12 [Medicago truncatula]
18079	ENU01873	AN161C1754: 4729..3810	57-78	909-934	NAP		g3368		96	8.00E-26			(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
18080	ENU01874	AN161C6862: 22-46	882-905	NAP			g1791305	610	149	1.00E-57	43	70	(U83489) sepin B [Emmericella nidulans]
18081	ENU01875	AN150C1_17 41:3..929	24-43	889-908	NAP		g1703202		168	4.00E-41	38	68	sterigmatocystin biosynthesis regulatory protein; sterigmatocystin synthesis transcriptional regulator aflR - Emmericella nidulans; (U34740) pathway specific transcription factor [Emmericella nidulans]
18082	ENU01876	AN161C352:9 95..69	23-42	888-907	NAP		g1176004	480	192	4.00E-48	39	82	hypothetical 40.4 KDa protein in PES4-HIS2 intergenic region; (D50617) YFR024C [Saccharomyces cerevisiae]
18083	ENU01877	AN161C4038: 71-93	936-957	NAP			g2160185	299	101	8.00E-21	26	42	(AC000132) Similar to S. pombe ISP4 (gbID83992). [Arabidopsis thaliana]
18084	ENU01878	AN161C1100 6:1241..312	32-53	897-919	NAP		g585251		77	1.00E-13			Polyketide synthase HETM; hetm protein - Anabaena sp. (PCC 7120); (L22883) polyketide synthase [Anabaena sp.]
18085	ENU01879	AN161C8862: 22-54	888-910	NAP			g3006183	381	97	9.00E-38	37	67	(AL022304) trp-ast repeats containing protein [Schizosaccharomyces pombe]
18086	ENU01880	AN161C1020 9:2555..1619	34-59	907-926	NAP		g2330840	417	118	1.00E-41	38	90	(Z98531) hypothetical protein [Schizosaccharomyces pombe]

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18095	ENNU01889	AN161C7499:	69-87	418-435	NAP		g2127839	180	65	2.00E-10	32	82	"deoxycytidine triphosphate deaminase homolog - Methanococcus jannaschii ; (U67553) deoxycytidine triphosphate deaminase, putative (dcd)
		1412..1003											[Methanococcus jannaschii]"
18096	ENNU01890	AN161C3183:	32-51	388-407	NAP		g400513		33	0.0007			NADH-ubiquinone oxidoreductase B22 subunit (complex I-B22) (CI-B22) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine ; (X64836) NADH-ubiquinone oxidoreductase complex B22 subunit [Bos taurus]
		568..985											gamma-adaptin - smut fungus (Ustilago maydis) ; (Z46804) gamma-adaptin [Ustilago maydis]
18097	ENNU01891	AN161C1610:	36-56	395-414	NAP		g1078673	1228	40	0.006	31	13	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
		1312..1732											(AL031603) 60s ribosomal protein [Schizosaccharomyces pombe]
18098	ENNU01892	AN161C4480:	22-44	382-401	NAP		g2465151	111	53	0.000001	40	74	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740) putative p450 monooxygenase [Emeticella nidulans]
		445..24											hypothetical protein YPL088w - yeast (Saccharomyces cerevisiae) ; (U43281) Lpg20p [Saccharomyces cerevisiae]
18099	ENNU01893	AN161C6633:	66-83	434-452	NAP		g3646455	432	61	0.000000	77	53	Scyralone dehydratase ; (D86079) scyralone dehydratase [Colletotrichum lagenarium]
		880..1308											hypothetical 66.5 KD protein in ALG9-RAP1 intergenic region ; probable membrane protein YNL218w - yeast (Saccharomyces cerevisiae) ; (Z71494) ORF YNL218w [Saccharomyces cerevisiae]
18100	ENNU01894	AN161C2205:	30-49	400-419	NAP		g2493389	179	56	0.000000	39	21	(AC005169) hypothetical protein [Arabidopsis thaliana]
		4095..4526											(M77661) putative pol polypeptide [Magnaporthe grisea]
18101	ENNU01895	AN161C6093:	31-49	409-426	NAP		g2132183	760	138	3.00E-32	50	42	
		2385..2822											
18102	ENNU01896	AN161C1021	53-72	429-448	NAP		g3024608	488	138	3.00E-44	63	69	
		1:862..1299											
18103	ENNU01897	AN161C1106	56-75	433-452	NAP		g1730822	804	157	3.00E-38	52	24	
		5:3087..3525											
18104	ENNU01898	AN161C1828:	55-72	434-453	NAP		g3687238	493	176	7.00E-44	57	53	
		420..860											
18105	ENNU01899	AN161C3632:	30-51	416-435	NAP		g538067	189	97	6.00E-20	36	10	
		9..456											

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18106	ENU01900	AN161C1108:	58-77	445-463	NAP		g731968	426	141	2.00E-33	50	45	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region ; hypothetical protein YJL213w - yeast
		4975..4527											(Saccharomyces cerevisiae) ; (Z34098) ORF [Saccharomyces cerevisiae] ; (Z49488) ORF YJL213w [Saccharomyces cerevisiae]
18107	ENU01901	AN161C4859:	71-90	462-481	NAP		g731347		56	7.00E-17			Metal resistance protein YCF1 (yeast cadmium factor 1) ; (L35237) metal resistance protein [Saccharomyces cerevisiae]
		2706..2254											(AF026204) No definition line found [Caenorhabditis elegans]
18108	ENU01902	AN161C3691:	40-59	432-451	NAP		g2435542	89	45	0.0004	37	70	"60S ribosomal protein YL16B ; ribosomal protein L6.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U22382) Rpl16bp: 60S ribosomal protein YL16B [Saccharomyces cerevisiae] "
18109	ENU01903	AN161C9317:	25-44	419-443	NAP		g1346942	399	125	2.00E-28	50	84	"Interferon-induced GTP-binding protein MX ; Mx resistance protein homolog - perch (fragment) ; (M27252) [Perca fluviatilis gene with homology to murine Mx genes, partial cds.], gene product [Perca fluviatilis] " (AL023518) hypothetical protein [Schizosaccharomyces pombe]
		5033..4573											[Schizosaccharomyces pombe] hypothetical 31.6 KD protein C2E12.03C in chromosome I ; (Z69726) unknown [Schizosaccharomyces pombe]
18110	ENU01904	AN161C1116	63-83	472-491	NAP		g127568	292	82	3.00E-15	31	51	(U31884) aromatic L-amino acid decarboxylase [Rattus norvegicus]
		4:4277..4747											Nitrate reductase 3 (NR) ; (U20450) nitrate reductase [Zea mays] (AF088906) clock-controlled gene-9 protein [Neurospora crassa]
18111	ENU01905	AN161C1389:	72-98	481-501	NAP		g3130056	206	80	7.00E-15	37	22	
		74..545											
18112	ENU01906	AN161C3296:	61-80	479-500	NAP		g1723416	297	104	4.00E-22	39	50	
		747..266											
18113	ENU01907	AN161C3109:	41-58	470-488	NAP		g975309	802	103	2.00E-31	49	29	
		2704..3193											
18114	ENU01908	AN161C3335:	36-55	465-484	NAP		g1352497	1224	112	5.00E-28	42	18	
		2067..2558											
18115	ENU01909	AN150C844_	27-46	460-479	NAP		g3746895		63	0.000000			
		1:539..45											

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18116	ENU01910	ANI61C1026	53-72	494-513	NAP		g465665	310	135	2.00E-31	41	68	"hypothetical 27.1 KD protein UFD4-CAP1 intergenic region ; hypothetical protein YKL009w - yeast (Saccharomyces cerevisiae) ; (S53418) ribosomal protein L10 homolog [Saccharomyces cerevisiae=yeast, Peptide, 236 aa] [Saccharomyces cerevisiae] ; (Z28009) ORF YKL009w [Saccharomyces cerevisiae] "
18117	ENU01911	ANI61C9065	58-76	502-521	NAP		g1491795	503	159	2.00E-38	41	18	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus] "
18118	ENU01912	ANI61C1043	51-68	498-517	NAP		g4107287	459	50	0.000000			(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
18119	ENU01913	ANI61C3562	55-73	505-524	NAP		g4586977	3318	176	1.00E-43	47	7	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]
18120	ENU01914	ANI61C5666	49-67	512-531	NAP		g3122291	661	161	4.00E-48	70	49	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) ; (AJ001000) inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) [Pichia pastoris] hypothetical 16.6 KD protein in ATL 5'region (ORF3) ; (D17366) ORF3 [Staphylococcus aureus] ; (L41499) ORF3 [Staphylococcus aureus] "(U21319) similar to alcohol dehydrogenase, highest similarity to B. japonicum FIXR protein (SP:FIXR_BRAJA_P05406) [Caenorhabditis elegans] "
18121	ENU01915	ANI61C3340	68-87	541-560	NAP		g1723227	109	39	0.017			(AC000133) ORF [Emmericella nidulans]
18122	ENU01916	ANI61C7507	50-69	528-547	NAP		g687834	45	39	0.023			"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe] ; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe] "
18123	ENU01917	ANI61C1802	24-44	505-524	NAP		g1870209	332	104	3.00E-22	41	32	
18124	ENU01918	ANI61C4995	54-71	537-556	NAP		g2498711	230	99	2.00E-20	34	31	

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18125	ENU01919	ANI61C4995:	54-71	537-556	NAP		g2498711	230	99	2.00E-20	34	31	"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe] ; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe]"
18126	ENU01920	ANI61C8394:	24-43	507-526	NAP		g117804	244	119	1.00E-26			cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Saccharomyces cerevisiae) ; (X03215) cytochrome b2 precursor [Saccharomyces cerevisiae] ; (Z46729) cytochrome b2 precursor [Saccharomyces cerevisiae] ; (AL022070) hsp gpr homolog [Schizosaccharomyces pombe] ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18127	ENU01921	ANI61C7977:	62-81	545-564	NAP		g2950485	313	137	5.00E-32	45	73	"High affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18128	ENU01922	ANI61C7152:	41-58	525-545	NAP		g3123032	275	125	2.00E-28	32	30	66 kDa stress protein p66 [Physarum polycephalum]
18129	ENU01923	ANI61C3573:	37-61	523-542	NAP		g1709181	434	45	0.000000	27	27	"High affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18130	ENU01924	ANI61C8580:	31-52	522-541	NAP		g2808541	871	108	2.00E-23	39	25	(Y16261) CRO1 protein [Podospira anserina]
18131	ENU01925	ANI61C8962:	65-84	559-578	NAP		g1351916	1951	272	1.00E-72	68	22	"AMP deaminase (myoadenylate deaminase) ; AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae) ; (Z46659) AMD1 gene, len: 810, CAl: 0.19, AMP deaminase [Saccharomyces cerevisiae]"
18132	ENU01926	ANI61C1026	38-57	548-567	NAP		g2440196	487	147	6.00E-35	48	64	(Z99532) myo-inositol transporter [Schizosaccharomyces pombe]

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18133	ENU01927	ANI61C6374:	59-78	570-588	NAP		g140499	649	184	5.00E-46	57	67	"putative 30.7 KD methyltransferase in TSM1-ARE1 intergenic region; hypothetical protein YCR047c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR047c, len:275 [Saccharomyces cerevisiae]"
18134	ENU01928	ANI61C8578:	55-73	585-604	NAP		g2493143	440	121	4.00E-27	71	88	Vacuolar ATP synthase 16 KD proteolipid subunit ; (U02877) vacuolar ATPase subunit c [Candida tropicalis] (Z99126) putative mannosyl transferase [Schizosaccharomyces pombe] (U78597) kinesin light chain [Plectonema boryanum] probable peroxisomal membrane protein PMP20 (allergen ASP F 3) ; (U58050) peroxisomal-like protein [Aspergillus fumigatus] cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7 [Schizosaccharomyces pombe]
18135	ENU01929	ANI61C3426:	51-70	583-602	NAP		g2398816	312	103	9.00E-22	30	46	"5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (methionine synthase, vitamin-B12 independent isozyme) (cobalamin-independent methionine synthase) (delta-P8 protein) ; 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - yeast (Saccharomyces cerevisiae) ; (U18839) Met6p: 5-methyltetrahydropteroyl triglutamate--homocysteine methyltransferase [Saccharomyces cerevisiae] ; (U32508) N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae]"
18136	ENU01930	ANI61C1156:	37-61	572-591	NAP		g2645229	156	67	9.00E-11	32	40	
18137	ENU01931	ANI61C5927:	63-81	604-623	NAP		g3914384	536	90	5.00E-45	65	86	
18138	ENU01932	ANI61C823:	68-87	614-633	NAP		g1168817	236	60	1.00E-18	33	16	
18139	ENU01933	ANI61C5908:	71-90	628-647	NAP		g730018	1750	317	4.00E-86	77	26	

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18140	ENU01934	ANI61C3096:	49-67	608-627	NAP		g3929350	3103	259	1.00E-68	65	22	Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052)
		2148..1528											multifunctional beta-oxidation protein [Neurospora crassa]
18141	ENU01935	ANI61C6914:	51-71	610-629	NAP		g4501859	550	101	4.00E-44			"acyl-Coenzyme A dehydrogenase, short/branched chain precursor ; acyl-CoA dehydrogenase, short/branched chain specific precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD) ; short/branched chain acyl-CoA dehydrogenase (EC 1.3.-.-) precursor - human ; (U12778) acyl-CoA dehydrogenase [Homo sapiens] " (AF034089) calcineurn subunit B [Neurospora crassa]
18142	ENU01936	ANI61C1103	49-68	612-631	NAP		g2645886	627	210	5.00E-54	87	92	quininate permease (quininate transporter) ; quininate transport protein - Emericella nidulans ; (X13525) quininate permease [Emericella nidulans]
18143	ENU01937	ANI61C8512:	47-67	611-631	NAP		g131768	252	73	9.00E-16	32	31	(AL031262) hypothetical protein [Schizosaccharomyces pombe]
		7.5341..4717											[Schizosaccharomyces pombe]
		26..652											cytochrome B ; ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Emericella nidulans mitochondrion (SGC3) ; (J01389) apocytochrome b [Emericella nidulans]
18144	ENU01938	ANI61C6933:	39-58	608-627	NAP		g3417428	214	75	3.00E-13	31	29	(AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum]
		1260..629											casein kinase II beta chain (CK II) ; (X74274) casein kinase II beta subunit [Schizosaccharomyces pombe]
18145	ENU01939	ANI61C3548:	33-56	593-623	NAP		g117840	1057	320	5.00E-87	98	54	
		918..286											
18146	ENU01940	ANI61C7842:	28-45	604-623	NAP		g4062842	290	80	1.00E-14	41	69	
		137..774											
18147	ENU01941	ANI61C4563:	50-71	631-649	NAP		g729881	641	226	1.00E-58	58	85	
		1004..363											

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18148	ENU01942	ANI61C9471: 43..685	64-83	645-664	NAP		g1718099	846	254	5.00E-67	76	54	vacuolar ATP synthase subunit AC39 (V-ATPase AC39 subunit) (V-ATPase 41 kDa subunit) ; (U36470) vacuolar ATPase 41 kDa subunit [Neurospora crassa]
18149	ENU01943	ANI61C2909: 756..108	45-62	628-651	NAP		g1723727	481	115	1.00E-31	62	42	hypothetical 41.0 kDa protein in YIP1-CBP4 intergenic region ; hypothetical protein YGR173w - yeast (Saccharomyces cerevisiae) ; (Z72958) ORF YGR173w [Saccharomyces cerevisiae]
18150	ENU01944	ANI61C6178: 682..24	32-51	625-648	NAP		g2894179	356	148	4.00E-35	43	65	(AJ223998) PCZA361.15 [Amycolatopsis orientalis]
18151	ENU01945	ANI61C1138: 3..2574..1916	53-72	650-669	NAP		g3810873	144	55	0.000000	32	45	(AB010465) lactonohydrolase [Fusarium oxysporum]
18152	ENU01946	ANI61C8219: 742..81	50-69	650-669	NAP		g1902911		89	4.00E-17			(D83988) reductase [Colletotrichum lagenarium]
18153	ENU01947	ANI61C7493: 4028..3367	67-84	667-686	NAP		g2494090	208	62	1.00E-11	37	55	hypothetical 33.3 kDa protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
18154	ENU01948	ANI61C1055: 7..133..538	31-50	635-653	NAP		g3023956	885	189	1.00E-47	42	16	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
18155	ENU01949	ANI61C3688: 4356..3691	39-58	643-662	NAP		g2983787	238	86	3.00E-16	39	46	"(AE000737) fructose-1,6-bisphosphate aldolase class II [Aquifex aeolicus]"
18156	ENU01950	ANI61C8586: 1110..441	39-58	647-666	NAP		g3004863	967	262	2.00E-69	57	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
18157	ENU01951	ANI61C2388: 4438..5116	56-75	673-692	NAP		g1170278	510	194	5.00E-49	56	62	ATP phosphoribosyltransferase ; ATP phosphoribosyltransferase (EC 2.4.2.17) - yeast (Candida albicans) ; (X83871) ATP phosphoribosyltransferase [Candida albicans]
18158	ENU01952	ANI61C508: 005..4326	69-88	687-706	NAP		g825440	927	183	2.00E-82	92	87	(L42299) RAS [Aspergillus fumigatus]

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18159	ENU01953	AN161C2966: 2334..1644	50-67	677-697	NAP		g127568	224	112	2.00E-24	37	58	"interferon-induced GTP-binding protein MX; Mx resistance protein homolog - perch (fragment); (M27252) [Perca fluviatilis gene with homology to murine Mx genes, partial cds,] gene product [Perca fluviatilis]"
18160	ENU01954	AN161C7836: 1578..882	51-70	687-705	NAP		g2687850	659	116	4.00E-45	45	34	(Y15839) fatty acid transporter protein [Cochiobolus heterostrophus]
18161	ENU01955	AN161C1016: 8:767..70	36-55	671-690	NAP		g1526987	423	110	3.00E-45	49	89	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]
18162	ENU01956	AN161C2322: 429..1130	66-85	706-725	NAP		g4481956	290	100	8.00E-28	51	36	(AL035637) putative uracil kinase-cytosine deaminase-bifunctional enzyme [Schizosaccharomyces pombe] (X89453) DRPLA [Rattus norvegicus]
18163	ENU01957	AN161C7012: 843..141	49-68	689-709	NAP		g995557		36	0.21			NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor - Neurospora crassa
18164	ENU01958	AN161C1806: 1112..402	27-46	671-695	NAP		g280478	446	117	2.00E-39	55	96	putative potassium transport protein C1F5.12; (Z68136) unknown [Schizosaccharomyces pombe]
18165	ENU01959	AN161C6073: 1834..1120	22-45	675-694	NAP		g1351299	260	126	1.00E-28	36	24	sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
18166	ENU01960	AN161C3790: 843..128	68-87	721-741	NAP		g1711561	304	122	3.00E-27	31	41	microtubule-associated protein YTM1; hypothetical protein YOR272w - yeast (Saccharomyces cerevisiae); (X89633) hypothetical protein [Saccharomyces cerevisiae]; (Z75180) ORF YOR272w [Saccharomyces cerevisiae]; (U92821) microtubule-associated protein [Saccharomyces cerevisiae]
18167	ENU01961	AN161C905:4 33..1165	60-79	731-750	NAP		g2494905	618	178	4.00E-44	48	49	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	at Score	Blast Score	Blast Prob	% id	% cvrg	Description
18168	ENU01962	ANI61C6665:	47-66	723-744	NAP	g1723254	673	130	1.00E-29	55	63		probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase ; (Z69369) putative phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerases [Schizosaccharomyces pombe]
18169	ENU01963	ANI61C2704:	70-89	754-773	NAP	g115595	225	67	4.00E-16	34	69		F-actin capping protein alpha subunit ; actin-capping protein alpha chain - yeast (Saccharomyces cerevisiae) ; (X61398) Capping Protein Alpha Subunit [Saccharomyces cerevisiae] ; (Z28007) ORF YKL007w [Saccharomyces cerevisiae] ; (S59773) CAP1 [Saccharomyces cerevisiae] transposase - fungus (Cochliobolus carbonum) (AL023794) hypothetical protein [Schizosaccharomyces pombe] unknown ; (AF075599) ubiquitin conjugating enzyme 12 [Homo sapiens] ; (AB012191) Nedd8-conjugating enzyme hUbc12 [Homo sapiens] (Z97050) iUvD [Mycobacterium tuberculosis] hypothetical 49.5 KDa protein in UBP3-PET122 intergenic region ; hypothetical protein YER152c - yeast (Saccharomyces cerevisiae) ; (U18917) Yer152cp [Saccharomyces cerevisiae] (AF080235) reductase homolog [Streptomyces cyanogenus]
18170	ENU01964	ANI50C1415	22-50	722-741	NAP	g2133335		221	5.00E-57	42	47		
18171	ENU01965	ANI61C7152:	72-91	778-797	NAP	g3192028	312	113	1.00E-24	36	85		
18172	ENU01966	ANI61C1188:	41-60	752-771	NAP	g4507791	510	148	8.00E-47	56	96		
18173	ENU01967	ANI61C1125	70-89	787-806	NAP	g2213526	342	121	7.00E-27	33	42		
18174	ENU01968	ANI61C1023	61-83	781-798	NAP	g731527	265	67	3.00E-23	37	51		
18175	ENU01969	ANI61C3627:	40-59	767-786	NAP	g4240421		97	3.00E-22				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18176	ENU01970	ANI61C3268:	71-90	801-821	NAP		g121146	1021	293	1.00E-78	66	47	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
18177	ENU01971	ANI61C9212:	65-84	791-816	NAP		g1168269	414	131	5.00E-30	41	76	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) ; (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger] ; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6 ; SPT6 protein - yeast (Saccharomyces cerevisiae) ; (M34391) SPT6 protein [Saccharomyces cerevisiae] ; (Z72899) ORF YGR116w [Saccharomyces cerevisiae]
18178	ENU01972	ANI61C1330:	66-84	800-819	NAP		g134854	907	123	4.00E-41	37	17	(U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
18179	ENU01973	ANI61C8126:	66-86	804-823	NAP		g1805251	1222	311	4.00E-84	55	47	(X91867) CPC3 protein [Neurospora crassa]
18180	ENU01974	ANI61C9741:	67-85	805-824	NAP		g1020413	119	83	2.00E-15	26	42	catalase ; catalase (EC 1.11.1.6) - Haemophilus influenzae (strain Rd KW20) ; (U32774) catalase (hkte) [Haemophilus influenzae Rd] (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]
18181	ENU01975	ANI61C9072:	37-57	780-799	NAP		g3860264	344	68	5.00E-22	39	54	
18182	ENU01976	ANI61C8695:	63-82	809-830	NAP		g1351702	765	129	2.00E-29	36	40	
18183	ENU01977	ANI61C1015	66-85	816-835	NAP		g3355628	557	111	1.00E-37	35	15	
18184	ENU01978	ANI50C1469	36-55	785-808	NAP		g1168784		83	7.00E-30	37	45	
18185	ENU01979	ANI61C3072:	28-47	781-804	NAP		g4454690		54	0.000001			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18186	ENU01980	ANI61C1073	70-87	828-847	NAP		g1351671	165	83	3.00E-15			hypothetical 25.4 KD protein C1F7.10 in chromosome I ; hypothetical protein SPAC1F7.10 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown
		4:1983..1164											
18187	ENU01981	ANI61C4097	56-75	814-834	NAP		g586299	630	203	2.00E-51	50	67	[Schizosaccharomyces pombe] hypothetical oxidoreductase in RPB5-CD28 intergenic region ; probable membrane protein YBR159w - yeast (Saccharomyces cerevisiae) ; (Z36028) ORF YBR159w [Saccharomyces cerevisiae]
		234..1054											
18188	ENU01982	ANI61C6237	71-91	836-855	NAP		g732189	735	157	9.00E-38	37	61	hypothetical 49.1 KD protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) ; (X78898) N1342 [Saccharomyces cerevisiae] ; (Z71483) ORF YNL207w [Saccharomyces cerevisiae]
		1362..2188											"GTP-binding protein YPT1 ; GTP-binding protein ypt1 - Neurospora crassa ; (S51252) NCYPT1=putative small GTP-binding protein [Neurospora crassa] ; small GTP-binding protein [Neurospora crassa] " (AL035210) halotolerance protein [Schizosaccharomyces pombe]
18189	ENU01983	ANI61C1754	22-44	790-809	NAP		g466171	827	215	3.00E-79	89	96	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans] (Z98602) putative siroheme synthase [Schizosaccharomyces pombe] (AL021815) putative cis-muconate cycloisomerase [Schizosaccharomyces pombe]
		3010..2181											
18190	ENU01984	ANI61C9551	26-45	812-831	NAP		g4160397	782	257	5.00E-68	49	76	
		5918..5071											
18191	ENU01985	ANI61C7226	42-61	839-858	NAP		g2498971	2547	599	e-171	99	58	
		967..1825											
18192	ENU01986	ANI61C7492	49-68	851-880	NAP		g2330809	571	217	7.00E-57	50	96	
		456..1329											
18193	ENU01987	ANI61C6496	42-61	868-887	NAP		g2879855	954	179	2.00E-44	48	45	
		695..61											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18194	ENU01988	ANI61C1410:	58-77	891-910	NAP		g3024813	280	125	3.00E-28	3		"vanillyl-alcohol oxidase (aryl-alcohol oxidase) (4-allylphenol oxidase) ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptyl)phenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptyl)phenol "
18195	ENU01989	ANI61C9556:	36-57	869-888	NAP		g3451313	242	65	1.00E-15	34	77	(AL031324) conserved hypothetical protein [Schizosaccharomyces pombe]
18196	ENU01990	ANI61C298:	60-79	897-916	NAP		g3024443	464	160	1.00E-38	38	92	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Zalerion arboricola ; (U33266) pyrroline carboxylate reductase [Zalerion arboricola]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18197	ENU01991	ANI61C8349:	64-83	903-922	NAP	g3738171	507	145	3.00E-40	44	87	87	"(AL031856) atp synthase gamma chain, mitochondrial precursor [Schizosaccharomyces pombe]"
		420..1320											probable NADP-dependent oxidoreductase P1 ; zeta-crystallin homolog - Arabidopsis thaliana ; (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
18198	ENU01992	ANI61C8021:	70-89	913-932	NAP	g2498731	206	50	2.00E-18	39	64	64	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618) RTM1 gene product [Saccharomyces cerevisiae]
18199	ENU01993	ANI61C3602:	22-46	881-900	NAP	g730689	261	75	1.00E-12	32	89	89	(AJ006852) alternative NADH-dehydrogenase [Yarrowia lipolytica] lipoamide acyltransferase component precursor of branched-chain alpha-keto acid dehydrogenase complex (E2) (Dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit) ; dihydrolipoamide transacylase precursor - mouse ; (L42996) acyltransferase [Mus musculus] ; branched chain alpha-ketoacid dehydrogenase:subunit=E2 [Mus musculus]
18200	ENU01994	ANI61C9410:	53-72	912-931	NAP	g3718005	1054	387	e-107	62	52	52	(D64005) nitrilase [Synechocystis sp.]
18201	ENU01995	ANI61C9218:	46-65	915-934	NAP	g1709438	621	242	3.00E-63				(D45894) thiamine-4 [Neurospora crassa]
		112..1032											(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]
		3037..2106											(AL049522) hypothetical protein [Schizosaccharomyces pombe]
18202	ENU01996	ANI61C3555:	61-80	937-956	NAP	g1001835	320	145	5.00E-34	33	79	79	(L02869) VPS17 [Saccharomyces cerevisiae]
18203	ENU01997	ANI61C8559:	50-75	929-948	NAP	g4432914	896	128	1.00E-51	59	46	46	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) ; hydroxyproline-rich glycoprotein precursor - common tobacco ; (X13885) extensin (AA 1-620) [Nicotiana tabacum]
18204	ENU01998	ANI61C980:2	72-89	952-972	NAP	g2909465	235	100	2.00E-20	29	96	96	
18205	ENU01999	ANI61C7233:	47-64	930-949	NAP	g4539600	403	88	5.00E-31	52	70	70	
18206	ENU02000	ANI61C5362:	42-62	931-948	NAP	g173177	577	210	1.00E-53	40	52	52	
18207	ENU02001	ANI61C1208:	25-44	913-933	NAP	g119714	150	53	0.000002	29	33	33	
		4167..5117											

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Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18208	ENU02002	ANI61C1065	43-62	933-952	NAP		g1708797	445	96	4.00E-19	39	22		LET1 protein - yeast (Kluyveromyces marxianus var. lactis) ; (X70373) LET1 [Kluyveromyces lactis]
		6:1262..2213												
18209	ENU02003	ANI61C1708	27-46	924-943	NAP		g3661614	2806	579	e-164	88	41		(AF093142) aconitase [Aspergillus terreus]
		595..1553												"fructose-2,6-bisphosphatase ; fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - yeast (Saccharomyces cerevisiae) ; (Z49430) ORF YJL155c [Saccharomyces cerevisiae]"
18210	ENU02004	ANI61C859	1-70	968-987	NAP		g1169587	994	294	6.00E-99	60	65		(Z97209) hypothetical protein [Schizosaccharomyces pombe]
		34..1093												"hypothetical 30.7 KD protein in RV5161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"
18211	ENU02005	ANI50C721_	38-57	936-955	NAP		g2239208		132	4.00E-30	35	30		(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
		1:18..977												3-dehydroshikimate dehydratase (DHS dehydratase) ; 3-dehydroshikimate dehydratase - Neurospora crassa ; (X14603) DHS dehydratase [Neurospora crassa] ; (M10139) 3-dehydroshikimate dehydratase [Neurospora crassa]
18212	ENU02006	ANI61C9205	45-64	963-982	NAP		g140459	376	49	4.00E-14	51	74		(U93867) RNA polymerase III subunit [Homo sapiens]
		4292..3314												(U94913) H-K-ATPase alpha 2b subunit [Rattus norvegicus]
18213	ENU02007	ANI61C1116	46-66	967-986	NAP		g1938424	274	85	3.00E-34	41	21		
		1:459..29												
18214	ENU02008	ANI61C7920	69-87	994-1015	NAP		g112790	456	199	3.00E-50	33	90		
		1937..949												
18215	ENU02009	ANI50C1679	39-62	967-986	NAP		g2228748		90	3.00E-17	23	52		
		9_1:1996..1007												
18216	ENU02010	ANI61C142	1-72	1002-1022	NAP		g2735428		54	0.000002				
		893..901												

Database Hit

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18217	ENU02011	AN161C5215:	39-58	977-996	NAP		g4093186	247	71	2.00E-11	30	91	"(AF106583) contains similarity to domains present in ubiquitin-regulatory proteins (Pfam: PF00789, Score=79.3, E=7.8e-20, N=1), C2H2-type zinc finger domain (Pfam: PF00096, Score=9.5, E=6.2, N=1) and ubiquitin-associated domains (Pfam: PF00... "(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18218	ENU02012	AN161C1002	44-64	986-1008	NAP		g1167523	219	62	1.00E-20	26	24	"hypothetical 76.1 KD protein in UNG1-OST6 intergenic region ; hypothetical protein YML020w - yeast (Saccharomyces cerevisiae) ; (Z46659) unknown orf, len: 664, CAl: 0.13 [Saccharomyces cerevisiae] "
18219	ENU02013	AN161C9368:	45-64	1001-1021	NAP		g2497103	512	138	4.00E-39	42	43	(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum] vegetaitle incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina] "glutamate decarboxylase, 67 KD isoform (GAD-67) (67 KD glutamic acid decarboxylase) ; glutamate decarboxylase (EC 4.1.1.15) 1 - cat ; (M18629) glutamic acid decarboxylase [Felis catus] "
18220	ENU02014	AN161C6615:	22-53	982-1001	NAP		g2326188	654	235	5.00E-61	46	92	splicing factor U2AF homolog - mouse ; (X64587) orf [Mus musculus] putative transcriptional regulatory protein in MKK2-COX11 intergenic region ; hypothetical protein YPL133c - yeast (Saccharomyces cerevisiae) ; (U43703) Lpi12p [Saccharomyces cerevisiae]
18221	ENU02015	AN161C5217:	49-68	1010-1029	NAP		g3023956	264	90	1.00E-22	33	21	hypothetical 63.5 KD protein C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
18222	ENU02016	AN161C3697:	40-59	1006-1024	NAP		g416884	658	253	1.00E-66	40	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18223	ENU02017	AN161C6281:	70-90	1045-1065	NAP		g110998	451	178	2.00E-49	42	61	
18224	ENU02018	AN161C3002:	63-82	1041-1061	NAP		g1730882	529	152	5.00E-54	41	69	
18225	ENU02019	AN161C1025	64-83	1044-1063	NAP		g1351690	393	73	2.00E-19	30	55	
18226	ENU02020	AN161C1002	44-64	1036-1055	NAP		g1167523	219	62	1.00E-20	26	25	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	at Score	Blast Score	Blast Prob	% id	% cvrg	Description
18227	ENU02021	AN161C6760:	63-85	1055-1075	NAP	g538067	1738	217	8.00E-56	36	24		(M77661) putative pol polypeptide [Magnaporthe grisea]
18228	ENU02022	AN161C1099	42-61	1039-1058	NAP	g3912972	328	125	9.00E-29	33	94		alcohol dehydrogenase II (AF008244) alcohol dehydrogenase II [Pichia stipitis]
18229	ENU02023	AN161C3608:	44-63	1045-1064	NAP	g2408068	769	159	3.00E-77	51	67		(Z99165) hypothetical protein [Schizosaccharomyces pombe]
18230	ENU02024	AN161C4301:	42-61	1046-1065	NAP	g2791498	176	111	8.00E-24	35	97		(AL021246) hypothetical protein Rv2458 [Mycobacterium tuberculosis]
18231	ENU02025	AN161C8515:	49-66	1054-1073	NAP	g543962	525	173	2.00E-42	45	88		cell division control protein 16; cdc16 protein - fission yeast [Schizosaccharomyces pombe]; (X71605) cdc16 [Schizosaccharomyces pombe]; (Z98981) cell division control protein 16 [Schizosaccharomyces pombe]
18232	ENU02026	AN161C9037:	39-58	1047-1077	NAP	g2385382	586	116	3.00E-52	42	97		(AJ001428) D-mandelate dehydrogenase [Rhodotorula graminis]; (AJ001429) D-mandelate dehydrogenase [Rhodotorula graminis]; putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe]
18233	ENU02027	AN161C3359:	70-88	1091-1110	NAP	g1351714	236	81	2.00E-14	27	62		"GNS1 protein; probable membrane protein YCR034w - yeast [Saccharomyces cerevisiae]; (X56909) YCR521 [Saccharomyces cerevisiae]; (S78624) YCR521 [Saccharomyces cerevisiae=yeast, Peptide, 347 aa] [Saccharomyces cerevisiae]; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae]; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae]"
18234	ENU02028	AN161C2496:	63-82	1084-1103	NAP	g140489	700	158	3.00E-69				(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
18235	ENU02029	AN161C9101:	63-82	1084-1104	NAP	g3114719	587	109	2.00E-49	43	16		
		3505..2422											

Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18236	ENU02030	ANI61C8453:	60-81	1106-1125	NAP		g1352980	846	215	8.00E-85	50	30	ATP-dependent RNA helicase DOB1 (MRNA transport regulator MTR4); SKI2 protein homolog YJL050w - yeast (Saccharomyces cerevisiae); (Z49325) ORF YJL050w [Saccharomyces cerevisiae] transposase - fungus (Cochliobolus carbonum)
18237	ENU02031	ANI61C119:1	22-56	1069-1088	NAP		g2133335	329	53	0.000003	27	64	(U51327) versicolirin B synthase [Aspergillus parasiticus]; (U51328) versicolirin B synthase [Aspergillus parasiticus]
18238	ENU02032	ANI61C360:2	60-83	1120-1139	NAP		g1293655	589	132	4.00E-30	37	53	(U74468) indole-3-acetaldehyde dehydrogenase [Usitiago maydis] calcium/calmodulin-dependent protein kinase (CMPK); Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans; (M74120) calmodulin-dependent protein kinase [Emericella nidulans]; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] sterigmatocystin 7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]
18239	ENU02033	ANI61C7661:	58-75	1123-1142	NAP		g1658175	809	279	1.00E-86	45	72	(AL031128) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=404.95; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P46821; 2-match_description=microtubule-associated protein ...
18240	ENU02034	ANI61C7147:	54-72	1125-1144	NAP		g3122300	1980	602	0	98	82	(Z25485) ACR1-protein [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe]
18241	ENU02035	ANI61C1107	44-63	1117-1136	NAP		g2498702	196	109	3.00E-23	33	30	
18242	ENU02036	ANI61C7320:	49-68	1129-1148	NAP		g3355742		47	0.0003			
18243	ENU02037	ANI61C6437:	22-40	1130-1147	NAP		g396595	782	236	7.00E-81	61	96	
18244	ENU02038	ANI61C7645:	22-46	1130-1149	NAP		g2408062	531	164	1.00E-39	35	58	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18245	ENU02039	ANI61C2531:	62-81	1179-1198	NAP		g2833229	626	116	4.00E-52	36	70	Laccase (benzenedio:xygen oxidoreductase) (urishiol oxidase) (diphenol oxidase)
18246	ENU02040	ANI61C6864:	32-51	1151-1170	NAP		g854534	764	184	1.00E-45	45	39	(X87634) oxidative stress resistance [Saccharomyces cerevisiae]
18247	ENU02041	ANI61C292:9	70-89	1199-1218	NAP		g2833081	416	99	2.00E-28	38	96	(AL021768) ATP binding protein-like [Arabidopsis thaliana]
18248	ENU02042	ANI61C2972:	52-71	1194-1213	NAP		g4507229	1009	242	e-102	47	74	"Succinic semialdehyde dehydrogenase ; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] ; (AL031230) d173M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24) [Homo sapiens] " calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18249	ENU02043	ANI61C1069	39-58	1185-1204	NAP		g728904	1065	177	1.00E-43	47	31	(AL022072) possible transmembrane protein [Schizosaccharomyces pombe]
18250	ENU02044	ANI61C7104:	51-70	1204-1223	NAP		g2950489	309	69	8.00E-11	45	53	Tetracycline resistance protein (transposon TN4351 / TN4400) ; NADP-requiring oxidoreductase - Bacteroides fragilis ; (M37699) tetracycline resistance protein [Transposon Tn4351]
18251	ENU02045	ANI61C3347:	44-63	1198-1217	NAP		g401172	183	107	2.00E-22	28	96	(AL049559) hypothetical protein [Schizosaccharomyces pombe]
18252	ENU02046	ANI61C9152:	24-46	1188-1206	NAP		g4581522	614	153	2.00E-36	32	42	hypothetical 43.5 KD protein in RPB9-ALG2 intergenic region ; hypothetical protein YGL067w - yeast (Saccharomyces cerevisiae) ; (Z72589) ORF YGL067w [Saccharomyces cerevisiae]
18253	ENU02047	ANI61C1022	22-42	1187-1206	NAP		g1723847	313	159	4.00E-38	32	93	

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18254	ENU02048	ANI61C8681:	2888..1653	45-64	1219-1238	NAP		g2499619	179	68	7.00E-15	32	21	probable serine/threonine-protein kinase YMR216C; probable membrane protein YMR216c - yeast (Saccharomyces cerevisiae); (Z49809) unknown [Saccharomyces cerevisiae]
18255	ENU02049	ANI61C3355:	22-41		1195-1215	NAP		g418150	856	122	1.00E-56			GABA-specific permease (GABA-specific transport protein); GABA transport protein - yeast (Saccharomyces cerevisiae); (X66472) GABA-specific permease [Saccharomyces cerevisiae]; (X99000) GABA transporter protein [Saccharomyces cerevisiae]; (Z74258) ORF YDL210w [Saccharomyces cerevisiae]; GABA transport protein [Saccharomyces cerevisiae]
18256	ENU02050	ANI61C6437:	60-79		1241-1260	NAP		g2497127	440	182	3.00E-45	32	90	hypothetical 48.4 KD protein in ARP9-IMP2 intergenic region; probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae); (Z49213) unknown [Saccharomyces cerevisiae]
18257	ENU02051	ANI61C1135	69-89		1256-1275	NAP		g2213553	595	183	3.00E-45	39	56	[Schizosaccharomyces pombe] (Z97052) hypothetical protein
18258	ENU02052	ANI61C7225:	64-82		1257-1276	NAP		g2497946	1369	279	e-120	62	77	"PRPD protein; (U73857) similar to yqjP of B. subtilis [Escherichia coli]; (AE000140) orf, hypothetical protein [Escherichia coli]"
18259	ENU02053	ANI61C4189:	39-59		1237-1256	NAP		g2978332	172	57	0.000000	33	51	(AB012140) arylesterase [Acetobacter pasteurianus]
18260	ENU02054	ANI61C4716:	50-69		1252-1271	NAP		g3183362	339	103	3.00E-21	38	74	hypothetical 48.0 KD protein C1B3.08 in chromosome I; (Z98598) hypothetical protein [Schizosaccharomyces pombe]
18261	ENU02055	ANI61C1046	33-52		1237-1255	NAP		g4038592	308	154	1.00E-36	30	32	(Y10403) RNA-directed RNA polymerase [Lycopersicon esculentum]
18262	ENU02056	ANI61C2205:	27-46		1231-1250	NAP		g3850125	458	131	8.00E-30	32	75	(AL033391) hypothetical membrane protein [Candida albicans]
18263	ENU02057	ANI61C7041:	25-44		1238-1257	NAP		g171124	387	78	1.00E-25	29	74	(M20319) aminotriazole resistance protein [Saccharomyces cerevisiae]
18264	ENU02058	ANI61C9605:	43-62		1263-1283	NAP		g3341974	931	360	9.00E-99	47	92	(AB012604) squalene synthase [Candida utilis]

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18265	ENU02059	ANI61C8226:	67-87	1298-1317	NAP	g4584836	424	424	150	1.00E-35	33	54	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
18266	ENU02060	ANI61C8226:	67-87	1298-1317	NAP	g4584836	424	424	150	1.00E-35	33	54	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
18267	ENU02061	ANI61C1064	47-66	1280-1299	NAP	g2565329	694	278	7.00E-77	45	88	(AF025290) cAMP-dependent protein kinase catalytic subunit [Ustilago maydis]	
18268	ENU02062	ANI61C4192:	24-43	1261-1279	NAP	g4160579	227	99	5.00E-20	37	49	(AL035218) hypothetical protein [Schizosaccharomyces pombe]	
18269	ENU02063	ANI61C5216:	48-68	1288-1307	NAP	g2661608	1696	246	e-118	53	69	(AL009197) hypothetical ctp synthase [Schizosaccharomyces pombe]	
18270	ENU02064	ANI61C2416:	23-43	1296-1315	NAP	g2239198	636	178	1.00E-62	55	99	(Z97209) putative tricarboxylate transport protein protein [Schizosaccharomyces pombe]	
18271	ENU02065	ANI61C7568:	53-72	1339-1361	NAP	g1709181	503	136	9.00E-39	34	70	"[Schizosaccharomyces pombe] "high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae] "	
18272	ENU02066	ANI61C1128	23-48	1317-1336	NAP	g2132491	152	44	5.00E-11	34	68	Probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]	
18273	ENU02067	ANI61C1016	22-41	1326-1345	NAP	g1169782	556	206	5.00E-60	37	91	Fusca protein FUS6 ; (L26498) FUS6 [Arabidopsis thaliana]	
18274	ENU02068	ANI61C3255:	44-63	1348-1367	NAP	g3023683	1913	560	e-180	90	86	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; 6beta-hydroxyhyoscyamine epoxidase (EC 1.14.11.14) - Aspergillus oryzae ; (D63941) enolase [Aspergillus oryzae] ; (D64113) enolase [Aspergillus oryzae] ; enolase [Aspergillus oryzae]	
18275	ENU02069	ANI61C1080	62-81	1389-1408	NAP	g4033481	233	63	2.00E-21	30	84	putative tarrate transporter ; (U32375) membrane protein [Agrobacterium vitis]	
18276	ENU02070	ANI61C7689:	71-90	1408-1426	NAP	g3882261	375	98	8.00E-25	31	54	(AB018313) KIAA0770 protein [Homo sapiens]	

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18277	ENU02071	ANI61C9422:	40-63	1379-1398	NAP		g4406656	214	102	4.00E-21	29	45	(AF131820) Unknown [Homo sapiens]
18278	ENU02072	124..1524 ANI61C3006:	40-59	1388-1407	NAP		g2493484	1127	342	e-110	53	81	glycerol kinase (ATP:glycerol 3-phosphotransferase) (glycerokinase) (GK) ; (U48403) glycerol kinase [Mus musculus]
18279	ENU02073	ANI61C6597:	44-63	1393-1413	NAP		g417699	1559	321	e-171			"histone deacetylase RPD3 (transcriptional regulatory protein RPD3) ; transcription regulator RPD3 - yeast (Saccharomyces cerevisiae) ; (S66438) RPD3 [Saccharomyces cerevisiae, Peptide, 433 aa] [Saccharomyces cerevisiae] ; (X83226) global transcriptional regulator [Saccharomyces cerevisiae] ; (Z71606) ORF YNL330c [Saccharomyces cerevisiae]"
18280	ENU02074	ANI61C1223:	24-45	1374-1393	NAP		g3023717	1095	437	e-121	58	86	ESA1 protein ; hypothetical protein YOR244w - yeast (Saccharomyces cerevisiae) ; (Z75152) ORF YOR244w [Saccharomyces cerevisiae] (U39201) acetolactate synthase [Magnaporthe grisea] (AF027868) Yoan [Bacillus subtilis] ; (Z29114) similar to hypothetical proteins [Bacillus subtilis] (U73857) galactoside O-acetyltransferase [Escherichia coli] (AL032671) predicted using GeneFinder [Caenorhabditis elegans] (AC004473) Contains similarity to golliath protein gblM97204 from D. melanogster. [Arabidopsis thaliana] Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides] (AF041050) 4-coumarate:CoA ligase [Populus tremuloides] (Z98529) conserved hypothetical protein [Schizosaccharomyces pombe]
18281	ENU02075	ANI61C1029	69-87	1431-1450	NAP		g1072104	2199	628	e-180	70	68	
18282	ENU02076	6:9675..8253 ANI61C7367:	47-64	1420-1439	NAP		g2619026	699	153	8.00E-73	43	96	
18283	ENU02077	ANI61C1141	45-65	1436-1454	NAP		g1657538	206	51	3.00E-14	40	26	
18284	ENU02078	4:1586..135 ANI50C5820	72-89	1467-1486	NAP		g3873654		43	0.005			
18285	ENU02079	3_1:2193..737 ANI61C8228:	57-80	1452-1471	NAP		g3249088	134	76	6.00E-13	25	27	
18286	ENU02080	ANI61C1073	41-59	1448-1467	NAP		g3915140	448	73	2.00E-19	33	74	
18287	ENU02081	ANI61C8810:	23-40	1443-1462	NAP		g3258637	442	128	3.00E-50	37	64	
18288	ENU02082	3452..1970 ANI61C3730:	52-71	1484-1501	NAP		g3859776		62	0.000000	41	38	

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18289	ENU02083	ANI61C3730:	72-91	1510-1529	NAP	g2648302	239	115	6.00E-25	43	49		"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
18290	ENU02084	ANI61C2434:	23-41	1481-1500	NAP	g1661227	633	234	1.00E-60	32	62		(U75973) NAAG-peptidase; NAALADase; prostate specific membrane antigen; PSM; PSMA [Rattus norvegicus] ; (AF040256) glutamate carboxypeptidase II [Rattus norvegicus]
18291	ENU02085	ANI61C1714:	24-43	1496-1515	NAP	g547880	693	102	7.00E-58	43	78		LYSINE-specific permease ; (U00007) lysine-specific permease [Escherichia coli] ; Lys permease [Escherichia coli] (AF017990) Fkbp39p
18292	ENU02086	ANI61C5953:	24-43	1512-1532	NAP	g3406742	509	157	2.00E-37	45	72		[Schizosaccharomyces pombe] ; (AL035548) Peptidyl Prolyl cis-trans isomerase [Schizosaccharomyces pombe]
18293	ENU02087	ANI61C1758:	24-45	1514-1533	NAP	g464369	566	118	7.00E-26	26	35		phenol 2-monooxygenase (phenol hydroxylase) ; (L04488) phenol hydroxylase [Trichosporon cutaneum]
18294	ENU02088	ANI61C1052	69-87	1591-1608	NAP	g2058299	938	317	e-105	44	95		(X98309) ARI protein [Drosophila melanogaster] ; (X98310) ARI protein [Drosophila melanogaster]
18295	ENU02089	ANI61C3068:	24-43	1582-1601	NAP	g130117	639	137	3.00E-39	35	80		[Drosophila melanogaster] phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18296	ENU02090	ANI61C4335:	45-64	1624-1643	NAP	g1706439	651	220	1.00E-65	35	81		[Neurospora crassa] Dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae] ; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
18297	ENU02091	ANI61C5680:	53-73	1638-1657	NAP	g2498564	186	60	0.000000	39	42		ML03 protein ; (L42551) ORF [Schizosaccharomyces pombe] ; (Z98270) Mlo3p [Schizosaccharomyces pombe]

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18298	ENU02092	ANI61C1080	32-51	1618-1637	NAP	g4033481	233	63	4.00E-22	29	90		putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
18299	ENU02093	ANI61C85111	53-72	1672-1691	NAP	g2494913	923	369	e-101	40	98		hypothetical 57.3 KD TRP-ASP repeats containing protein in POM152-REC114 intergenic region ; hypothetical protein YMR131c - yeast (Saccharomyces cerevisiae) ; (Z48622) unknown [Saccharomyces cerevisiae] "(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici] "
18300	ENU02094	ANI61C7716	34-53	1655-1674	NAP	g799150	1915	531	e-150	54	69		probable membrane protein YDR294c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr294cp [Saccharomyces cerevisiae] hypothetical protein YDL037c - yeast (Saccharomyces cerevisiae) ; (Z71781) unknown [Saccharomyces cerevisiae] ; (Z74085) ORF YDL037c [Saccharomyces cerevisiae] (AF041049) 4-coumarate:CoA ligase [Populus tremuloides] (AF036097) flavocytochrome b subunit [Bos taurus] (D86086) canalicular multispecific organic anion transporter [Rattus norvegicus] (Y16045) leucine-rich repeat protein [Arabidopsis thaliana] Uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe] (Y16834) hexose transporter [Candida albicans] hypothetical 87.0 KD protein in PAN1-PR1 intergenic region ; hypothetical protein YIR007w - yeast (Saccharomyces cerevisiae)
18301	ENU02095	ANI61C5161	53-72	1680-1700	NAP	g2132493	1168	379	e-104	51	86		
18302	ENU02096	ANI61C1048	63-83	1692-1713	NAP	g2131317		40	0.04				
18303	ENU02097	ANI61C5282	56-74	1705-1724	NAP	g3258635	526	219	3.00E-61	32	99		
18304	ENU02098	ANI61C1054	41-60	1693-1713	NAP	g2921400	606	257	1.00E-74	33	90		
18305	ENU02099	ANI61C1542	47-66	1713-1731	NAP	g1405353	614	100	3.00E-55	35	30		
18306	ENU02100	ANI61C7473	71-90	1762-1781	NAP	g2760084	228	126	4.00E-28	31	49		
18307	ENU02101	ANI61C1883	68-87	1760-1779	NAP	g2492816	1271	176	e-114	50	84		
18308	ENU02102	ANI61C1014	68-88	1821-1852	NAP	g3336839	795	100	4.00E-78	40	95		
18309	ENU02103	ANI61C9693	71-90	1864-1883	NAP	g731909	427	85	2.00E-30	36	31		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18310	ENU02104	ANI61C5240:	67-86	1924-	NAP		g1613878	1680	499	e-140	45	49	(U72236) <i>Moda</i> [Dicyostelium discoideum]
18311	ENU02105	755..2676	46-63	1924-	NAP		g3877738	122	44	0.003			(Z74473) predicted using GeneFinder [Caenorhabditis elegans]
18312	ENU02106	11354..10547	50-69	1995-	NAP		g3702646	601	135	4.00E-63	34	73	(AL031825) putative membrane transport protein
18313	ENU02107	ANI61C1125:	52-71	2051-	NAP		g129307	885	272	e-101	39	93	[Schizosaccharomyces pombe] L- amino acid oxidase precursor (LAO) ; L- amino- acid oxidase (EC 1.4.3.2)
18314	ENU02108	193..2253	35-54	2034-	NAP		g3417415	462	102	2.00E-48	44	50	precursor - Neurospora crassa (AL031261) phosphoserine phosphatase [Schizosaccharomyces pombe]
18315	ENU02109	4657..6718	53-76	2060-	NAP		g2501570	395	137	1.00E-36	35	71	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae] probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae) ; (Z74122) ORF YDL074c
18316	ENU02110	ANI61C1122	34-53	2050-	NAP		g2132428	356	153	4.00E-36	28	40	[Saccharomyces cerevisiae] (AL034490) hypothetical proten [Schizosaccharomyces pombe]
18317	ENU02111	6:1866..2040	24-45	2080-	NAP		g4008552	334	100	4.00E-26	35	57	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum]"
18318	ENU02112	ANI61C7956:	63-82	2145-	NAP		g119830	757	661	0	47	36	"hypothetical 77.5 KD protein in PRP1-STE3 intergenic region ; hypothetical protein YKL179c - yeast (Saccharomyces cerevisiae) ; (X74151) previously orf13 and orf14 [2], now merged; homologous to human CENP-E [Saccharomyces cerevisiae] ; (Z28179) ORF YKL179c
18319	ENU02113	1265..3436	22-57	2132-	NAP		g549740	469	113	4.00E-41	28	94	[Saccharomyces cerevisiae]" (AL021747) hypothetical protein [Schizosaccharomyces pombe]
18320	ENU02114	ANI61C6804:	61-80	2201-	NAP		g2842464	260	63	0.000000	26	93	
		3811..6011		2219						008			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18321	ENU02115	AN161S2760:	43-62	2188-2207	NAP		g2072788	89	1.00E-16	27	20		(U64574) cell cycle inhibitor Nif1 [Schizosaccharomyces pombe]; (AL035065) cell cycle inhibitor nif1. [Schizosaccharomyces pombe]
18322	ENU02116	AN161C3865:	38-57	2198-2217	NAP		g1350600	3129	1186	0	77	88	Ribonucleoside-diphosphate reductase large chain (ribonucleotide reductase); CDC22 protein - fission yeast (Schizosaccharomyces pombe); (Z67998) Cdc22p [Schizosaccharomyces pombe]
18323	ENU02117	AN161C2081:	54-73	2213-2235	NAP		g125935	437	195	1.00E-48	28	70	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (M59935) negative-acting regulatory protein [Emmericella nidulans]; (M77664) repressor protein [Emmericella nidulans]
18324	ENU02118	AN161C9003:	63-85	2272-2291	NAP		g168082	1305	439	e-140	40	78	Maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z26167) ORF YBR298c [Saccharomyces cerevisiae]
18325	ENU02119	AN161C594:	67-86	2369-2388	NAP		g585446	772	120	1.00E-83	37	70	hypothetical 175.8 K D protein in GND1-IK11 intergenic region; hypothetical protein YHR186c - yeast (Saccharomyces cerevisiae); (U00030) Yhr186cp [Saccharomyces cerevisiae] (X86780) polyketide synthase [Streptomyces hygroscopicus] probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae); (Z73573) ORF YPL217c [Saccharomyces cerevisiae]
18326	ENU02120	AN161C1055	52-71	2415-2434	NAP		g731756	867	236	6.00E-79	37	42	"probable glucan 1,3-beta-glucosidase precursor (exo-1,3-beta-glucanase); (Z70721) putative 1,3-beta-d-glucanohydrolase [Schizosaccharomyces pombe]"
18327	ENU02121	AN161C8706:	66-85	2452-2472	NAP		g987102	493	132	2.00E-62	36	8	
18328	ENU02122	AN161C1003	72-90	2497-2516	NAP		g2133002	2342	503	e-141	45	65	
18329	ENU02123	AN161C1125	72-91	2498-2516	NAP		g1706727	841	332	7.00E-90	42	48	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18330	ENU02124	ANI61C1003	72-90	2497-	NAP		g2133002	2342	503	e-141	45	65	probable membrane protein YPL217c-yeast (Saccharomyces cerevisiae) ; (Z73573) ORF YPL217c [Saccharomyces cerevisiae]
18331	ENU02125	ANI61C9304	24-47	2476-2495	NAP		g2132957	207	51	0.000000	42	14	probable membrane protein YOR378w-yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae]
18332	ENU02126	ANI61C3630	62-81	2518-2537	NAP		g1002380		39	0.14			(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]
18333	ENU02127	ANI61C648	2	58-77	NAP		g4502897	719	222	1.00E-80	40	47	cleft lip and palate associated transmembrane protein 1 ; (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] ; (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]
18334	ENU02128	ANI61C7559	67-86	2707-2727	NAP		g2853114	361	92	1.00E-17	26	25	(AL021766) hypothetical protein [Schizosaccharomyces pombe]
18335	ENU02129	ANI61C220	2	49-69	NAP		g3913731	1354	504	e-156	42	82	probable mannosyl-oligosaccharide glucosidase (processing A-glucosidase I) ; (Z98603) hypothetical protein [Schizosaccharomyces pombe]
18336	ENU02130	ANI61C8057	45-66	2887-2906	NAP		g4176548	1115	288	e-109	54	57	(AL035259) putative Ca-calmodulin-dependent serine-threonine-protein kinase [Schizosaccharomyces pombe]
18337	ENU02131	ANI61C1412	66-85	203-223	NAP		g133186	400	111	6.00E-25	71	65	Guanyl-specific ribonuclease PB1 ; ribonuclease T1 (EC 3.1.27.3) - Penicillium brevicompactum ; RNase [Penicillium brevicompactum]
18338	ENU02132	ANI61C1055	30-50	163-189	NAP		g2493874	127	64	9.00E-11	42	94	cytochrome C oxidase assembly protein COX17 ; COX17 protein - yeast (Saccharomyces cerevisiae) ; (L75948) approximately 300 nucleotides distal from helicase gene [Saccharomyces cerevisiae] ; (Z73114) ORF YLL009c [Saccharomyces cerevisiae]

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18339	ENU02133	AN161C1360:	22-50	164-183	NAP		g2833211	238	46	0.000000	62	50	NADH-ubiquinone oxidoreductase 10.5 KD subunit (complex I) (CI); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 10.5K chain - Neurospora crassa ; (X69929) NUO-10.5 [Neurospora crassa]
		1556..1353								07			
18340	ENU02134	AN161C480:4	55-77	202-222	NAP		g99521	416	137	1.00E-32	91	45	nad5 intron 1 protein 459 - Sugar beet mitochondrion (fragment) ; (X55786) ORF459 [Beta vulgaris] (AC000104) EST gb T45093 comes from this gene. [Arabidopsis thaliana] phenol hydroxylase - imperfect fungus (Trichosporon beigeli)
		32..223											"(AE000352)orf, hypothetical protein [Escherichia coli]"
18341	ENU02135	AN161C7399:	23-42	172-192	NAP		g1903364		44	0.0002			"mitochondrial 60S ribosomal protein L33 (YML33) ; ribosomal protein L30, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49704) Mpr133p [Saccharomyces cerevisiae]"
		82..293											30S ribosomal protein S15 (BS18) ; (Z80835) ribosomal protein S15 [Bacillus subtilis] ; (Z99112) ribosomal protein S15 (BS18) [Bacillus subtilis] (AL031179) splicing factor [Schizosaccharomyces pombe]
18342	ENU02136	AN161C8581:	70-89	232-251	NAP		g102033	98	42	0.0007			"DNA-directed RNA polymerases I, II, and III 7.7 KD polypeptide (ABC10-alpha) ; DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast (Saccharomyces cerevisiae) ; (U23378) RNA polymerase I, II and III subunit ABC10 alpha [Saccharomyces cerevisiae] ; (U10397) Rpb12p: RNA polymerase II subunit [Saccharomyces cerevisiae]"
		4554..4777											(AC000133) pyrC [Emmericella nidulans]
18343	ENU02137	AN161C3361:	24-43	187-206	NAP		g1789035	162	62	4.00E-10	46	84	
		1117..893											
18344	ENU02138	AN161C5161:	51-70	215-235	NAP		g1710603	169	62	6.00E-10	38	87	
		5997..5772											
18345	ENU02139	AN161C3149:	31-49	197-218	NAP		g2507327	156	51	0.000001	44	86	
		77..306											
18346	ENU02140	AN161C7173:	71-90	241-267	NAP		g3395591	176	70	2.00E-12			
		1312..1550											
18347	ENU02141	AN161C4095:	53-72	231-250	NAP		g3647370	210	80	3.00E-15	50	84	
		457..696											
18348	ENU02142	AN161C8881:	59-79	240-259	NAP		g730606	134	56	0.000000	45	88	
		2362..2604								05			
18349	ENU02143	AN161C1355:	59-78	230-261	NAP		g1870226	531	187	2.00E-47	98	86	
		1288..1532											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18350	ENU02144	AN161S4306:	22-55	190-225	NAP		g2315135	415	166	3.00E-41	100	100	(AB003522) beta subunit of coupling factor one [Arabidopsis thaliana]
18351	ENU02145	AN161S3217:	35-56	215-242	NAP								
18352	ENU02146	AN161C1479:	22-50	215-235	NAP		g4586031	147	56	0.000000	59	94	(AC007109) unknown protein [Arabidopsis thaliana]
18353	ENU02147	AN161C7312:	53-76	252-271	NAP		g1352897	133	56	0.000000			(AC007109) unknown protein [Arabidopsis thaliana]
		2010..2265											hypothetical 11.3 KD protein in MIRI-STE18 intergenic region ; probable membrane protein YJR085c - yeast (Saccharomyces cerevisiae) ; (Z49585) ORF YJR085c [Saccharomyces cerevisiae] ; (L47993) ORF YJR085c [Saccharomyces cerevisiae]
		3506..3246											Rub1
18354	ENU02148	AN161C9353:	39-62	247-266	NAP		g4139493	187	87	4.00E-17	64	92	(AF047427) unknown [Pasteurella haemolytica]
18355	ENU02149	AN161C5287:	31-55	234-261	NAP		g3978168	135	55	0.000000			(U12823) hemolysin [Acanthamoeba polyphaga]
18356	ENU02150	AN161C1253:	26-49	242-261	NAP		g607954	218	66	6.00E-11	62	80	Chloroplast 50S ribosomal protein L23 ; (X65615) ribosomal protein L23 [Sinapis alba]
18357	ENU02151	AN161S4051:	22-53	223-258	NAP		g1350634	490	195	7.00E-50	100	100	(AJ223315) rAsp f7 [Aspergillus fumigatus]
18358	ENU02152	AN161C1068	49-68	270-289	NAP		g2879888	453	155	5.00E-38	75	84	(X95503) zinc finger protein [Mus musculus] ; (X95504) zinc finger protein [Mus musculus]
18359	ENU02153	AN161C563:2	53-72	275-296	NAP		g2326720	48	34	0.27	32	12	"Thioredoxin ; thioredoxin - Emericella nidulans ; thioredoxin [Aspergillus nidulans, Peptide, 109 aa]"
18360	ENU02154	AN161C6455:	23-44	249-268	NAP		g267125	269	96	8.00E-20	53	87	"Keratin, type I cytoskeletal 47 KD ; (X04805) keratin B1 [Xenopus laevis]"
18361	ENU02155	AN161C3233:	48-69	284-305	NAP		g1346341		32	1.5			(AC004680) unknown protein [Arabidopsis thaliana]
18362	ENU02156	AN161C1135	26-45	253-284	NAP		g3420051	477	189	5.00E-48	74	91	[Arabidopsis thaliana]
		8:3396..3096											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18363	ENU02157	ANI61C4231:	31-51	264-292	NAP		g3334316	170	59	0.00000001			"DNA-directed RNA polymerases I, II, and III 8.3 KD polypeptide (ABC10-beta) ; (D89596) RNA polymerase II subunit Rpb10 [Schizosaccharomyces pombe] ; (U80219) RNA polymerases I-III common subunit Rpb10 [Schizosaccharomyces pombe] ; (AF027818) RNA polymerases I, II and III subunit Rpb10 [Schizosaccharomyces pombe] ; (Z98598) dna-directed ma polymerases i, ii, and iii 8.3 kd polypeptide(abc10-beta).dna-directed ma polymerases i, ii, and iii 8.3 kd polypeptide(abc10-beta). [Schizosaccharomyces pombe]" (AC000133) ORF [Emeticella nidulans]
18364	ENU02158	ANI61C5142:	47-66	289-309	NAP		g1870220	97	41	0.002			suppressor of Ty (S.cerevisiae) 4 homolog 1 ; transcription initiation protein SPT4 homolog 1 ; (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] ; (U38818) SPT4H [Homo sapiens] ; (U38817) SPT4H [Homo sapiens] ; (U43154) Supt4h [Mus musculus] ; (U96809) chromatin structural protein homolog [Mus musculus]
18365	ENU02159	ANI61C2477:	22-57	262-287	NAP		g4507311		92	1.00E-18			ribosomal protein L38 ; 60S ribosomal protein L38 ; ribosomal protein L38 - rat ; ribosomal protein L38 - human ; (X57007) ribosomal protein L38 [Rattus rattus] ; (Z26876) ribosomal protein [Homo sapiens]
18366	ENU02160	ANI61C5703:	61-80	307-326	NAP		g4506645	167	61	0.000000002			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18367	ENU02161	ANI61C914:1	22-55	272-291	NAP		g731363	131	57	0.000000	03		PET100 protein precursor ; probable membrane protein YDR079w - yeast (Saccharomyces cerevisiae) ; (X82086) 1 putative transmembrane spans [Saccharomyces cerevisiae] ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74375) ORF YDR079w [Saccharomyces cerevisiae] ; (U91943) cytochrome c oxidase-specific assembly factor [Saccharomyces cerevisiae]
18368	ENU02162	ANI61C1597: 24-50		271-294	NAP		g2656010	201	76	5.00E-14	29	71	(Z99165) hypothetical protein [Schizosaccharomyces pombe] (AC007195) putative blue copper-binding protein II [Arabidopsis thaliana]
18369	ENU02163	ANI61C4533: 24-52		267-295	NAP		g458971	572	221	1.00E-57	97	98	"Histone H3.2, minor; histone H3.3-like protein - Arabidopsis thaliana ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (U09458) histone H3.2 [Medicago sativa] ; (U09460) histone H3.2 [Medicago sativa] ; (U09461) histone H3.2 [Medicago sativa] ; (U09464) histone H3.2 [Medicago sativa] ; (U09465) histone H3.2 [Medicago sativa] ; (X79714) histone H3 [Lolium temulentum] ; (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] ; (AF024716) histone 3 [Gossypium hirsutum] ; (AB015760) histone H3 [Nicotiana tabacum] ; (AF093633) histone H3 [Oryza sativa] ; (AF109910) histone H3 [Porteresia coarctata] ; (AL035708) histone H3.3 [Arabidopsis thaliana] ; (AL035708) Histone H3 [Arabidopsis thaliana] " (AC000133) mt2 [Emmericella nidulans]
18370	ENU02164	ANI61C466:4	65-84	318-337	NAP		g417103	338	141	1.00E-33			
18371	ENU02165	ANI61C5625: 23-50		270-295	NAP		g1870224	569	224	2.00E-58	98	99	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18372	ENU02166	ANI61C1062	31-50	282-303	NAP		g465533	166	46	0.00008	32	87	hypothetical 11.5 KD protein in HTB2-NTH2 intergenic region ; hypothetical protein YBL001c - yeast
		2:5429..5743											(Saccharomyces cerevisiae) ; (Z26494) unknown [Saccharomyces cerevisiae] ; (Z35762) ORF YBL001c [Saccharomyces cerevisiae] ; ORF YBL0105 [Saccharomyces cerevisiae] (U12823) hemolysin [Acanthamoeba polyphaga]
18373	ENU02167	ANI61C1253	29-53	273-303	NAP		g607954	218	57	2.00E-11	57	91	(U12823) hemolysin [Acanthamoeba polyphaga]
		6112..5796											Conidiation-specific protein 6 ; (L26036) conidiation protein [Neurospora crassa]
18374	ENU02168	ANI61C5247	22-50	276-296	NAP		g461773	98	46	0.00006	34	91	(U12823) hemolysin [Acanthamoeba polyphaga]
		3049..2733											cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
18375	ENU02169	ANI61C1253	29-53	273-303	NAP		g607954	218	57	2.00E-11	57	91	hypothetical protein YDR286c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr286cp [Saccharomyces cerevisiae] "(S53434) L46=ribosomal protein [Kluyveromyces marxianus, Peptide, 51 aa] [Kluyveromyces marxianus] " epoxide hydrolase [Rattus norvegicus]
		6112..5796											(AC005278) Similar to gb U85207 smRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb AA612141 comes from this gene. [Arabidopsis thaliana]
18376	ENU02170	ANI61C3429	22-50	278-297	NAP		g117803	132	78	2.00E-14	44	15	(Z98595) 60s ribosomal protein 122 [Schizosaccharomyces pombe]
		379..62											
18377	ENU02171	ANI61C592	22-53	279-300	NAP		g2131413	70	49	0.000009	23	92	
		05..1225											
18378	ENU02172	ANI61C7935	22-54	282-302	NAP		g263485	139	33	0.6			
		802..902											
18379	ENU02173	ANI61C1965	62-86	323-343	NAP		g228278	148	56	0.000000	31	95	
		393..70								07			
18380	ENU02174	ANI61C8199	24-49	287-306	NAP		g3850571	286	100	5.00E-21	57	95	
		2534..2210											
18381	ENU02175	ANI61C7018	24-43	288-310	NAP		g4581479	335	104	2.00E-22	60	74	
		469..141											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18382	ENU02176	AN161C107:1	22-54	286-308	NAP		g1723740	99	50	0.000004	31	82	hypothetical 12.4 KD protein in NAB1A-GPI1 intergenic region ; hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae) ; (Z73000) ORF YGR215w [Saccharomyces cerevisiae]
18383	ENU02177	AN161C1034	27-46	292-315	NAP		g586501	138	64	4.00E-10	35	92	hypothetical 13.2 KD protein in ORC2-TIP1 intergenic region ; hypothetical protein YBR062c - yeast (Saccharomyces cerevisiae) ; (Z25931) ORF YBR062c [Saccharomyces cerevisiae]
18384	ENU02178	AN161C2076: 1448..1116	37-56	295-327	NAP		g3850102	437	161	1.00E-39	67	77	(A1033338) putative golgi membrane protein-sorting protein [Schizosaccharomyces pombe]
18385	ENU02179	AN161C4334: 606..943	22-51	297-317	NAP		g2132826	91	56	0.000000	34	93	probable membrane protein YOL026c - yeast (Saccharomyces cerevisiae) ; (Z74768) ORF YOL026c [Saccharomyces cerevisiae]
18386	ENU02180	AN161C6137: 3737..4075	35-53	312-331	NAP		g2131721	217	64	1.00E-17	52	91	[Saccharomyces cerevisiae] hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mrs11p [Saccharomyces cerevisiae] ; (U10555) Mrs11p [Saccharomyces cerevisiae]
18387	ENU02181	AN161C4486: 475..137	72-92	350-369	NAP		g1175403	164	60	0.000000	36	54	hypothetical 19.0 KD protein C31A2.08 in chromosome I ; hypothetical protein SPAC31A2.08 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe]
18388	ENU02182	AN161C5870: 684..1024	60-79	334-358	NAP		g2281089	152	74	3.00E-13	54	81	(AC002333) Sm protein F isolate [Arabidopsis thaliana]
18389	ENU02183	AN161C3916: 2424..2765	61-88	339-360	NAP		g3183357		41	0.002			hypothetical 13.4 KD protein C17H9.07 in chromosome I ; (Z28597) hypothetical protein [Schizosaccharomyces pombe]
18390	ENU02184	AN161C3209: 50..393	70-89	351-371	NAP		g2498272	267	98	2.00E-20	46	77	Cyanate lyase (cyanate hydrolase) (cyanase) ; (U59481) cyanate lyase [Synechococcus PCC7942] ; (AB000100) cyanase [Synechococcus sp.]

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18391	ENU02185	AN161C8982:	33-51	317-336	NAP		g2983605	238	100	4.00E-21	46	72	(AE000725) ribose 5-phosphate isomerase B [Aquitex acolicus]
18392	ENU02186	7793..7448 AN161C1601:	56-77	341-361	NAP		g1351714		52	0.000002			putative transporter C11D3.18C; (Z68166) unknown
18393	ENU02187	AN161C5803:	22-43	309-327	NAP		g3183399	125	55	0.000000	28	91	[Schizosaccharomyces pombe] hypothetical 13.9 KD protein C2E11.03C in chromosome I; (AL031181) very hypothetical protein [Schizosaccharomyces pombe]; (AL035064) very hypothetical protein [Schizosaccharomyces pombe]
18394	ENU02188	AN161C1064	29-54	314-335	NAP		g731777	149	61	1.00E-10	38	97	"hypothetical 11.0 KD protein in FAA3-MAS3 intergenic region; hypothetical protein YIL008w - yeast (Saccharomyces cerevisiae); (Z38113) orf. len: 99, CAl=0.21 [Saccharomyces cerevisiae]"
18395	ENU02189	AN161C4009:	52-71	342-359	NAP		g2276355	328	101	2.00E-21	60	80	(Z97992) putative small ribonuclear protein [Schizosaccharomyces pombe]
18396	ENU02190	872..523 AN161C6138:	35-68	322-343	NAP		g1363744	260	41	0.004	38	45	hypothetical protein YLR435w - yeast (Saccharomyces cerevisiae); (U21094) Ylr435wp [Saccharomyces cerevisiae] (AC000133) ORF [Emicella nidulans]
18397	ENU02191	AN161C1127	42-62	329-352	NAP		g1870220	685	234	2.00E-61	98	87	hypothetical 10.7 KD protein C17C9.09C in chromosome I; (Z73099) hypothetical protein [Schizosaccharomyces pombe]
18398	ENU02192	4:431..79 AN161C9645:	54-74	347-366	NAP		g1723568		48	0.00002			small nuclear ribonucleoprotein polypeptide E; U1 and U2 small nuclear ribonucleoprotein E (SNRNP-E); small nuclear ribonucleoprotein E - human; (X12466) snRNP E protein (AA 1-92) [Homo sapiens]; (L19064) small nuclear ribonucleoprotein E [Gallus gallus]; (X65702) SmeE protein [Gallus gallus]; (M37716) small nuclear RNA protein (snRNP E) [Homo sapiens]
18399	ENU02193	AN161C1000	26-45	307-339	NAP		g4507129	169	68	2.00E-11			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
18400	ENU02194	AN161C9311:	44-63	341-360	NAP		g1175442	759	138	1.00E-32	58	39	hypothetical protein C22F3.01 in chromosome I ; hypothetical protein SPAC22F3.01 - fission yeast (Schizosaccharomyces pombe) (fragment) ; (Z54285) unknown [Schizosaccharomyces pombe]
		3740..3382											Lectin precursor (agglutinin); lectin precursor - rice ; (M24504) lectin [Oryza sativa]
18401	ENU02195	AN161C8065:	65-84	364-383	NAP		g113509	78	68	2.00E-11	35	45	60S ribosomal protein L35
		714..354											
18402	ENU02196	AN161C5436:	34-59	334-353	NAP		g2833359	268	45	0.0002	57	73	"40S ribosomal protein S15 (S12) ; ribosomal protein S12, cytosolic - Podospora anserina ; (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]"
		564..925											
18403	ENU02197	AN161C4673:	28-57	329-350	NAP		g464706	506	108	1.00E-37	78	76	(AL035263) weak similarity to chick phosphatidylethanolamine site rol acetyltransferase [Schizosaccharomyces pombe]
		38..402											putative protein transport protein SEC61 gamma subunit ; hypothetical protein SPAC4G8.02c - fission yeast (Schizosaccharomyces pombe) ; (Z56276) putative protein transport protein sec61-gamma subunit [Schizosaccharomyces pombe]
18404	ENU02198	AN161C7221:	50-72	353-372	NAP		g4176531	1107	89	1.00E-17	34	18	nuclear transport factor 2 (NTF-2) (nuclear transport factor P10) ; hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae]
		1542..1906											
18405	ENU02199	AN161C9819:	31-56	337-356	NAP		g1351034	167	47	0.000000	52	95	hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae]
		4967..4600											
18406	ENU02200	AN161C3164:	69-88	368-394	NAP		g731437	244	53	2.00E-15	44	81	hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae]
		630..263											
18407	ENU02201	AN161C4957:	60-79	368-393	NAP		g3810851	851	96	1.00E-19	33	15	hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae]
		460..85											
18408	ENU02202	AN161C6549:	63-84	378-397	NAP		g3183481	299	92	1.00E-18	51	56	hypothetical 23.0 KD protein in SNF2-CPA1 intergenic region ; hypothetical protein YOR294w - yeast (Saccharomyces cerevisiae) ; (Z75202) ORF YOR294w [Saccharomyces cerevisiae]
		905..529											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18409	ENU02203	ANI61C1235:	24-43	341-362	NAP		g114663	685	167	4.00E-41	97	88	"ATP synthase protein 9, mitochondrial precursor (LIPID-binding protein); (M30144) mitochondrial ATP synthase precursor [Emmericella nidulans]"
18410	ENU02204	ANI61C2997:	61-89	381-400	NAP		g1362228	448	161	2.00E-39	60	54	pac2 protein - fission yeast (Schizosaccharomyces pombe); (D43748) Pac2p [Schizosaccharomyces pombe]; (Z98979) camp independent regulatory protein
18411	ENU02205	ANI61C7253:	51-70	375-394	NAP		g3005841	341	143	7.00E-34	54	80	[Schizosaccharomyces pombe] (AJ002026) rAsp f 13 [Aspergillus fumigatus]
18412	ENU02206	ANI61C8384:	67-86	392-411	NAP		g3451473	587	121	2.00E-27	50	41	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]
18413	ENU02207	ANI61C6419:	69-88	389-414	NAP		g2492777	314	99	9.00E-21	40	35	hypothetical ZINC-type alcohol dehydrogenase-like protein in pre5-FET4 intergenic region; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae); (Z54141) unknown [Saccharomyces cerevisiae] (Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis]
18414	ENU02208	ANI61C1015:	63-91	390-410	NAP		g2213500	173	85	3.00E-16	39	76	[Mycobacterium tuberculosis] (X99300) unknown epidymal protein [Mus musculus]
18415	ENU02209	ANI61C2495:	24-55	343-371	NAP		g1430862	90	61	0.000000	26	91	(Z99259) small nuclear ribonucleoprotein
18416	ENU02210	ANI61C9745:	30-56	358-377	NAP		g2414614	177	43	0.000000	50	60	[Schizosaccharomyces pombe] ubiquitin-like protein SMT3; SMT3 protein - yeast (Saccharomyces cerevisiae); (U27233) Smt3p [Saccharomyces cerevisiae]; (U33057) suppressor of MIF2 mutations; CAI: 0.31 [Saccharomyces cerevisiae]
18417	ENU02211	ANI61C2576:	22-53	351-370	NAP		g2501450	201	76	7.00E-17	46	94	hypothetical 14.1 KD protein C31A2.02 in chromosome I; hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe); (Z50113) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emmericella nidulans]
18418	ENU02212	ANI61C1557:	55-75	386-406	NAP		g1175395	290	80	5.00E-15	43	84	
18419	ENU02213	ANI61C1098:	22-54	349-373	NAP		g1870220	169	81	3.00E-15	39	97	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18420	ENU02214	ANI61C727:1	45-64	362-397	NAP		g1708982	550	129	1.00E-29	52	23	Ammonium transporter MEP3 ; ammonium transport protein MEP3 - yeast (Saccharomyces cerevisiae) ; (U40829) Similar to B. subtilis membrane protein NrgA (Swiss Prot. accession number Q07429) [Saccharomyces cerevisiae] "(AB007633) Myo3 [Schizosaccharomyces pombe] ; (Z98762) SPAC4A8.05c, myosin heavy chain, len:2104aa, similar eg. to MYO2_DICD1, P08799, myosin ii heavy chain; non muscle, (2116aa), fasta scores, opt: 2488, E0.0, (29.5% identit y in 2167 aa overlap), PS00017 ATP/GTP-bind...
18421	ENU02215	ANI61C7854: 785..1181	45-72	376-399	NAP		g2828348	362	64	5.00E-10			
18422	ENU02216	ANI61C5660: 1057..1454	68-88	396-423	NAP		g3023324	414	133	5.00E-31	48	76	"ATP synthase D chain, mitochondrial ; (AF019223) F1Fo-ATP synthase subunit 7 [Kluveromyces lactis]" DNA-directed RNA polymerase II 13.3 KD polypeptide (RPB11) (RPB14) ; (D85818) RNA polymerase II subunit RPB14 [Mus musculus] (AF099136) vacuolar ATP synthase subunit F [Neurospora crassa] (X89714) rhamnogalacturonan acetyltransferase [Aspergillus aculeatus] (Z28052) ORF YKL053c-a [Saccharomyces cerevisiae] ; (Z28054) ORF YKL053c-a [Saccharomyces cerevisiae]
18423	ENU02217	ANI61C9131: 580..181	54-73	389-411	NAP		g2500634	198	56	3.00E-12	52	70	
18424	ENU02218	ANI61C6203: 9440..9041	52-73	381-409	NAP		g4426615	398	73	2.00E-15	57	75	
18425	ENU02219	ANI61C5382: 1245..845	22-50	356-379	NAP		g1004217	840	127	6.00E-31	64	47	
18426	ENU02220	ANI61C1044 2:1486..1886	36-58	374-394	NAP		g2980812	86	37	0.003			
18427	ENU02221	ANI61C4350: 2224..1823	69-89	408-428	NAP		g3451060		34	0.38			(AL031326) putative protein [Arabidopsis thaliana]
18428	ENU02222	ANI61C9613: 1012..610	55-77	390-415	NAP		g71107	635	154	2.00E-42	76	63	"ribosomal protein L11.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z72870) ORF YGR085c [Saccharomyces cerevisiae]" (AC007196) unknown protein [Arabidopsis thaliana]
18429	ENU02223	ANI61C1800: 1807..2209	31-50	372-391	NAP		g4582434	207	36	1.00E-11	54	87	(AB011378) MAT-2 protein [Fusarium oxysporum]
18430	ENU02224	ANI61C7401: 1335..930	46-65	389-409	NAP		g3168589	206	59	4.00E-19	38	93	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18431	ENU02225	ANI61C6584:	35-56	380-401	NAP		g322266	1653	245	1.00E-64	82	28	(AF077355) protein phosphatase 2A regulatory B subunit [Neurospora crassa]
18432	ENU02226	ANI61C5101:	27-51	377-394	NAP		g3676762	443	105	7.00E-32	71	90	(AF087136) RS6/L7A ribosomal protein homolog [Schizosaccharomyces pombe]
18433	ENU02227	ANI61C4456:	43-62	388-411	NAP		g1082211	148	57	1.00E-10	31	3	"ankyrin 3, long form - human ; (U13616) ankyrin G [Homo sapiens]"
18434	ENU02228	ANI61C5487:	52-71	400-421	NAP		g131668	218	59	0.000000	49	85	Oleate-induced peroxisomal protein POX18 (lipid-transfer protein) (PXP-18) ; POX18 protein - yeast (Candida tropicalis) ; lipid transfer protein - imperfect fungus (Candida tropicalis) ; (X53633) POX18 [Candida tropicalis] ; (M24440) peroxisomal protein [Candida tropicalis]
18435	ENU02229	ANI61C1012	57-76	407-429	NAP		g730548	446	112	1.00E-24	76	55	"probable 60S ribosomal protein L27 ; ribosomal protein L27.e.A, cytosolic - yeast (Saccharomyces cerevisiae) ; (U10400) Rpl27p: Probable 60S ribosomal protein L27 [Saccharomyces cerevisiae]"
18436	ENU02230	ANI61C7031:	49-68	404-423	NAP		g113701	702	99	1.00E-20			Acetamidase ; amds protein - Emmericella nidulans ; (M16371) acetamidase enzyme [Emmericella nidulans]
18437	ENU02231	ANI61C1047	39-61	395-414	NAP		g3915963	1420	152	9.00E-37	60	8	ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
18438	ENU02232	ANI61C3552:	25-44	383-402	NAP		g3249567	200	52	4.00E-14	50	87	(AF047694) glutaredoxin [Vernicia fordii]
18439	ENU02233	ANI61C8615:	22-40	379-399	NAP		g2833220	579	101	1.00E-32	68	33	hypothetical 35.7 KD protein in DNL4-SLG1 intergenic region ; hypothetical protein YOR006c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UND313 [Saccharomyces cerevisiae] ; (Z74914) ORF YOR006c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18440	ENU02234	ANI61C1677: 47-67	4351..4771	396-425	NAP		g418574	520	106	8.00E-23	38	45	mitochondrial carrier protein YMC1 precursor ; (X67122) mitochondrial carrier protein [Saccharomyces cerevisiae]
18441	ENU02235	ANI61C662:8	26-47	382-406	NAP		g3850125	193	94	6.00E-19	35	27	(AL033391) hypothetical membrane protein [Candida albicans]
18442	ENU02236	ANI61C1479: 45-64	3298..2876	405-425	NAP		g627570	180	68	3.00E-11			phosphorylation regulatory protein HP-10 - human
18443	ENU02237	ANI61C3138: 24-52	896..1319	386-405	NAP		g2493096	103	57	0.000000	30	96	"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] ; (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe]
18444	ENU02238	ANI61C7858: 60-79	4680..4257	414-441	NAP		g2293314		69	2.00E-11			(Y08703) SlyA protein [Sinorhizobium meliloti]
18445	ENU02239	ANI61C394:1	09..533	71-91	434-453	NAP	g3006160	456	165	2.00E-40	51	33	(AL022070) hypothetical protein [Schizosaccharomyces pombe]
18446	ENU02240	ANI61C1107	2:909..1333	33-53	397-415	NAP	g1926396		33	1.2			"probable transporter FEN2 ; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR028c, len:512 [Saccharomyces cerevisiae] "
18447	ENU02241	ANI61C506:1	142..717	28-48	391-411	NAP	g2950478	276	79	1.00E-14	39	82	(AB005295) HY5 [Arabidopsis thaliana] ; (AB005456) HY5 [Arabidopsis thaliana]
18448	ENU02242	ANI61C3144: 22-43	1556..1130	22-43	385-406	NAP	g140479	260	102	1.00E-21	39	27	protein transport protein SEC9 ; SEC9 protein - yeast (Saccharomyces cerevisiae) ; (L34336) Sec9 [Saccharomyces cerevisiae] ; (Z72794) ORF YGR009c [Saccharomyces cerevisiae]
18449	ENU02243	ANI61S1388: 58-78	37..465	425-444	NAP		g2244709	136	46	0.0001	33	78	
18450	ENU02244	ANI61C7468: 39-58	3382..3811	405-426	NAP		g730733	368	83	9.00E-16	50	15	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18451	ENU02245	ANI61C9311	38-57	398-425	NAP		g731668	517	74	6.00E-13	31	31	SSF1 protein ; SSF1 protein - yeast (Saccharomyces cerevisiae) ; (U00061) Ssf1p [Saccharomyces cerevisiae] ; (U18113) Ssf1p [Saccharomyces cerevisiae]
18452	ENU02246	ANI61C8081	67-86	436-455	NAP		g1710760	218	56	4.00E-10	84	73	probable 40S ribosomal protein S28 (S33) ; (Z70691) ribosomal protein S28 [Schizosaccharomyces pombe] ; (AL031545) probable 40s ribosomal protein 28s [Schizosaccharomyces pombe]
18453	ENU02247	ANI61C6597	72-94	434-461	NAP		g1923256	980	169	1.00E-41	53	46	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]
18454	ENU02248	ANI61C1463	50-69	420-440	NAP		g1073534	224	72	8.00E-14	37	40	iucB protein - Escherichia coli ; (X76100) iucB [Escherichia coli]
18455	ENU02249	ANI61C1898	37-64	409-428	NAP		g2271497	316	84	4.00E-16	45	39	(AF009672) unknown [Acinetobacter sp. ADP1]
18456	ENU02250	ANI61C7592	25-44	394-416	NAP		g1176485	251	101	3.00E-21	42	96	hypothetical 16.2 KD protein in IME2-MEF2 intergenic region ; probable membrane protein YJL104w - yeast (Saccharomyces cerevisiae) ; (X85021) orf 8 [Saccharomyces cerevisiae] ; (Z49379) ORF YJL104w [Saccharomyces cerevisiae]
18457	ENU02251	ANI61C5414	24-43	381-416	NAP		g731459	168	73	1.00E-12	38	84	hypothetical 17.1 KD protein in SAH1-ME14 intergenic region ; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer044cp [Saccharomyces cerevisiae] (AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
18458	ENU02252	ANI61C9241	67-88	430-460	NAP		g4538668	98	45	0.0002	32	73	Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase) ; lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z75104) ORF YOR196c [Saccharomyces cerevisiae]
18459	ENU02253	ANI61C1281	60-79	434-453	NAP		g417254	1206	211	2.00E-54	69	35	(Z92669) hypothetical protein Rv0223c [Mycobacterium tuberculosis]
18460	ENU02254	ANI61C1100	51-74	410-444	NAP		g1871596	180	78	2.00E-14	29	29	

Seq num	Seq id	Contig	Source	5 pos	Primer	3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18461	ENU02255	ANI61C3253:	72-92	444-465	NAP			g1703247	561	221	2.00E-57	70	39	"fructose-bisphosphate aldolase ; (L42380) fructose 1,6 biphosphate-aldolase [Neurospora crassa]"	
18462	ENU02256	ANI61C426:5	72-91	441-467	NAP			g729580	697	200	5.00E-51	61	20	"1,4-alpha-glucan branching enzyme (glycogen branching enzyme) ; 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - yeast (Saccharomyces cerevisiae) ; (U18530) 1,4-alpha-glucan branching enzyme [Saccharomyces cerevisiae]"	
18463	ENU02257	ANI61C9851:	59-80	435-454	NAP			g3128287	134	63	9.00E-10	33	86	(AF010496) hypothetical protein [Rhodobacter capsulatus]	
18464	ENU02258	ANI61C2552:	63-82	440-459	NAP			g2131439	192	83	9.00E-16	34	28	hypothetical protein YDR348c - yeast (Saccharomyces cerevisiae) ; (U51032) Ydr348cp [Saccharomyces cerevisiae]	
18465	ENU02259	ANI61C8575:	23-46	400-419	NAP			g4507485		38	0.05			thrombospondin 1 ; (X14787) precursor polypeptide (AA -31 to 1139) [Homo sapiens]	
18466	ENU02260	ANI61C9787:	53-75	427-449	NAP			g1175439	258	55	3.00E-14	38	15	hypothetical 107.1 KD protein C24H6.11C in chromosome 1 ; hypothetical protein SPAC24H6.11c - fission yeast (Schizosaccharomyces pombe) ; (Z54142) hypothetical protein [Schizosaccharomyces pombe]	
18467	ENU02261	ANI61C1796:	38-58	415-435	NAP			g118513	517	155	1.00E-37	54	39	Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASA DH) ; aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - yeast (Saccharomyces cerevisiae) ; (X15649) aspartic semi-aldehyde dehydrogenase (AA 1-365) [Saccharomyces cerevisiae] ; (Z50046) Hom2p [Saccharomyces cerevisiae]	
18468	ENU02262	ANI61C9323:	62-81	425-459	NAP			g793875	274	111	3.00E-24	42	98	(Z49149) 100% identity in 135 aa ov with the CSE1 protein from S. cerevisiae. This ORF is incomplete. [Saccharomyces cerevisiae] ; HRC135 gene [Saccharomyces cerevisiae]	
18469	ENU02263	ANI61C1144	69-97	434-467	NAP			g1805251	235	87	8.00E-17	36	26	(U58946) transposase [Aspergillus awamori]	

Sequence Overview

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18470	ENU02264	ANI61C1465	22-50	399-420	NAP		g133131	116	48	0.00004	37	79	"mitochondrial 60S ribosomal protein L31 precursor (YML31) ; ribosomal protein Yml31 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X15099) precursor rpL31 protein [Saccharomyces cerevisiae] ; (Z28138) ORF YKL138c [Saccharomyces cerevisiae]"
18471	ENU02265	ANI61C6213	60-81	438-458	NAP		g1723832	368	72	3.00E-17	58	62	hypothetical 15.9 KD protein in OLE1-DUP1 intergenic region ; probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) ; (Z72576) ORF YGL054c [Saccharomyces cerevisiae]
18472	ENU02266	ANI61C3405	35-59	415-434	NAP		g1170186	200	54	0.000000	34	19	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UF1) ; probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae) ; (Z49308) ORF YJL033w [Saccharomyces cerevisiae]
18473	ENU02267	ANI61C3640	71-91	451-472	NAP		g1805251	1188	93	8.00E-19	37	26	(U58946) transposase [Aspergillus awamori]
18474	ENU02268	ANI61C7618	63-84	444-464	NAP		g1710803	714	92	1.00E-18	31	23	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRF588; EMBL:SCRTG2X:M97691; PIR:B44344:B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
18475	ENU02269	ANI61C2182	38-57	418-440	NAP		g731298	256	105	2.00E-22	37	24	probable transporter SEO1 ; probable membrane protein YAL067c - yeast (Saccharomyces cerevisiae) ; (U12980) Seo1p; putative membrane protein [Saccharomyces cerevisiae]
18476	ENU02270	ANI61C6415	65-84	449-468	NAP		g3873405		43	0.002			(U17129) unknown [Rhodococcus erythropolis]

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18477	ENU02271	ANI61C9683:	71-92	452-475	NAP		g465011	1037	261	1.00E-69	97	43	Uricase (urate oxidase) ; urate oxidase (EC 1.7.3.3) - Emericella nidulans ; (X72210) urate oxidase [Emericella nidulans]
18478	ENU02272	ANI61C3079:	27-53	413-432	NAP		g171183	383	129	1.00E-29	45	34	(M61194) CDC14 [Saccharomyces cerevisiae]
18479	ENU02273	ANI61C7257:	30-49	407-436	NAP		g1723218	294	107	2.00E-23	51	83	hypothetical 19.5 KD protein C3H8.07C in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
18480	ENU02274	ANI61C6494:	22-50	409-428	NAP		g1850768	177	88	4.00E-17	47	89	(AB001289) YNL157W homolog [Schizosaccharomyces pombe]
18481	ENU02275	ANI61C497:	31-49	414-438	NAP		g3023637	2950	213	4.00E-55	68	12	probable ATP-dependent RNA helicase HRH1 (DEAH box protein 8) ; probable RNA helicase 1 - human ; (D50487) RNA helicase (HRH1) [Homo sapiens]
18482	ENU02276	ANI61C1049	39-69	428-447	NAP		g3024439	1855	234	2.00E-61	84	35	26S PROTEASE regulatory subunit 6B homolog ; (U15601) 26S proteasome subunit [Aspergillus niger]
18483	ENU02277	ANI61C3576:	26-54	416-435	NAP		g3169068	276	56	5.00E-18	67	84	(AL023704) putative transcription factor ita small subunit [Schizosaccharomyces pombe]
18484	ENU02278	ANI61C2679:	64-84	443-473	NAP		g2132651	286	127	3.00E-29	42	25	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
18485	ENU02279	ANI61C1083	24-48	403-435	NAP		g3265058	703	165	2.00E-40	91	84	(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
18486	ENU02280	ANI61C3200:	70-91	462-481	NAP		g1078650	546	136	9.00E-42	81	61	"peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioides)"
18487	ENU02281	ANI61C5329:	61-80	451-472	NAP		g131768	605	68	3.00E-11			quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]

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18488	ENU02282	ANI61C7023:	22-49	414-434	NAP		g465702	221	83	2.00E-20	42	64	probable ribosomal protein B0303.15 in chromosome III ; ribosomal protein L11 homolog - <i>Caenorhabditis elegans</i> ; (M77697) ribosomal protein L11 [<i>Caenorhabditis elegans</i>] (AC000133) GAP04 [Emricella nidulans]
18489	ENU02283	ANI61C1355:	60-79	451-473	NAP		g1870214	839	267	4.00E-74	98	68	hypothetical protein YPR100w - yeast (<i>Saccharomyces cerevisiae</i>) ; (U32445)
18490	ENU02284	ANI61C1024:	26-47	420-440	NAP		g2132281	217	76	2.00E-20	41	94	Note that there is a 357 codon ORF contained within this ORF on the other strand [<i>Saccharomyces cerevisiae</i>] "Lysyl-TRNA synthetase, cytoplasmic (lysine--TRNA ligase) (LYSRS) ; lysine--TRNA ligase (EC 6.1.1.6) - yeast (<i>Saccharomyces cerevisiae</i>) ; (J04186) lysyl-TRNA synthetase [<i>Saccharomyces cerevisiae</i>] ; (Z68196) Krs1p [<i>Saccharomyces cerevisiae</i>] ; (Z74333) ORF YDR037w [<i>Saccharomyces cerevisiae</i>] "
18491	ENU02285	ANI61C2432:	25-44	421-440	NAP		g135139	698	241	3.00E-63	75	25	3-Isopropylmalate dehydratase (isopropylmalate isomerase) (alpha-IPM isomerase) (IPMI) ; (D63833) 3-isopropylmalate dehydratase [<i>Rhizopus niveus</i>] ; alpha-isopropylmalate isomerase [<i>Rhizopus niveus</i>] (AJ001732) r-Asp f 4 [<i>Aspergillus fumigatus</i>] (AC004077) putative urease accessory protein [<i>Arabidopsis thaliana</i>] ; (AC004481) putative urease accessory protein [<i>Arabidopsis thaliana</i>] (Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene; ...
18492	ENU02286	ANI61C1783:	52-72	445-467	NAP		g2492643	621	195	1.00E-49	66	19	
18493	ENU02287	ANI61C4724:	56-78	451-471	NAP		g3005839	485	125	2.00E-28	53	52	
18494	ENU02288	ANI61C7180:	51-70	450-469	NAP		g3128220	721	195	2.00E-49	62	55	
18495	ENU02289	ANI61C9804:	71-95	470-489	NAP		g3876465	129	39	0.0005	63	80	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18496	ENU02290	ANI61C5930:	24-59	424-443	NAP		g3646479	526	70	1.00E-11	37	91	(AJ010981) putative transposase [Talaromyces stripiatus]
18497	ENU02291	ANI61C7029:	64-84	464-483	NAP		g1169238	935	169	1.00E-41	56	30	"glutamate decarboxylase (GAD) ; glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia ; (L16797) glutamate decarboxylase [Petunia hybrida] ; (L16977) glutamate decarboxylase [Petunia hybrida]"
18498	ENU02292	ANI61C8332:	33-52	432-452	NAP		g3378330	347	131	4.00E-30	40	79	(AF079317) unknown [Sphingomonas aromaticivorans]
18499	ENU02293	ANI61C9046:	46-66	441-466	NAP		g731511	805	189	1.00E-47	63	58	hypothetical 29.7 KD protein in RSP5-PAK1 intergenic region ; hypothetical protein YER126c - yeast (Saccharomyces cerevisiae) ; (U18916) Yer126cp [Saccharomyces cerevisiae]
18500	ENU02294	ANI61C1064:	22-46	417-442	NAP		g4490325	104	58	0.000000	25	70	(AL035656) hypothetical protein [Arabidopsis thaliana]
18501	ENU02295	ANI61C7541:	42-61	443-462	NAP		g1730544	909	163	3.00E-53	73	53	Prohibitin ; prohibitin - yeast (Saccharomyces cerevisiae) ; (Z72917) ORF YGR132c [Saccharomyces cerevisiae]
18502	ENU02296	ANI61C3317:	32-51	433-452	NAP		g729318	784	106	1.00E-28	49	35	"2,2-dialkylglycine decarboxylase (DGD) ; (J05282) 2,2-dialkylglycine decarboxylase structural protein [Pseudomonas cepacia]"
18503	ENU02297	ANI61C5842:	68-99	463-488	NAP		g2909465	226	78	3.00E-14			(AL021930) hypothetical protein Ry0276 [Mycobacterium tuberculosis]
18504	ENU02298	ANI61C1473:	72-91	471-493	NAP		g3747050	380	115	1.00E-25	68	85	(AF093540) ribosomal protein L26 [Zea mays]
18505	ENU02299	ANI61C2300:	64-83	464-486	NAP		g462565	294	71	3.00E-12	32	31	Mannose-6-phosphate isomerase (phosphomannose isomerase) (PMI) (phosphohexomutase) ; mannose-6-phosphate isomerase (EC 5.3.1.8) - yeast (Candida albicans) ; (X82024) mannose-6-phosphate isomerase [Candida albicans]
18506	ENU02300	ANI61C5903:	33-54	433-455	NAP		g2132260	318	86	2.00E-16	46	37	hypothetical protein YPR040w - yeast (Saccharomyces cerevisiae) ; (Z68111) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18507	ENU02301	ANI61C7819:	23-42	425-445	NAP		g4235093	357	118	2.00E-27	43	19	(AF108944) beta-xylosidase [Aspergillus niger]
18508	ENU02302	2..466 ANI61C4975:	68-88	473-492	NAP		g1749584	415	157	6.00E-38	45	74	(D89188) unnamed protein product [Schizosaccharomyces pombe]
18509	ENU02303	2990..2524 ANI61C2732:	72-94	461-496	NAP		g1722894	465	187	3.00E-47	56	47	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase); xylosidase/arabinosidase - Bacteroides ovatus (strain V975) ; (U04957) xylosidase/arabinosidase [Bacteroides ovatus] ; xylosidase-arabinosidase [Bacteroides ovatus]"
18510	ENU02304	ANI61C1138:	22-41	428-447	NAP		g1931638	414	145	2.00E-34	42	12	[Bacteroides ovatus]" (U95973) transcription factor rush-1 alpha isolog [Arabidopsis thaliana]
18511	ENU02305	8699..9166 ANI61C2853:	34-53	436-459	NAP		g731448	70	43	0.001	31	62	hypothetical 18.3 KD protein in GAL83-YPT8 intergenic region ; hypothetical protein YER030w - yeast (Saccharomyces cerevisiae) ; (U18778) Yer030wp [Saccharomyces cerevisiae] probable stermatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emmentella nidulans]
18512	ENU02306	ANI61C3640:	67-87	459-493	NAP		g2493387	267	96	1.00E-19	38	27	(AL034353) putative acetyltransferase [Schizosaccharomyces pombe]
18513	ENU02307	ANI61C1140:	48-67	452-474	NAP		g3925776	258	108	3.00E-23	39	94	[Schizosaccharomyces pombe] (AF047464) Trp1
18514	ENU02308	668..1136 ANI61C1115	62-81	470-489	NAP		g2896142	984	85	2.00E-16	40	15	[Schizosaccharomyces pombe] (AL022299) ribosomal protein [Schizosaccharomyces pombe] ; (AJ001133) ribosomal protein L7 [Schizosaccharomyces pombe]
18515	ENU02309	5:3351..3820 ANI61C2532:	24-46	432-451	NAP		g3006140	622	220	6.00E-57	68	60	(U70852) weak similarity to neutral endopeptidases [Caenorhabditis elegans] (AF095903) unknown [Sinorhizobium meliloti]
18516	ENU02310	2369..2839 ANI61C8155:	64-84	468-492	NAP		g1572791	63	42	0.003			
18517	ENU02311	ANI61C5147:	69-100	477-498	NAP		g4580321		36	0.12			

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18518	ENU02312	ANI61C8277:	68-87	478-497	NAP		g134975	495	101	3.00E-31	52	23	Heat shock protein STI1 ; stress-induced protein STI1 - yeast (Saccharomyces cerevisiae) ; (M28486)
		1289..818											heat shock protein STI1 [Saccharomyces cerevisiae] ; (X87331)
													STI1 heat shock protein [Saccharomyces cerevisiae] ; (Z74935)
													ORF YOR027w [Saccharomyces cerevisiae]
18519	ENU02313	ANI61C4165:	22-55	432-452	NAP		g548437	364	146	7.00E-35	47	18	OSH1 protein ; SWH1 protein (version 1) - yeast (Saccharomyces cerevisiae) ; (L28920) Osh1p [Saccharomyces cerevisiae]
		5..478											(AF039376) polypeptide [Arabidopsis arenosa]
18520	ENU02314	ANI61C102:1	28-46	435-460	NAP		g2865437	214	83	1.00E-15			hypothetical 34.1 KD protein C11D3.03C in chromosome I ; (Z68166) unknown
		415..1889											[Schizosaccharomyces pombe]
18521	ENU02315	ANI61C1075	23-44	435-455	NAP		g1351700	696	137	7.00E-42	57	46	CUT8 protein ; (D31772) ORF [Schizosaccharomyces pombe] ; (Z73099) protein kinase
		2:1531..1057											[Schizosaccharomyces pombe]
18522	ENU02316	ANI61C8453:	59-81	464-491	NAP		g729231	249	108	2.00E-23	33	60	[Schizosaccharomyces pombe]
		1035..561											(Z73099) protein kinase
													[Schizosaccharomyces pombe]
18523	ENU02317	ANI61C2468:	54-74	461-486	NAP		g3702336	566	134	4.00E-31	46	45	(AC005397) putative 3-methyl-2-oxobutanoate hydroxyl-methyl-transferase [Arabidopsis thaliana]
		374..848											hypothetical zinc finger protein ZK686.4 in chromosome III ; ZK686.4
18524	ENU02318	ANI61C2736:	35-60	448-467	NAP		g466044	150	72	2.00E-12	28	37	protein - Caenorhabditis elegans ; (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]
		518..44											(Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis]
18525	ENU02319	ANI61C9206:	22-43	436-455	NAP		g2213500	133	66	2.00E-10	35	91	[Mycobacterium tuberculosis]
		3099..3574											(AL023859) putative tRNA splicing endonuclease gamma subunit [Schizosaccharomyces pombe]
18526	ENU02320	ANI61C1049	25-47	439-458	NAP		g3218411	386	98	4.00E-20	31	55	(AF079317) unknown [Sphingomonas aromaticivorans]
		4:875..1350											
18527	ENU02321	ANI61C7100:	59-78	472-493	NAP		g3378265	1233	150	3.00E-45	67	35	
		517..41											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18528	ENU02322	ANI61C1087	63-85	475-497	NAP		g1934614	269	109	1.00E-23	36	14	(U93874) cytochrome P450 102 [Bacillus subtilis] ; (Z99117) similar to cytochrome P450 / NADPH-cytochrome P450 reductase [Bacillus subtilis]
18529	ENU02323	ANI61C35:18	41-60	456-475	NAP		g2498971	502	66	2.00E-10			putative sterigmatocystin biosynthesis monoxygenase STCW ; (U34740) putative FAD-containing monoxygenase [Emmericella nidulans] "(U40939) Similar to dihydroflavonol-4-reductase (maize, petunia, tomato). [Caenorhabditis elegans] "
18530	ENU02324	ANI61C8224: 1960..1483	66-84	467-501	NAP		g1072179	109	40	0.009			(U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi] "(AF125459) contains similarity to enoyl-CoA hydratases/isomerases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans] "(Z95556) fadD35 [Mycobacterium tuberculosis] (AE001038) enoyl-CoA hydratase (fad-3) [Archaeoglobus fulgidus] probable serine/threonine-protein kinase YOL045W ; hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae) ; (Z74788) ORF YOL045w [Saccharomyces cerevisiae]
18531	ENU02325	ANI61C2974: 648..169	51-70	464-486	NAP		g1438949	424	69	1.00E-18	42	28	hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region ; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe13p [Saccharomyces cerevisiae]
18532	ENU02326	ANI61C3312: 1079..601	30-49	447-466	NAP		g4226133		34	0.00006			
18533	ENU02327	ANI61C7634: 551..72	40-68	458-477	NAP		g2113938	551	105	2.00E-30	51	25	
18534	ENU02328	ANI61C2961: 41..520	62-81	480-499	NAP		g2649635	292	124	4.00E-28	40	61	
18535	ENU02329	ANI61C9447: 1448..1928	63-82	481-501	NAP		g2499624	662	187	4.00E-47	68	12	
18536	ENU02330	ANI61C7555: 3253..3734	46-66	455-485	NAP		g3025275	375	102	2.00E-38	59	94	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18537	ENU02331	AN161C465:6	51-70	467-491	NAP		g4557817	1328	187	5.00E-47	57	30	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor (succinyl-CoA:3-oxoacid CoA-transferase) (OXCCT); (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]
18538	ENU02332	AN161C1508: 42-62		458-482	NAP		g1363392	267	113	8.00E-25	36	24	beta-glucosidase/xylosidase - Erwinia chrysanthemi
18539	ENU02333	AN161C4557: 57-84		474-497	NAP		g3451474	563	224	3.00E-58	63	25	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]
18540	ENU02334	AN161C2769: 44-63		465-484	NAP		g729079	644	134	4.00E-31	61	41	"Carboxy-cis,cis-muconate cyclase (3-carboxy-cis,cis-muconate lactonizing enzyme) (CMLE) ; carboxy-cis,cis-muconate cyclase (EC 5.5.1.5) - Neurospora crassa ; (L27538) 3-carboxy-cis,cis-muconate cyclase [Neurospora crassa] "
18541	ENU02335	AN161C323:4	22-41	444-463	NAP		g349686	238	119	1.00E-26	39	16	Manganese resistance protein; hypothetical protein YKL064w - yeast (Saccharomyces cerevisiae) ; (X75781) B969 [Saccharomyces cerevisiae] ; (Z28064) ORF YKL064w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] (AB025252) reverse transcriptase [Magnaporthe grisea] (D87924) ORF 6 [Actinomyadura hibiscus]
18542	ENU02336	AN161C1029	60-79	482-501	NAP		g4586458	163	85	2.00E-16	35	55	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
18543	ENU02337	AN161C1099	25-42	446-466	NAP		g2580447		86	2.00E-16		80	tuberos scleros protein 2 - human
18544	ENU02338	AN161C2925: 70-89		492-511	NAP		g3650394	157	75	2.00E-13	33	80	hibiscus
18545	ENU02339	AN161C349:7	23-53	445-464	NAP		g631482	273	68	4.00E-11			(AL031540) uroporphyrin methyltransferase
18546	ENU02340	AN161S1334: 61-82		484-503	NAP		g3581882	492	197	5.00E-50	59	32	[Schizosaccharomyces pombe] (AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
18547	ENU02341	AN161C9558: 65-84		488-507	NAP		g3395556	695	156	8.00E-38	50	48	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18548	ENU02342	ANI61C1812:	46-67	468-488	NAP		g2440206	412	122	2.00E-27	42	20	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
18549	ENU02343	ANI61C5509:	27-46	451-470	NAP		g140400	1065	201	3.00E-51	65	50	"hypothetical 37.2 KD protein in CHA1-PRD1 intergenic region ; hypothetical protein YCL059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL059c, len:316 [Saccharomyces cerevisiae]"
18550	ENU02344	ANI61C6930:	26-46	450-469	NAP		g2160183	316	47	0.000000	47	42	"(AC000132) Identical to A. thaliana U2 SnRNP-specific A' protein (gb X69137). ESTs gb ATTS0705, gb ATTS0339 come from this gene. [Arabidopsis thaliana]"
18551	ENU02345	ANI61C9624:	22-57	446-466	NAP		g2842472	174	83	1.00E-15	31	65	(AL021747) preg-like protein. [Schizosaccharomyces pombe]
18552	ENU02346	ANI61C1031	22-56	445-466	NAP		g731810	335	92	2.00E-18	65	94	"probable 60S ribosomal protein YIL052C ; ribosomal protein L34.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77, RL34_RAT P11250 60S ribosomal protein L34 [Saccharomyces cerevisiae]"
18553	ENU02347	ANI61C6624:	68-87	491-512	NAP		g1749648		32	2.5			"(D89220) similar to Saccharomyces cerevisiae glutathion-dependent formaldehyde dehydrogenase, SWISS-PROT Accession Number P32771 [Schizosaccharomyces pombe]"
18554	ENU02348	ANI61C2275:	69-88	493-513	NAP		g731935	374	138	2.00E-32	52	24	hypothetical 66.4 KD protein in SMC3-MRPL8 intergenic region ; hypothetical protein YJL069c - yeast (Saccharomyces cerevisiae) ; (Z34288) HRE594 [Saccharomyces cerevisiae] ; (X88851) hypothetical protein [Saccharomyces cerevisiae] ; (Z49344) ORF YJL069c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18555	ENU02349	ANI61C1036	50-69	462-495	NAP		g128478	171	93	1.00E-18	38	75	Nodulation protein L ; nodulation protein nodL - Rhizobium leguminosarum bv. viciae plasmid pRL1J1 ; (Y00548) nodL [Rhizobium leguminosarum] ; (X17557) nodL [Rhizobium leguminosarum] (Z99295) hypothetical protein [Schizosaccharomyces pombe]
18556	ENU02350	ANI61C7084	30-53	455-475	NAP		g2414606	252	81	4.00E-15			"splicing factor, arginine/serine-rich 2 ; splicing factor, arginine/serine-rich 2 (splicing factor SC35) (SC-35) (splicing component, 35 KD) (PR264 protein) ; splicing factor SC35 - human ; (M90104) splicing factor [Homo sapiens]"
18557	ENU02351	ANI61C4309	43-63	469-488	NAP		g4506899	173	53	0.000001	42	68	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18558	ENU02352	ANI61C9255	57-86	472-502	NAP		g1730714	220	86	1.00E-16	37	66	hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18559	ENU02353	ANI61C4912	50-70	473-495	NAP		g2707187	301	116	1.00E-25	67	96	hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18560	ENU02354	ANI61C9554	23-46	450-469	NAP		g2131127	277	102	2.00E-21	71	57	hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18561	ENU02355	ANI61C6119	25-46	450-471	NAP		g586387	199	87	8.00E-17	46	31	hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18562	ENU02356	ANI61C1090	35-54	463-482	NAP		g2673951	1172	247	3.00E-65	89	10	hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18563	ENU02357	ANI50C1_11	66-86	484-514	NAP		g2493561	117	2.00E-33				Cytosine deaminase (cytosine aminohydrolase); hypothetical protein YPR062w - yeast (Saccharomyces cerevisiae); (Z49219) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]; (U5193) cytosine deaminase [Saccharomyces cerevisiae]; (AF005261) cytosine deaminase [Saccharomyces cerevisiae]
18564	ENU02358	ANI61C2752:	40-59	469-488	NAP		g2493540	965	314	3.00E-85	99	22	catalase B; (U80672) catalase [Emmericella nidulans]
18565	ENU02359	ANI61C6673:	27-49	447-476	NAP		g731886	189	88	3.00E-17	32	83	"hypothetical 22.0 KD protein in FOX3-UBP7 intergenic region; probable membrane protein YIL157c - yeast (Saccharomyces cerevisiae); (Z38059) orf, len 197, CAl: 0.19 [Saccharomyces cerevisiae]"
18566	ENU02360	ANI61C1188:	42-63	471-491	NAP		g729839	985	240	4.00E-79	89	41	ketol -acid reductoisomerase precursor (acetohydroxy -acid reductoisomerase) (alpha -keto -beta -hydroxylacyl reductoisomerase); alpha -keto -beta -hydroxylacyl reductoisomerase - Neurospora crassa; (M84189) alpha -keto -beta -hydroxylacyl reductoisomerase [Neurospora crassa] (AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae] (AL031540) short chain dehydrogenase [Schizosaccharomyces pombe]
18567	ENU02361	ANI61C9579:	45-65	473-494	NAP		g2979688	923	169	1.00E-41	73	46	Probable nicotinate phosphoribosyltransferase (NAPRTASE); probable nicotinate phosphoribosyltransferase (EC 2.4.2.11) - yeast (Saccharomyces cerevisiae); (Z75117) ORF YOR209c [Saccharomyces cerevisiae]
18568	ENU02362	ANI61C6739:	37-56	467-486	NAP		g3581884	362	58	3.00E-17	46	50	Coatomer beta subunit (beta-coat protein) (beta-COP); beta-COP protein - rat; (X57228) beta COP [Rattus norvegicus]
18569	ENU02363	ANI61C8503:	71-90	500-520	NAP		g2507262	786	64	4.00E-21	42	33	
18570	ENU02364	ANI61C5428:	23-42	446-474	NAP		g116923	715	222	9.00E-58	62	17	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18571	ENU02365	AN161C4891:	22-47	455-474	NAP		g2132942	275	110	7.00E-24	36	31	[Saccharomyces cerevisiae] probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c
18572	ENU02366	AN161C8291:	70-89	500-523	NAP		g548818	283	85	1.00E-25	57	85	[Saccharomyces cerevisiae] "DNA-directed RNA polymerases I, II, and III 15 KD polypeptide (RPABC6) ; (L00597) RNA polymerase small common phosphorylated subunit [Schizosaccharomyces pombe] ; (L25592) RNA polymerase [Schizosaccharomyces pombe] ; (AL023518) dna-directed RNA polymerase [Schizosaccharomyces pombe] "
18573	ENU02367	AN161C2932:	64-83	499-518	NAP		g3850092	819	149	9.00E-50	72	32	(AL033389) argininosuccinate lyase [Schizosaccharomyces pombe]
18574	ENU02368	AN161C8403:	48-69	483-502	NAP		g1353060	439	185	1.00E-46	58	89	"3-hydroxyanthranilate 3,4-dioxygenase (3-HAO) (3-hydroxyanthranilic acid dioxygenase) (3-hydroxyanthranilate oxygenase) ; hypothetical protein YJR025c - yeast (Saccharomyces cerevisiae) ; (Z49525) ORF YJR025c [Saccharomyces cerevisiae] ; (X87297) J1550 [Saccharomyces cerevisiae] " (U60989) putative transposase [Magnaporthe grisea]
18575	ENU02369	AN161C171:	1 24-54	452-478	NAP		g1408257	305	117	6.00E-26	35	29	putative enoyl-CoA hydratase ; (Z73101) echA6 [Mycobacterium tuberculosis]
18576	ENU02370	AN161C7500:	54-73	489-509	NAP		g1706568	140	85	3.00E-16	34	64	Adaptin complex small chain homolog C3OD11.05 ; hypothetical protein SPAC30D11.05 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) adaptin complex small chain homolog [Schizosaccharomyces pombe]
18577	ENU02371	AN161C6450:	57-77	492-512	NAP		g1351658	351	131	4.00E-30	54	79	(U77369) transcription factor dMax [Drosophila melanogaster]
18578	ENU02372	AN161C7324:	28-48	455-483	NAP		g1763539	77	55	0.000000	32	67	
		3468..3965							3				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18579	ENU02373	ANI61C5863:	29-51	466-485	NAP		g1169869	267	50	0.00001			"eukaryotic translation initiation factor 3 gamma subunit (EIF-3 gamma) (EIF3 P62) (translation initiation factor EIF3, P62 subunit) (GCD10 protein); GCD10 protein - yeast (Saccharomyces cerevisiae); (X83511) Gcd10p [Saccharomyces cerevisiae]; (Z71338) ORF YNL062c [Saccharomyces cerevisiae]; (U12141) Gcd10p [Saccharomyces cerevisiae]"
18580	ENU02374	ANI61C3397:	27-47	453-483	NAP		g4206286	1929	173	5.00E-43	52	16	(AF043332) plasma membrane H(+)-ATPase [Emertella nidulans] (AL022103) hypothetical protein [Schizosaccharomyces pombe]
18581	ENU02375	ANI61C1097	24-52	461-480	NAP		g2956778	409	80	2.00E-28	51	32	cyclin-dependent kinases regulatory subunit (cell division control protein CKS1); protein kinase CDC28 complex subunit CKS1 - yeast (Saccharomyces cerevisiae); (M26033) protein kinase [Saccharomyces cerevisiae]; (X75891) CKS1 [Saccharomyces cerevisiae]; (Z36004) ORF YBR135w [Saccharomyces cerevisiae]; CKS1 gene [Saccharomyces cerevisiae]
18582	ENU02376	ANI61C3024:	67-86	503-523	NAP		g116484	296	87	8.00E-26			Isoleucyl-TRNA synthetase (isoleucine--TRNA ligase) (ILERS); (D90907) isoleucyl-tRNA synthetase [Synechocystis sp.]
18583	ENU02377	ANI61C1300:	23-44	459-480	NAP		g2501011	453	77	9.00E-14	28	16	hypothetical 30.5 KD protein C30A5.3 in chromosome III; C30A5 protein - Caenorhabditis elegans; (L10990) putative [Caenorhabditis elegans] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe]
18584	ENU02378	ANI61C6297:	58-77	497-516	NAP		g465677	196	109	1.00E-23	37	60	
18585	ENU02379	ANI61C298:3	65-85	504-523	NAP		g3192023	220	79	2.00E-14	32	33	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18586	ENU02380	ANI61C462:6	39-58	478-497	NAP		g4504799	837	127	2.00E-34	63	32	isovaleryl Coenzyme A dehydrogenase ; isovaleryl-CoA dehydrogenase precursor (IVD) ; isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human ; (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]
18587	ENU02381	ANI61C9323: 38-59		477-497	NAP		g1077341	137	50	0.000000	40	88	"hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae) ; (U17243) This gene is in the -2 reading frame. There are also overlapping ORFs in the -3 reading frame, and in the +1 reading (on the other strand). The longest ORF was arbitrarily chosen as L8003.11 [Saccharomyces cerevisiae]" (U89492) arylsulfatase [Neurospora crassa]
18588	ENU02382	ANI61C1396: 52-74		492-511	NAP		g2873363	212	108	4.00E-23	37	23	Anthranilate synthase component I ; anthranilate synthase (EC 4.1.3.27) component I - yeast (Saccharomyces cerevisiae) ; (X68327) anthranilate synthase (component 1) [Saccharomyces cerevisiae] ; (U18839) Trp2p: anthranilate synthase component I [Saccharomyces cerevisiae]
18589	ENU02383	ANI61C9179: 56-75		494-515	NAP		g731012	1431	217	5.00E-56	74	31	Anthranilate synthase component I ; anthranilate synthase (EC 4.1.3.27) component I - yeast (Saccharomyces cerevisiae) ; (X68327) anthranilate synthase (component 1) [Saccharomyces cerevisiae]
18590	ENU02384	ANI61C6172: 70-89		511-530	NAP		g3169083	279	81	6.00E-15	36	49	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18591	ENU02385	ANI61C3386: 65-86		506-525	NAP		g2495634		69	3.00E-11			hypothetical 43.3 KD protein in EVGS-GLK intergenic region ; (AE000325) putative enzyme [Escherichia coli]
18592	ENU02386	ANI61C6376: 46-65		486-506	NAP		g3219935	546	215	6.00E-56	70	92	probable peptidyl-prolyl cis-trans isomerase C57A10.03 ; (Z94864) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18593	ENU02387	ANI61C2093:	42-62	484-503	NAP		g1711596	231	91	5.00E-18	40	16	putative sulfate transporter YPR003C ; probable membrane protein YPR003c - yeast (Saccharomyces cerevisiae) ; (Z48951) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz3p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] "mitochondrial 60S ribosomal protein L30 precursor (YML30) ; ribosomal protein Yml30 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0864 [Saccharomyces cerevisiae] ; (Z71528) ORF YNL252c [Saccharomyces cerevisiae] "
18594	ENU02388	ANI61C2410:	22-43	462-484	NAP		g1710602	192	73	9.00E-13	30	57	hypothetical 47.3 KD protein C17G8.13C in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe] alpha-glucosidase (EC 3.2.1.20) MAL62 - yeast (Candida albicans) ; (M94674) alpha-glucosidase [Candida albicans] (AL023777) ma binding protein [Schizosaccharomyces pombe] 40S ribosomal protein S17 ; (M13933) ribosomal protein S17 [Crictulius griseus] ; (D25213) ribosomal protein S17 [Mus musculus] sorbitol dehydrogenase (L-iditol 2-dehydrogenase) ; L-iditol 2-dehydrogenase (EC 1.1.1.14) precursor - mouse ; (U27014) sorbitol dehydrogenase precursor [Mus musculus domesticus] hypothetical 45.7 KD protein in RPS3-PSD1 intergenic region ; hypothetical protein YNL175c - yeast (Saccharomyces cerevisiae) ; (Z71451) ORF YNL175c [Saccharomyces cerevisiae]
18595	ENU02389	ANI61C6738:	27-55	458-489	NAP		g1723485	364	152	2.00E-36	43	41	
18596	ENU02390	ANI61C8016:	59-78	488-522	NAP		g323015	1408	118	3.00E-26	37	29	
18597	ENU02391	ANI61C7458:	22-45	462-485	NAP		g3184100	327	145	2.00E-34	43	61	
18598	ENU02392	ANI61C1126:	66-89	511-530	NAP		g133820	334	92	1.00E-31	62	91	
18599	ENU02393	ANI61C4302:	34-63	477-498	NAP		g2492773	574	96	1.00E-19	37	41	
18600	ENU02394	ANI61C879:	5-46-68	491-510	NAP		g1730806	196	87	6.00E-17	31	36	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18601	ENU02395	ANI61C631:1	53-73	489-517	NAP		g2497216	123	62	0.000000	28	22	hypothetical 83.4 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR277w - yeast
		24..617								003			(Saccharomyces cerevisiae) ; (Z49704) unknown [Saccharomyces cerevisiae] (U34346) unknown [Paracoccus denitrificans]
18602	ENU02396	ANI61C8419: 34-54		470-498	NAP		g1002864	555	198	2.00E-50	53	85	(AB001288) ribosomal protein S23 homolog [Schizosaccharomyces pombe]
		3562..3056											(AB023225) KIAA1018 protein [Homo sapiens]
18603	ENU02397	ANI61C2838: 45-64		488-510	NAP		g1850766	614	144	1.00E-56	86	86	hypothetical 21.6 KD protein F37A4.2 in chromosome III ; F37A4.2 protein - Caenorhabditis elegans ; (U00032) F37A4.2 gene product [Caenorhabditis elegans]
		298..805											Aspergillopepsin II precursor (acid protease A) (protase A) ; aspergillopepsin II (EC 3.4.23.19) precursor - Aspergillus niger (var. macrosporus) ; (M68871) acid proteinase A [Aspergillus niger] ; acid protease A [Aspergillus niger macrosporus]
18604	ENU02398	ANI61C4555: 47-79		491-512	NAP		g4589686	210	100	1.00E-20	33	16	hypothetical 65.3 KD protein in pre3-SAG1 intergenic region ; hypothetical protein YJR001w - yeast
		28..535											(Saccharomyces cerevisiae) ; (X87611) ORF YJR83.4 [Saccharomyces cerevisiae] ; (Z49501) ORF YJR001w [Saccharomyces cerevisiae] "
18605	ENU02399	ANI61C7287: 45-66		492-511	NAP		g1176711	137	59	0.000000	22	89	(S80872) putative Tc1-matrin class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]
		842..750											"
18606	ENU02400	ANI50C1_10 35:32..540	40-59	480-506	NAP		g131056		237	4.00E-62	69	60	
18607	ENU02401	ANI61C5560: 53-73		501-520	NAP		g1353046	190	45	0.0003	37	22	
		638..129											
18608	ENU02402	ANI61C9150: 26-50		464-493	NAP		g1911486	388	90	4.00E-34	51	52	
		217..726											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18609	ENU02403	ANI61C8849:	72-93	520-539	NAP		g2497193	499	152	2.00E-36	44	33	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae] (AL031349) N-acetyltransferase [Schizosaccharomyces pombe] (Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAL: 0.19 [Saccharomyces cerevisiae]
18610	ENU02404	ANI61C6707:	62-81	508-530	NAP		g3451464	370	111	1.00E-35	59	88	(AF097181) tufellin-interacting protein 10 [Mus musculus]
18611	ENU02405	ANI61C5252:	65-90	505-533	NAP		g3549891	562	102	2.00E-21	46	28	(U57100) orf256; putative triose phosphate isomerase [Brucella abortus]
18612	ENU02406	ANI61C4094:	22-47	472-491	NAP		g1711561	283	110	6.00E-24	34	29	proline-specific permease (proline transport protein) ; (X79797) proline permease [Emmericella nidulans] hypothetical 15.7 KD protein in NUP85-SSC1 intergenic region ; probable membrane protein YJR044c - yeast (Saccharomyces cerevisiae) ; (Z49544) ORF YJR044c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae] (Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
18613	ENU02407	ANI61C3490:	22-45	472-491	NAP		g3851164	163	62	0.000000	23	32	
18614	ENU02408	ANI61C7357:	70-96	521-540	NAP		g4204901	215	71	7.00E-12	38	66	
18615	ENU02409	ANI61C5347:	46-65	495-516	NAP		g3929399		96	1.00E-19			
18616	ENU02410	ANI61C6339:	34-54	480-506	NAP		g1352881	180	66	2.00E-10	37	94	
18617	ENU02411	ANI61C6057:	60-79	512-533	NAP		g4150918	288	113	7.00E-28	50	70	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18618	ENU02412	ANI61C3771:	22-41	470-496	NAP		g417274	407	181	3.00E-45			mitochondrial import inner membrane translocase subunit TIM23
		875..359											(mitochondrial protein import protein 3) (mitochondrial protein import protein MAS6) (membrane import machinery protein MIM23); mitochondrial inner membrane protein MIM23 - yeast (Saccharomyces cerevisiae); (X71633) MAS6 [Saccharomyces cerevisiae]; (X74161) MIM23 [Saccharomyces cerevisiae]; (Z71632) ORF YNR017 ^w [Saccharomyces cerevisiae] (AF048992) ribonuclease H1 [Schizosaccharomyces pombe] (AL031535) transcription initiation factor tffid 60 kd subu nit [Schizosaccharomyces pombe] (X96943) Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] (AL033391) hypothetical membrane protein [Candida albicans] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] hypothetical 63.0 KD protein in PYC2-PDB1 intergenic region; probable membrane protein YBR220c - yeast (Saccharomyces cerevisiae); (Z36088) ORF YBR220c [Saccharomyces cerevisiae] (AL033396) putative alcohol phosphatidyl transferase [Candida albicans]
18625	ENU02419	ANI61C4950:	27-58	486-506	NAP		g3850144	198	75	1.00E-17	36	60	"Cleavage and polyadenylation specificity factor, 160 KD subunit (CPSF 160 KD subunit); (U37012) cleavage and polyadenylation specificity factor [Homo sapiens]"
		575..54											
18626	ENU02420	ANI61C9832:	22-57	483-502	NAP		g1706102	133	77	7.00E-14	32	11	
		82..604											
18621	ENU02415	ANI61C1050	36-55	491-512	NAP		g1524045	459	132	1.00E-30	42	38	
		5:5005..5523											
18622	ENU02416	ANI61C3996:	23-44	480-499	NAP		g3850125	542	115	2.00E-25	41	32	
		6129..5611											
18623	ENU02417	ANI61C8551:	32-54	489-508	NAP		g3549879	436	88	1.00E-22	40	28	
		3297..2779											
18624	ENU02418	ANI61C1086	60-79	520-539	NAP		g586338	913	126	9.00E-29	43	26	
		9:3385..3906											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18627	ENU02421	ANI61C6709:	23-46	472-503	NAP		g2500360	157	64	6.00E-15	38	60	60S ribosomal protein L14; ribosomal protein L14 - rat; (X94242) ribosomal protein L14 [Rattus norvegicus] hypothetical 55.1 KD protein in TRX1-RTA1 intergenic region; hypothetical protein YGR211w - yeast (Saccharomyces cerevisiae); (Z72996) ORF YGR211w [Saccharomyces cerevisiae]; (AF019769) zinc finger protein [Saccharomyces cerevisiae] (U81509) urease [Coccidioides immitis] (U68040) polyketide synthase [Cochliobolus heterostrophus] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (X96943) Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] "(AE000952) methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit (mmdC) [Archaeoglobus fulgidus]" (AE000855) endonuclease III [Methanobacterium thermoautotrophicum] "CAT5 protein (ubiquinone biosynthesis protein COQ7); CAT5 protein - yeast (Saccharomyces cerevisiae); (X82930) CAT5 [Saccharomyces cerevisiae]; (X90518) putative [Saccharomyces cerevisiae]; (X94335) YOR3284c [Saccharomyces cerevisiae]; (Z75033) ORF YOR125c [Saccharomyces cerevisiae]; (S81938) COQ7 [Saccharomyces cerevisiae, Peptide, 272 aa] [Saccharomyces cerevisiae]" (AE000352) putative transport protein [Escherichia coli]
18628	ENU02422	ANI61C5035:	40-60	499-521	NAP		g1723738	548	164	4.00E-40	43	34	
18629	ENU02423	ANI61C1400:	36-55	497-517	NAP		g2580518	3042	136	5.00E-39	66	15	
18630	ENU02424	ANI61C1002	29-48	489-510	NAP		g1546072	1185	68	5.00E-11	29	6	
18631	ENU02425	ANI61C1767:	53-74	510-534	NAP		g1438947	697	272	1.00E-72	67	35	
18632	ENU02426	ANI61C1570:	22-53	484-503	NAP		g1524045	385	66	8.00E-17	42	33	
18633	ENU02427	ANI61C2430:	22-53	474-504	NAP		g2648307	127	59	0.000000	32	99	
18634	ENU02428	ANI61C8832:	54-73	516-536	NAP		g2621854	84	52	0.000002	29	52	
18635	ENU02429	ANI61C303:9	28-48	491-510	NAP		g1168783	381	118	1.00E-34			
18636	ENU02430	ANI61C3361:	34-53	498-517	NAP		g1789036	257	61	0.000000	33	56	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18637	ENU02431	ANI61C9483:	32-51	484-515	NAP		g133887	234	94	8.00E-19	54	96	"mitochondrial ribosomal protein S24 ; ribosomal protein S16, mitochondrial - Neurospora crassa ; (X06360) cyt-21 [Neurospora crassa] ; (J03533) ribosomal protein S-24 [Neurospora crassa]"
18638	ENU02432	ANI61C2362:	48-67	510-531	NAP		g699196	316	104	4.00E-22			(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
18639	ENU02433	ANI61C9152:	63-82	525-546	NAP		g133336	145	53	1.00E-12			DNA-directed RNA polymerase II 32 KD polypeptide (B32) ; DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB4 - yeast (Saccharomyces cerevisiae) ; (X58099) RPB4 [Saccharomyces cerevisiae] ; (M27253) RNA polymerase II subunit RPB4 [Saccharomyces cerevisiae] ; (X87371) RNA polymerase II subunit 4 [Saccharomyces cerevisiae] ; (Z49415) ORF YJL140w [Saccharomyces cerevisiae]
18640	ENU02434	ANI61C2487:	61-82	525-544	NAP		g2983039	285	132	2.00E-30	41	30	(AE000686) proline-tRNA synthetase [Aquifex aeolicus]
18641	ENU02435	ANI50C3497	28-47	492-512	NAP		g462739		109	2.00E-23	38	26	NPL4 protein ; NPL4 protein - yeast (Saccharomyces cerevisiae) ; (X72224) NPL4 [Saccharomyces cerevisiae] ; (X74437) open reading frame YBR12.31 [Saccharomyces cerevisiae] ; (Z36039) ORF YBR170c [Saccharomyces cerevisiae]
18642	ENU02436	ANI61C383:5	61-80	526-545	NAP		g399112	199	91	6.00E-18	33	16	beta-galactosidase (lactase) ; beta-galactosidase (EC 3.2.1.23) - yeast (Kluyveromyces marxianus var. lactis) ; (M84410) beta-D-galactosidase [Kluyveromyces lactis]
18643	ENU02437	ANI61C6528:	28-49	488-513	NAP		g3880440	190	69	2.00E-11	32	96	(Z82062) cDNA EST yk415c12.5 comes from this gene [Caenorhabditis elegans]

Sequence Database

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18644	ENU02438	ANI61C6109:	23-43	482-509	NAP		g3123100	351	99	6.00E-33	50	99	"hypothetical 15.9 KD protein C4A8.02C in chromosome I ; (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ_ECOLI, P32698, hypothetical 15.7 kd protein, (138aa), fast a scores, opt:403, E0: 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe]"
		1824..1296											
18645	ENU02439	ANI61C5925:	38-57	504-524	NAP		g543649	245	86	2.00E-21	53	91	hypothetical protein 133 - Rhodococcus erythropolis (fragment) ; (D14454) P47K protein [Rhodococcus erythropolis] ; ORF P47K [Rhodococcus erythropolis]
		1611..1083											
18646	ENU02440	ANI61C7364:	22-50	490-509	NAP		g585656	249	86	2.00E-16			Pyridoxamine 5'-phosphate oxidase (PNP/PMF oxidase) ; pyridoxamine-phosphate oxidase (EC 1.4.3.5) - yeast (Saccharomyces cerevisiae) ; (X76992) pyridoxamine-phosphate oxidase [Saccharomyces cerevisiae] ; (X76078) YBR0321 [Saccharomyces cerevisiae] ; (Z35904) ORF YBR035c [Saccharomyces cerevisiae] ; ORF YBR0321 [Saccharomyces cerevisiae] (AL023554) zinc finger protein [Schizosaccharomyces pombe] (AF034090) MAPKK kinase [Neurospora crassa]
		2988..3517											
18647	ENU02441	ANI61C137:	1 22-42	484-510	NAP		g3133097	114	48	0.00005	30	35	SAP1 protein ; hypothetical protein YER047c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer047cp [Saccharomyces cerevisiae] (AJ000084) putative acetyl transferase [Proteus mirabilis]
		940..1410											
18648	ENU02442	ANI61C1321:	23-47	490-511	NAP		g2654103	751	250	4.00E-66	67	25	sterigmatocystin 7-O-methyltransferase precursor ; (L25836) O-methyltransferase [Aspergillus flavus]
		82..612											
18649	ENU02443	ANI61C7991:	27-55	496-516	NAP		g731461	793	138	4.00E-41	57	19	hypothetical 59.3 KD protein C17C9.16C in chromosome I ; (Z73099) hypothetical protein [Schizosaccharomyces pombe]
		555..23											
18650	ENU02444	ANI61C8177:	61-81	531-550	NAP		g3395518	124	60	0.000000	28	88	
		4238..3705											
18651	ENU02445	ANI61C3627:	56-77	525-546	NAP		g2498701	127	63	0.000000	33	37	
		3038..3570											
18652	ENU02446	ANI61C8243:	41-62	507-531	NAP		g1723574	549	74	8.00E-13	33	33	
		920..388											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18653	ENU02447	ANI61C8767: 28-48	2767..2233	501-520	NAP	g3334833	66	2.00E-10					(AJ007932) ketoreductase [Streptomyces argillaceus]
18654	ENU02448	ANI61C4182: 35-54	1253..1788	497-528	NAP	g2330829	826	182	2.00E-45	52	11		(Z98530) hypothetical protein [Schizosaccharomyces pombe]
18655	ENU02449	ANI61C7614: 28-47	13..544	502-521	NAP	g118066	259	104	5.00E-22	35	32		cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
18656	ENU02450	ANI61C6208: 32-51	618..83	503-525	NAP	g1350839	257	114	5.00E-25	52	60		RIBOSE 5-phosphate isomerase (phosphoRIBOisomerase) ; (L35034) ribose 5-phosphate isomerase [Mus musculus]
18657	ENU02451	ANI61C8852: 60-79	1907..1371	530-554	NAP	g2832629	60	0.000000	01				(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]
18658	ENU02452	ANI61C1084: 39-60	3503..2966	513-534	NAP	g2131743	361	129	1.00E-29	52	85		hypothetical protein YLR009w - yeast (Saccharomyces cerevisiae) ; (Z73181) ORF YLR009w [Saccharomyces cerevisiae]
18659	ENU02453	ANI61C1271: 44-63	116..653	517-539	NAP	g1729996	667	228	2.00E-59	62	60		TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
18660	ENU02454	ANI61C1190: 25-44	4015..3476	502-522	NAP	g999873	616	106	9.00E-23	49	51		Lipase (E.C.3.1.1.3) [Triacylglycerol Acylhydrolase]
18661	ENU02455	ANI61C1070: 29-49	6:4348..4887	506-526	NAP	g1351617	728	138	4.00E-32	45	31		hypothetical 62.6 KD protein C29E6.02 in chromosome I ; (Z66525) unknown [Schizosaccharomyces pombe]
18662	ENU02456	ANI61C2194: 46-72	25..564	524-543	NAP	g1705519	153	68	3.00E-12	31	31		Benzaldehyde lyase (benzoin aldolase) (BL) (BZL) ; (U04048) benzaldehyde lyase [Pseudomonas fluorescens]
18663	ENU02457	ANI61C3754: 24-47	1807..1268	496-521	NAP	g2498971	574	110	8.00E-24	32	36		putative sterigmatoctin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
18664	ENU02458	ANI61C9710: 22-44	559..1099	487-520	NAP	g3192040	147	48	0.00004	28	98		(AL023796) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18665	ENU02459	ANI61C7140:	29-48	54..594	505-527	NAP		g4505495	239	104	6.00E-22			8-oxoguanine DNA glycosylase ; (Y11731) DNA glycosylase/AP lyase [Homo sapiens] ; (Y11838) 8-oxoguanine DNA glycosylase homolog 1 [Homo sapiens] ; (AB000410) hOGG1 [Homo sapiens] ; (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo sapiens] ; (U88527) 8-hydroxyguanine glycosylase [Homo sapiens]
18666	ENU02460	ANI61C3964:	40-59	3178..2638	515-538	NAP		g2492754	582	76	1.00E-18	42	57	sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans]
18667	ENU02461	ANI61C2208:	61-80	1388..848	540-559	NAP		g1730712	372	78	4.00E-14	29	35	hypothetical 56.2 KD protein in UME3-HDA1 intergenic region ; hypothetical protein YNL022c - yeast (Saccharomyces cerevisiae) ; (Z71298) ORF YNL022c [Saccharomyces cerevisiae]
18668	ENU02462	ANI61C6637:	36-57	72..613	512-535	NAP		g1722203	276	101	5.00E-21	41	17	(M29688) DNA mismatch repair protein [Saccharomyces cerevisiae]
18669	ENU02463	ANI61C9213:	48-71	1179..638	523-547	NAP		g3642873	690	257	3.00E-68	66	85	(AF026523) manganese superoxide dismutase; Mn-SOD [Penicillium chrysogenum] ; (AF026790) manganese superoxide dismutase [Penicillium chrysogenum]
18670	ENU02464	ANI61C8484:	52-71	726..1267	532-551	NAP		g1470090	92	50	0.00001	27	38	(U62028) negative acting factor [Fusarium solani f. sp. pisi]

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18671	ENU02465	ANI61C1889:	41-61	516-540	NAP		g1346554	42	0.000000	1			probable myosin regulatory light chain ; (Z46793) similar to myosin regulatory light chain 2; cDNA EST EMBL:TO1273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h1.3 comes from this gene; cDN...; (Z34801) similar to myosin regulatory light chain 2; cDNA EST EMBL:TO1273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h1.3 comes from this gene; cDN...
18672	ENU02466	ANI61C7908:	50-69	526-550	NAP		g3929362	397	97	3.00E-24	41	29	Pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]
18673	ENU02467	ANI61C2918:	49-68	526-550	NAP		g118572	180	59	0.000000	007		Granaticin polyketide synthase putative ketoacyl reductase 2 (ORF6) ; granaticin-producing polyketide synthase chain 6 - Streptomyces violaceoruber ; (X16144) ketoacyl reductase (AA 1-289) [Streptomyces violaceoruber] ; (X16300) ORF 6 (AA 1-249) [Streptomyces violaceoruber] ; (AJ011500) gra-orf6 [Streptomyces violaceoruber]
18674	ENU02468	ANI61C6924:	34-53	516-535	NAP		g4503609	375	50	3.00E-19			"electron-transfer-flavoprotein, beta polypeptide ; electron transfer flavoprotein beta-subunit (beta-ETF) ; electron transfer flavoprotein beta chain - human ; Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution ; (X71129) electron transfer flavoprotein beta subunit [Homo sapiens]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18675	ENU02469	ANI61C1036	37-56	521-540	NAP		g3560474	209	80	2.00E-19	32	51	(U81312) S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
		7:900..1447											
18676	ENU02470	ANI61C1112	72-93	556-575	NAP		g450864	536	198	2.00E-50	54	32	(L27993) alkaline phosphatase [Neurospora crassa]
		2:63..608											"hypothetical oxidoreductase in LYS1-HYR1 intergenic region ; probable
18677	ENU02471	ANI61C4008	32-56	512-535	NAP		g731922	414	130	8.00E-30	43	64	membrane protein YIR035c - yeast (Saccharomyces cerevisiae) ; (Z38061) orf, len 254, CAl: 0.24, 52.1% similar to orf complement(33925..34716), similar to DH11 human P28845 corticosteroid 11-beta-dehydrogenase [Saccharomyces cerevisiae] "
		89..634											"ADP,ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT) ; (Z49974) adenine nucleotide carrier
18678	ENU02472	ANI61C2566	53-77	533-557	NAP		g2497980	772	203	6.00E-75	83	51	[Schizosaccharomyces pombe] ; (AL023634) adp/atp translocase [Schizosaccharomyces pombe] "
		547..1											hypothetical 17.2 KD protein C3H1.03 in chromosome I ; (Z68144) hypothetical protein
18679	ENU02473	ANI61C3960	23-51	503-529	NAP		g1351687	108	49	0.00002	28	98	[Schizosaccharomyces pombe] alpha-glucosidase precursor (maltase) ; (D45356) alpha-glucosidase [Aspergillus niger]
		1663..2211											(AL022002) hypothetical protein Rv1672c [Mycobacterium tuberculosis] eukaryotic translation initiation factor 2 beta subunit (EIF-2-beta) ; translation initiation factor eIF-2 beta chain - yeast (Saccharomyces cerevisiae) ; (M21813) translation initiation factor eIF2 beta-subunit [Saccharomyces cerevisiae] ; (Z67751) SUI3 [Saccharomyces cerevisiae] ; (Z73594) ORF YPL237w [Saccharomyces cerevisiae] (AL022071) fructosyl amine [Schizosaccharomyces pombe]
18680	ENU02474	ANI61C8321	50-76	536-556	NAP		g3023267	658	212	6.00E-65	66	18	
		87..635											
18681	ENU02475	ANI61C6620	43-64	531-551	NAP		g2916970	194	33	1.3			
		826..1376											
18682	ENU02476	ANI61C3952	72-91	560-580	NAP		g124205	193	62	0.000000			
		556..331											
18683	ENU02477	ANI61C5937	31-53	520-539	NAP		g2950465	215	76	3.00E-18	38	39	
		1283..733											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18684	ENU02478	ANI61C8339:	25-44	512-533	NAP		g1730644	243	100	1.00E-20	28	27	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae] (AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
18685	ENU02479	ANI61C1708:	22-51	509-530	NAP		g3810866	60	0.000000	01			"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]
18686	ENU02480	ANI61C1532:	39-58	518-548	NAP		g461623	823	146	1.00E-34	53	17	"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]
18687	ENU02481	ANI61C9801:	23-45	513-532	NAP		g4106673	413	153	6.00E-37	54	38	[Schizosaccharomyces pombe] Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans] (AL023590) amino acid permease [Schizosaccharomyces pombe]
18688	ENU02482	ANI61C1130:	65-84	555-574	NAP		g133264	313	66	4.00E-14	59	81	hypothetical 61.8 KD peptide in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae] (X76302) nucleic acid binding protein [Homo sapiens] (AF029913) unknown [Cochliobolus heterostrophus] ; (AF027687) unknown [Cochliobolus heterostrophus]
18689	ENU02483	ANI61C1027:	69-88	560-579	NAP		g3136040	706	142	2.00E-33	39	34	hypothetical 27.3 KD protein in REF2-CBS2 intergenic region ; hypothetical protein YDR196c - yeast (Saccharomyces cerevisiae) ; (Z48784) unknown [Saccharomyces cerevisiae]
18690	ENU02484	ANI61C9766:	47-66	535-557	NAP		g1175977	465	136	1.00E-31	37	34	hypothetical 61.8 KD peptide in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae] (X76302) nucleic acid binding protein [Homo sapiens] (AF029913) unknown [Cochliobolus heterostrophus] ; (AF027687) unknown [Cochliobolus heterostrophus]
18691	ENU02485	ANI61C8436:	37-64	519-547	NAP		g431953	194	39	0.023	36	80	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae] (AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
18692	ENU02486	ANI61C6527:	24-53	516-535	NAP		g2583216	389	152	1.00E-36	47	82	"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]
18693	ENU02487	ANI61C1190:	47-66	540-559	NAP		g2833198	332	128	3.00E-29	52	67	"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18694	ENU02488	ANI61C3516:	29-48	522-541	NAP		g3687456	303	127	8.00E-30	44	97	(AL031798) hypothetical protein [Schizosaccharomyces pombe]
18695	ENU02489	ANI50C392_	22-50	515-535	NAP		g2144770		209	1.00E-53	65	59	"acidic ribosomal protein P0,e, cytosolic - yeast (Saccharomyces cerevisiae) ; (M37326) ribosomal protein L10e [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (U19028) Rpl10ep [Saccharomyces cerevisiae] "
18696	ENU02490	ANI61C7084:	24-43	518-537	NAP		g2414606	252	104	6.00E-22	46	94	(Z99295) hypothetical protein [Schizosaccharomyces pombe]
18697	ENU02491	ANI61C7236:	27-48	522-541	NAP		g548420	373	84	6.00E-31	54	90	mitochondrial import receptor subunit TOM20 (mitochondrial 20 K D outer membrane protein) (MOM19 protein) (translocase of outer membrane 20 K D subunit) ; (M80528) mitochondrial outer membrane protein 19 [Neurospora crassa]
18698	ENU02492	ANI61C7717:	68-87	550-583	NAP		g4456822	352	141	5.00E-33	42	100	(AL035548) hypothetical oligoribonuclease [Schizosaccharomyces pombe]
18699	ENU02493	ANI61C4632:	68-87	564-583	NAP		g2351250	325	89	3.00E-17	43	25	(U23425) ropy-2 [Neurospora crassa]
18700	ENU02494	ANI61C1096	71-97	554-587	NAP		g2498530	198	100	9.00E-21	40	56	mitochondrial inheritance component MDm12 ; (U64674) mitochondrial inheritance component Mdm12p [Schizosaccharomyces pombe]
18701	ENU02495	ANI61C1484:	50-83	546-567	NAP		g2708305	766	154	2.00E-43	47	35	(AF016369) U4/U6 small nuclear ribonucleoprotein hPrp4 [Homo sapiens]
18702	ENU02496	ANI61C3181:	42-65	537-559	NAP		g1054845	1435	159	2.00E-57	62	39	(X92680) allelic to VPS4 [Saccharomyces cerevisiae]
18703	ENU02497	ANI61C9072:	72-94	569-589	NAP		g1764098	178	31	0.000003	37	20	(U81794) putative permease [Uromyces fabae]
18704	ENU02498	ANI61C2133:	66-88	562-584	NAP		g1877327		60	0.000000			(Z92771) hypothetical protein Rv3272 [Mycobacterium tuberculosis]
		927..1487									01		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18705	ENU02499	ANI61C884:7	29-49	528-547	NAP		g2500493	324	98	3.00E-27	66	97	putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae) ; (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
18706	ENU02500	ANI61C8267: 774..213	45-66	543-564	NAP		g481285	342	130	9.00E-30	38	26	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger ; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger] ; NADPH cytochrome P450 reductase [Aspergillus niger] (AJ223998) PCZA361.9 [Amycolatopsis orientalis] (AL023592) putative phosphatidylinositol- glycan-class c protein [Schizosaccharomyces pombe] myoSIN-2 isoform ; myosin myo2 - yeast (Saccharomyces cerevisiae) ; (M35532) myosin I isoform (myo2) [Saccharomyces cerevisiae] ; (Z75234) ORF YOR326w [Saccharomyces cerevisiae]
18707	ENU02501	ANI61C8414: 2231..2792	48-67	548-567	NAP		g2894160	229	71	4.00E-18	38	59	Deoxyribose-phosphate aldolase (phosphodeoxyribosaldolase) (deoxyribosaldolase) ; deoxyribose aldolase (deoC) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32791) deoxyribose-phosphate aldolase (deoC) [Haemophilus influenzae Rd]
18708	ENU02502	ANI61C9773: 22-44	22-44	523-542	NAP		g3136049	270	129	2.00E-29	40	56	hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae) ; (U55021) O3615p [Saccharomyces cerevisiae] ; (Z75078) ORF YOR171c [Saccharomyces cerevisiae] (AF027979) carnitine acetyl transferase [Magnaporthe grisea] (Z97210) hypothetical protein [Schizosaccharomyces pombe]
18709	ENU02503	ANI61C8325: 3431..2869	54-75	553-574	NAP		g127736	322	62	4.00E-18	43	9	
18710	ENU02504	ANI61C3214: 2968..2406	56-76	557-576	NAP		g1169268	326	108	2.00E-23	43	81	
18711	ENU02505	ANI61C1078 7:2457..1894	44-65	546-565	NAP		g2132075	519	117	5.00E-26	30	30	
18712	ENU02506	ANI61C8080: 10..573	31-59	533-552	NAP		g2688966	991	259	1.00E-68	64	30	
18713	ENU02507	ANI61C1189: 9840..9276	41-60	539-563	NAP		g2239219	194	46	0.000000	34	79	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18714	ENJU02508	AN161C6833: 52-71	52-71	553-574	NAP		g3041696	845	214	4.00E-55	63	60	"Acetolactate synthase small subunit precursor (AHAS) (acetohydroxy-acid synthase small subunit) (ALS) ; (X59720) YCL009c, len:309 [Saccharomyces cerevisiae]"
18715	ENJU02509	AN161C7768: 72-91	72-91	575-594	NAP		g3130049	632	142	4.00E-51	69	52	(AL023518) Tal1p transaldolase [Schizosaccharomyces pombe]
18716	ENJU02510	AN161C5105: 70-91	70-91	573-593	NAP		g1762781	477	198	2.00E-50	51	18	(U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana]
18717	ENJU02511	AN161C6332: 69-96	69-96	573-592	NAP		g1175934	861	61	3.00E-14	34	15	hypothetical 117.8 KD protein in STE2-FRS2 intergenic region ; probable membrane protein YFL025c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL025C [Saccharomyces cerevisiae]
18718	ENJU02512	AN161C9824: 65-90	65-90	570-589	NAP		g2370595	1364	167	6.00E-41	60	19	(AJ001414) GTPase activating protein [Yarrowia lipolytica]
18719	ENJU02513	AN161C1043: 47-67	47-67	552-571	NAP		g2492633	987	207	4.00E-53	56	44	probable glutaryl-CoA dehydrogenase precursor (GCD) ; (Z66513) similar to acyl-CoA dehydrogenase; cDNA EST EMBL:D70283 comes from this gene; cDNA EST EMBL:D66714 comes from this gene; cDNA EST EMBL:D70641 comes from this gene; cDNA EST EMBL:D70573 comes from this gene; cDNA EST EM...
18720	ENJU02514	AN161C4425: 27-47	27-47	532-551	NAP		g3868940	433	84	6.00E-25	42	40	(AB015054) Alg2 [Rhizomucor pusillus] ; (AB015055) Alg2 [Rhizomucor pusillus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18721	ENU02515	AN161C1211	35-65	541-560	NAP		g4506439	556	129	4.00E-47			retinoblastoma-binding protein 7 ; histone acetyltransferase type B subunit 2 (retinoblastoma binding protein P46) (retinoblastoma-binding protein 7) ; retinoblastoma-binding protein RbAp46 - human ; (X72841) IEF 7442 [Homo sapiens] ; (U35143) retinoblastoma-binding protein RbAp46 [Homo sapiens] ; (AF090306) retinoblastoma binding protein [Rattus norvegicus] ; retinoblastoma-binding protein [Homo sapiens]
18722	ENU02516	AN161C4036	50-69	559-576	NAP		g729327	166	41	0.0006	25	47	glucose 1-dehydrogenase IV (GLCDH-IV) ; glucose 1-dehydrogenase (EC 1.1.1.47) - Bacillus megaterium ; (D10626) glucose dehydrogenase [Bacillus megaterium]
18723	ENU02517	AN161C3865	60-81	566-586	NAP		g4587575	251	109	1.00E-23	39	59	"(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb AA585719, gb AA728503 and gb T22272 come from this gene. [Arabidopsis thaliana]" (U81827) 8 kDa cytoplasmic dynein light chain [Emeticella nidulans] (D85924) myosin [Mus musculus]
18724	ENU02518	AN161C6288	48-68	551-574	NAP		g4099025	316	62	2.00E-16	84	97	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
18725	ENU02519	AN161C7365	46-65	549-572	NAP		g1945080	48	0.00005				[Schizosaccharomyces pombe]
18726	ENU02520	AN161C1062	30-51	538-558	NAP		g2842503	301	80	5.00E-27	43	75	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
18727	ENU02521	AN161C6548	44-63	553-572	NAP		g729712	1373	225	2.00E-58			casein kinase I homolog HHP1 ; hhp1 protein - fission yeast (Schizosaccharomyces pombe) ; casein kinase-I homolog hhp1 - Yeast (Schizosaccharomyces pombe) ; (X78871) Hhp1 protein kinase [Schizosaccharomyces pombe] ; (U10863) casein kinase-I [Schizosaccharomyces pombe] ; (AL031261) casein kinase i homologue [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18728	ENU02522	AN161C1038	43-68	553-572	NAP		g2842501	81	7.00E-15				(AL021748) putative quinine oxidoreductase [Schizosaccharomyces pombe]
18729	ENU02523	AN161C7455: 9	23-42	533-552	NAP		g4506235	165	69	2.00E-11	36	73	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 ; 26S proteasome regulatory subunit P27 ; (AB003177) proteasome subunit p27 [Homo sapiens]"
18730	ENU02524	AN161C1020	61-80	561-591	NAP		g3929392	633	201	4.00E-62	82	57	vacuolar ATP synthase subunit D (V-ATPase D subunit) ; (AF053230) vacuolar ATPase subunit D [Neurospora crassa]
18731	ENU02525	AN150C1_10	26-46	538-557	NAP		g416837		84	6.00E-16	34	40	cytochrome P450-TERP (cytochrome P450 108) ; cytochrome P450terp - Pseudomonas sp ; (M91440) P450terp [Pseudomonas sp.]
18732	ENU02526	AN161C8486: 319..894	42-64	554-574	NAP		g3560214	806	207	5.00E-53	67	30	(AL031536) tma splicing protein [Schizosaccharomyces pombe]
18733	ENU02527	AN161C9210: 378..952	62-83	572-594	NAP		g126192	739	106	2.00E-22			2-isopropylmalate synthase (alpha-isopropylmalate synthase) (alpha-IPM synthetase) ; 2-isopropylmalate synthase (EC 4.1.3.12) - yeast (Saccharomyces cerevisiae) ; (M12893) alpha-isopropylmalate synthase (EC 4.1.3.12) long form [Saccharomyces cerevisiae] ; (Z50161) 2-isopropylmalate Synthase [Saccharomyces cerevisiae] ; (Z71380) ORF YNL104c [Saccharomyces cerevisiae]
18734	ENU02528	AN161C6322: 2524..1949	55-73	569-588	NAP		g3873823	169	59	0.000000	39	72	(Z73422) predicted using Genefinder [Caenorhabditis elegans]
18735	ENU02529	AN161C5608: 1306..731	71-91	581-604	NAP		g1173624	114	65	3.00E-10	27	36	(U34744) cytochrome P-450 [Phlaenopsis sp. "hybrid SM9108"]
18736	ENU02530	AN161C8209: 1438..2014	43-62	557-577	NAP		g3114281	437	186	9.00E-47	46	84	"Chain M, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 1, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18737	ENU02531	AN161C1107	22-44	536-556	NAP		g1730718	297	140	8.00E-33	43	31	probable mannosyltransferase KTR5 ; probable membrane protein YNL029c - yeast (Saccharomyces cerevisiae) ; (Z71305) ORF YNL029c [Saccharomyces cerevisiae]
18738	ENU02532	AN161C1137	56-75	563-591	NAP		g731738	596	122	3.00E-27	37	12	DNA replication helicase DNA2 ; probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae) ; (U00027) Dna2p: DNA replication helicase [Saccharomyces cerevisiae]
18739	ENU02533	AN161C2857	24-59	533-559	NAP		g2130462	205	100	7.00E-21	36	30	poly A polymerase (EC 2.7.7.-) - fission yeast (Schizosaccharomyces pombe) ; (X79705) polymerase [Schizosaccharomyces pombe] ; (AL035216) poly A polymerase [Schizosaccharomyces pombe]
18740	ENU02534	AN161C3020	34-54	543-569	NAP		g133341	289	91	6.00E-18	51	96	DNA-directed RNA polymerase II 14.2 KD polypeptide (B12.6) ; DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB9 - yeast (Saccharomyces cerevisiae) ; (M73060) RNA polymerase II subunit RPB9 [Saccharomyces cerevisiae] ; (Z72592) ORF YGL070c [Saccharomyces cerevisiae]
18741	ENU02535	AN161C2411	53-72	570-589	NAP		g1351662	660	205	2.00E-52	48	30	hypothetical 74.4 KD protein C30D11.09 in chromosome I ; hypothetical protein SPAC30D11.09 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe]
18742	ENU02536	AN161C9242	36-57	553-573	NAP		g2633748	305	94	6.00E-19	38	76	(Z99111) similar to glucose 1-dehydrogenase [Bacillus subtilis] (AF008220) yteR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18743	ENU02537	AN161C8858	23-45	536-560	NAP		g2293194	303	99	3.00E-20			

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Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18744	ENU02538	ANI61C508:2	28-56	545-565	NAP		g1077558	33	0.005				hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae) ; (X84162) unknown [Saccharomyces cerevisiae] ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74359) ORF YDR063w [Saccharomyces cerevisiae] (Z99753) hypothetical protein [Schizosaccharomyces pombe]
18745	ENU02539	ANI61C7498: 22-52		540-559	NAP		g2465148	135	75	4.00E-13	32	45	[Schizosaccharomyces pombe]
18746	ENU02540	ANI61C464:7	45-73	556-582	NAP		g1708006	215	105	2.00E-22	37	95	probable glucokinase (gluconate kinase) ; (Z69727) probable glucokinase [Schizosaccharomyces pombe]
18747	ENU02541	ANI61C1052	23-49	534-561	NAP		g3873699	160	94	1.00E-18	44	85	(Z73102) predicted using Genefinder; Similarity to viral non-structural proteins (SW:POLN_EEVV3); cDNA EST EMBL:D65747 comes from this gene; cDNA EST EMBL:D69295 comes from this gene; cDNA EST EMBL:C10380 comes from this gene;
18748	ENU02542	ANI61C7840: 38-57		557-577	NAP		g1705999	291	123	1.00E-27	33	37	Coatmer delta subunit (delta-coat protein) (delta-COP) ; (X94265) coat protein delta-cop [Bos primigenius] (Z99168) putative heat shock transcription factor [Schizosaccharomyces pombe]
18749	ENU02543	ANI61C2563: 65-85		584-604	NAP		g3327019	230	89	1.00E-18	41	28	"fructose-bisphosphate aldolase ; (Y11135) fructose-1,6-bisphosphate aldolase type II [Bacillus stearothermophilus]" probable calcium-binding protein ALG-2 (PMP41) (ALG-257) ; (U49112) ALG-2 [Mus musculus]
18750	ENU02544	ANI61C9392: 47-66		555-586	NAP		g4033506	206	86	2.00E-16	35	60	sterigmatocystin biosynthesis regulatory protein ; sterigmatocystin synthesis transcriptional regulator aflR - Emericella nidulans ; (U34740) pathway specific transcription factor [Emericella nidulans]
18751	ENU02545	ANI61C9841: 37-56		544-576	NAP		g2506252	340	145	2.00E-34	39	97	(L07492) sugar transport protein [Saccharomyces cerevisiae]
18752	ENU02546	ANI61C9701: 66-87		586-605	NAP		g1703202	228	67	1.00E-10	35	44	
18753	ENU02547	ANI61C537:8	36-55	543-575	NAP		g409547	138	45	0.0006	38	24	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18754	ENU02548	ANI61C9833: 27-46	27-46	545-567	NAP		g3877351	308	75	9.00E-18			(Z66520) similar to ERG-3 like protein [Caenorhabditis elegans]
18755	ENU02549	ANI61C215:8 22-41	22-41	543-562	NAP		g3881138	159	85	5.00E-16	38	96	(AL023846) Y52B11.C.1 [Caenorhabditis elegans]
18756	ENU02550	ANI61C1039 72-92	72-92	596-615	NAP		g2804470		64	0.000000			(AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]
18757	ENU02551	ANI61C3473: 42-61	42-61	556-585	NAP		g465713	216	71	9.00E-18	32	67	hypothetical 30.3 KD protein in APE1/LAP4-CWP1 intergenic region ; hypothetical protein YKL099c - yeast (Saccharomyces cerevisiae) ; (X71133) YKL449 [Saccharomyces cerevisiae] ; (Z28099) ORF YKL099c [Saccharomyces cerevisiae]
18758	ENU02552	ANI61C1071 27-47	27-47	551-570	NAP		g4506617	391	102	1.00E-27	59	67	ribosomal protein L17 ; 60S ribosomal protein L17 (L23) ; ribosomal protein L17 - human ; (X53777) putative ribosomal protein (AA 1-184) [Homo sapiens]
18759	ENU02553	ANI61C8712: 58-77	58-77	577-602	NAP		g2498702	79	48	0.00007	34	38	sternmatocysin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
18760	ENU02554	ANI61C2827: 31-60	31-60	556-575	NAP		g114988	1001	363	e-100	98	16	Kinesin-like protein BIMC ; kinesin-related protein bimC - Emericella nidulans ; (M32075) kinesin-like protein (bimC) [Emericella nidulans]
18761	ENU02555	ANI61C9570: 44-63	44-63	568-589	NAP		g1084581	396	118	4.00E-36	50	89	hypothetical protein YER007c-a - yeast (Saccharomyces cerevisiae) ; (U18778) Yel007c-ap [Saccharomyces cerevisiae]
18762	ENU02556	ANI61C7729: 31-50	31-50	557-576	NAP		g2231082	1314	100	8.00E-21	37	19	(Y07891) dynamin-related protein [Schizosaccharomyces pombe]
18763	ENU02557	ANI61C4165: 69-95	69-95	591-614	NAP		g3264834	1030	187	4.00E-47	50	55	(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18764	ENU02558	ANI61C8730:	71-90	594-616	NAP		g130879	580	131	1.00E-48			Proteasome component PUP1 precursor (macropain subunit PUP1) (proteinase YSCE subunit PUP1) (multicatalytic endopeptidase complex subunit PUP1) ; probable multicatalytic endopeptidase complex (EC 3.4.99.46) chain PUP1 - yeast (Saccharomyces cerevisiae) ; (X61189) PUP1 [Saccharomyces cerevisiae] ; (U55020) Pup1p [Saccharomyces cerevisiae] ; (Z75065) ORF YOR157c [Saccharomyces cerevisiae]
18765	ENU02559	ANI61C1935:	52-71	576-598	NAP		g2117760	802	92	1.00E-25	50	33	"aspartate transaminase (EC 2.6.1.1), cytosolic - yeast (Saccharomyces cerevisiae) ; (Z73199) ORF YLR027c [Saccharomyces cerevisiae] "
18766	ENU02560	ANI61C6513:	22-47	545-568	NAP		g3184113	116	66	2.00E-10	35	30	(AL023780) zinc finger protein [Schizosaccharomyces pombe] (L48797) toxin pump [Cochliobolus carbonum]
18767	ENU02561	ANI61C886:1	40-59	565-587	NAP		g1063421	252	84	6.00E-16	28	34	Autophagy serine/threonine-protein kinase APCI1 ; probable membrane protein YGL180w - yeast (Saccharomyces cerevisiae) ; (X91489) putative ser/thr protein kinase [Saccharomyces cerevisiae] ; (Z72702) ORF YGL180w [Saccharomyces cerevisiae] ; (D29991) Apg1p [Saccharomyces cerevisiae]
18768	ENU02562	ANI61C5484:	72-92	590-619	NAP		g1730043	222	77	2.00E-17	39	19	nuclear protein SNF7 ; SNF7 protein - yeast (Saccharomyces cerevisiae) ; (Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18769	ENU02563	ANI61C4438:	68-86	594-615	NAP		g730759	197	49	0.000000	33	71	(Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18770	ENU02564	ANI61C7200:	48-70	571-596	NAP		g3834684	121	66	2.00E-10	30	86	(AF100925) mating type protein MAT-1-3 [Gibberella fujikuroi]
18771	ENU02565	ANI61C1125	59-78	584-607	NAP		g464786	235	94	1.00E-26	34	28	SPT10 protein ; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae) ; (L24435) SPT10 [Saccharomyces cerevisiae] ; (Z49402) ORF YJL127c [Saccharomyces cerevisiae]

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18772	ENU02566	AN161C8336:	59-88	589-608	NAP		g3722	816	258	2.00E-68	63	32	(X52633) GAP1 protein (AA 1-601)
18773	ENU02567	834..243 AN161C7975:	36-55	566-585	NAP		g4056551	666	154	9.00E-57	62	33	[Saccharomyces cerevisiae] (AL034583) putative elongation initiation factor subunit
18774	ENU02568	AN161C1803:	65-100	582-615	NAP		g1805251	273	101	4.00E-21	35	34	[Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]
18775	ENU02569	44..636 AN161C1115	53-73	584-603	NAP		g1723280	354	106	1.00E-22	43	52	hypothetical 34.8 KD protein C4H3.04C in chromosome I ; (Z69380) unknown [Schizosaccharomyces pombe]
18776	ENU02570	AN161C8494:	59-80	589-610	NAP		g3913497	637	84	3.00E-33	54	58	putative carboxymethylglutaminylase (dieneolase hydrolase) (DLH) ; hypothetical protein YDL086w - yeast (Saccharomyces cerevisiae) ; (Z74134) ORF YDL086w [Saccharomyces cerevisiae]
18777	ENU02571	AN161C6927:	47-66	568-599	NAP		g729230	652	191	1.00E-64	82	12	chromosome segregation protein CUT3 ; cut3 protein - fission yeast (Schizosaccharomyces pombe) ; (D30788) cut3 protein [Schizosaccharomyces pombe]
18778	ENU02572	AN161C4306:	37-57	558-589	NAP		g2132076	302	64	2.00E-18	33	44	hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) ; (U55021) O3625p [Saccharomyces cerevisiae] ; (Z75081) ORF YOR173w [Saccharomyces cerevisiae]
18779	ENU02573	AN161C6203:	62-81	582-615	NAP		g4322563	441	103	3.00E-40	60	91	(AF089838) phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae]
18780	ENU02574	AN161C1145	71-94	605-624	NAP		g2257524	619	127	2.00E-41	56	62	(AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe]
18781	ENU02575	AN161C941:	28-46	560-581	NAP		g539079	440	147	2.00E-37	54	14	peroxisomal assembly protein 5 - yeast (Pichia pastoris)

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18782	ENU02576	AN161C3194:	23-43	547-577	NAP		g133371	207	74	7.00E-18			DNA-directed RNA polymerases I and III 16 KD polypeptide (AC19) ; DNA-directed RNA polymerase (EC 2.7.7.6) I/III chain AC19 - yeast
		726..130											(Saccharomyces cerevisiae) ; (M64991) AC19 RNA polymerase subunit [Saccharomyces cerevisiae] ; (Z69382) Subunit of RNA polymerase I and III [Saccharomyces cerevisiae] ; (Z71390) ORF YNL113w [Saccharomyces cerevisiae]
18783	ENU02577	AN161C8284:	40-59	573-595	NAP		g461540	796	171	7.00E-57			"phospho-2-dehydro-3-deoxyheptone aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptone aldolase) (DAHPh synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptone aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptone aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae] "
		197..794											(AL035260) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]
18784	ENU02578	AN161C1878:	45-65	572-601	NAP		g4176538	316	67	1.00E-10	37	51	(AL035260) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]
		1258..660											hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
18785	ENU02579	AN161C3975:	66-86	587-622	NAP		g1351702	337	76	2.00E-13	31	36	(AL022245) ser/thr protein kinase [Schizosaccharomyces pombe] ; (AL031603) protein kinase. [Schizosaccharomyces pombe] (AL023781) hypothetical protein [Schizosaccharomyces pombe]
		1819..2417											
18786	ENU02580	AN161C9713:	63-86	594-619	NAP		g2995375	924	212	4.00E-59	66	46	(AL022245) ser/thr protein kinase [Schizosaccharomyces pombe] ; (AL031603) protein kinase. [Schizosaccharomyces pombe] (AL023781) hypothetical protein [Schizosaccharomyces pombe]
		1295..697											
18787	ENU02581	AN161C3218:	70-89	606-626	NAP		g3184080	394	68	4.00E-11	60	85	(AL023781) hypothetical protein [Schizosaccharomyces pombe]
		1079..1677											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18788	ENU02582	ANI61C1056	46-65	578-602	NAP		g1722905	157	66	3.00E-14	34	26	"endo-1,4-beta-xylosyltransferase D precursor (xylosyltransferase D) (XYLD) ; endo-1,4-beta-xylosyltransferase (EC 3.2.1.8) D - Cellulomonas fimi ; (X76729) endo-1,4-beta-xylosyltransferase [Cellulomonas fimi]"
18789	ENU02583	ANI61C1120	72-91	610-629	NAP		g3184056		56	0.000000			(AL023776) hypothetical protein [Schizosaccharomyces pombe]
18790	ENU02584	ANI61C8956	25-46	555-582	NAP		g2598037	257	60	3.00E-17	31	43	(AJ01272) manganese resistance I protein [Saccharomyces cerevisiae]
18791	ENU02585	ANI61C7700	22-55	561-580	NAP		g133264	341	73	7.00E-21	52	96	Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
18792	ENU02586	ANI61C5260	44-63	581-602	NAP		g1710503	609	161	3.00E-46	69	85	"probable 60S ribosomal protein L18 (RP28) ; ribosomal protein L18.e, cytosolic - fission yeast [Schizosaccharomyces pombe] ; (AL031528) 60S ribosomal protein 118 [Schizosaccharomyces pombe]"
18793	ENU02587	ANI61C3974	48-79	588-607	NAP		g120609	630	199	4.00E-53			Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracil phosphoribosyltransferase (EC 2.4.2.9) chain FUR1 - yeast [Saccharomyces cerevisiae] ; (M36485) uracil phosphoribosyltransferase (FUR1) [Saccharomyces cerevisiae] ; (U10398) Fur1p; Uracil phosphoribosyltransferase [Saccharomyces cerevisiae] ; (X79811) FUR1 [Saccharomyces cerevisiae] hypothetical protein YPL225w - yeast [Saccharomyces cerevisiae] ; (Z73581) ORF YPL225w [Saccharomyces cerevisiae]
18794	ENU02588	ANI61C1048	27-46	564-586	NAP		g2132237	287	112	2.00E-24	48	93	(AL034433) hypothetical protein [Schizosaccharomyces pombe] (X78082) NADH:ubiquinone oxidoreductase (complex I) [Neurospora crassa]
18795	ENU02589	ANI61C7255	30-49	565-589	NAP		g4007771	210	100	1.00E-20	29	30	
18796	ENU02590	ANI61C8977	33-54	570-592	NAP		g577597	347	138	3.00E-32	49	79	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18797	ENU02591	ANI61C7354:	69-88	610-629	NAP		g586551	490	87	8.00E-17	35	53	Hypothetical 33.5 KD protein in MRPS9-YSW1 intergenic region; probable membrane protein YBR147w - yeast (Saccharomyces cerevisiae); (Z36016) ORF YBR147w [Saccharomyces cerevisiae]
18798	ENU02592	ANI61C8993:	22-53	564-582	NAP		g1170922	293	101	1.00E-30	39	37	Ammonium transporter MEP2; ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae); (X83608) ammonium transporter [Saccharomyces cerevisiae]; (Z46843) NH3 permease [Saccharomyces cerevisiae]; (Z71418) ORF YNL142w [Saccharomyces cerevisiae] (X60381) ORF2 [Saccharomyces cerevisiae]
18799	ENU02593	ANI61C8845:	22-49	563-582	NAP		g388249	198	106	2.00E-22	39	60	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae); (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18800	ENU02594	ANI61C3564:	39-58	578-600	NAP		g1352984	365	114	6.00E-25	42	68	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana; (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana] (AL023589) membrane transporter [Schizosaccharomyces pombe] hypothetical zinc metalloproteinase T16A9.4 cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450I1A [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18801	ENU02595	ANI61C3979:	43-62	585-604	NAP		g1352982		52	0.000004			
18802	ENU02596	ANI61C1076:	32-51	574-593	NAP		g1361982	354	167	5.00E-41	44	34	
18803	ENU02597	ANI61C3755:	34-53	577-596	NAP		g3135990	322	97	1.00E-25	45	30	
18804	ENU02598	ANI61C5967:	35-55	576-597	NAP		g2499919	494	134	3.00E-31	45	20	
18805	ENU02599	ANI61C4286:	23-50	559-587	NAP		g1083278	163	87	1.00E-16	33	27	

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
18806	ENU02600	ANI61C197	6	25-46	566-589	NAP		g1911486	466	102	2.00E-21	49	61	"(S80872) putative TcI-nariner class transposase/IS630-TcI homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
18807	ENU02601	ANI61C9009	45-64		589-609	NAP		g2619026	435	155	3.00E-37	43	46	(AF027868) Yoan [Bacillus subtilis]; (Z99114) similar to hypothetical proteins [Bacillus subtilis]
18808	ENU02602	ANI61C6045	34-53		570-598	NAP		g1749484	203	76	1.00E-13	41	47	"(D89138) similar to Saccharomyces cerevisiae ORF YGL208W, EMBL Accession Number Z72730 [Schizosaccharomyces pombe]"
18809	ENU02603	ANI61C1111	28-49		570-593	NAP		g2498970	485	157	6.00E-38	40	73	putative sterigmatocystin biosynthesis protein STCQ; (U34740) similar to A. parasiticus putative aflatoxin biosynthesis protein [Emmericella nidulans]
18810	ENU02604	ANI61C1209	55-78		600-621	NAP		g2132284	367	91	1.00E-36	39	89	hypothetical protein YPR107c - yeast (Saccharomyces cerevisiae); (U32445) P8283.17 gene product [Saccharomyces cerevisiae]
18811	ENU02605	ANI61C4438	68-86		612-634	NAP		g730759	197	49	0.000000	35	74	nuclear protein SNF7; SNF7 protein - yeast (Saccharomyces cerevisiae); (Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18812	ENU02606	ANI61C5883	29-48		564-595	NAP		g731875	437	148	3.00E-35	39	65	"mitochondrial FAD carrier protein FLX1; carrier protein FLX1, inner membrane - yeast (Saccharomyces cerevisiae); (Z38059) orf, len: 311, CAI: 0.12, similar to peroxisomal membrane protein and mitochondrial carrier proteins [Saccharomyces cerevisiae]; (L41168) inner membrane carrier protein [Saccharomyces cerevisiae]"
18813	ENU02607	ANI61C7524	66-86		614-633	NAP		g128337	1671	324	2.00E-88	98	29	G2-specific protein kinase NIMA (never in mitosis); probable protein kinase nima (EC 2.7.1.-) - Emmericella nidulans; (M20249) never in mitosis protein [Emmericella nidulans]

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18814	ENU02608	ANI61C1107	24-42	565-591	NAP		g2879805	600	131	3.00E-30	37	12	(AL021813) hypothetical protein [Schizosaccharomyces pombe]
18815	ENU02609	ANI61C8051	36-55	585-604	NAP		g1706087	910	173	7.00E-43	50	37	cytochrome P450-DIT2 (cytochrome P450 56) ; cytochrome P450 56 - yeast (Saccharomyces cerevisiae) ; (U32274) Dit2p: cytochrome P450; CAL: 0.13 [Saccharomyces cerevisiae]
18816	ENU02610	ANI61C757:1	22-46	571-590	NAP		g126597	577	203	8.00E-59	58	87	"N,O-diacetylmutamidase (lysozyme CH) ; lysozyme (EC 3.2.1.17) - fungus (Chalara sp.)"
18817	ENU02611	ANI61C8231:1	61-81	594-629	NAP		g130117	813	110	9.00E-24	49	27	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18818	ENU02612	ANI61C3107:1	43-62	591-612	NAP		g730334	405	108	3.00E-23	32	35	putative polyketide biosynthesis protein PKSJ ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksJ [Bacillus subtilis] ; (Z99113) pksJ [Bacillus subtilis]
18819	ENU02613	ANI61C7361:1	63-82	613-632	NAP		g3687462	370	100	5.00E-29	45	91	(AL031798) coatomer zeta subunit [Schizosaccharomyces pombe]
18820	ENU02614	ANI61C9833:1	42-61	592-611	NAP		g1723488	87	61	0.000000	42	8	hypothetical 104.0 KD protein C32A11.03C in chromosome I ; (Z69796) unknown [Schizosaccharomyces pombe]
18821	ENU02615	ANI61C8431:1	72-92	611-641	NAP		g2914565	413	141	1.00E-36	48	70	"Chain A, Yeast Chorismate Mutase, T226s Mutant, Complex With Trp"

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18822	ENU02616	ANI61C3868:	22-45	572-593	NAP		g417817	409	176	1.00E-43			protein-S isoprenylcysteine O-methyltransferase (isoprenylcysteine carboxylmethyltransferase) ; farnesyl cysteine carboxyl-methyltransferase - yeast (Saccharomyces cerevisiae) ; (L07952) farnesyl cysteine carboxyl-methyltransferase [Saccharomyces cerevisiae] ; (L15442) isoprenylcysteine carboxyl methyltransferase [Saccharomyces cerevisiae] ; (U33007) Ste14p: farnesyl cysteine carboxyl-methyltransferase; YDR410C; CAL: 0.12 [Saccharomyces cerevisiae]
18823	ENU02617	ANI61C3365:	53-72	592-624	NAP		g3116144	110	54	0.000001	27	64	(AL023290) hypothetical protein [Schizosaccharomyces pombe]
18824	ENU02618	ANI61C502:6	49-72	596-621	NAP		g482219	290	113	8.00E-25	38	20	hypothetical protein ZK757.3 - Caenorhabditis elegans
18825	ENU02619	ANI61C1027	72-93	620-644	NAP		g2494676	1242	123	7.00E-28	38	36	EPD1 protein precursor ; (AB005130) EPD1 [Candida maltosa]
18826	ENU02620	ANI61C1166:	44-67	597-616	NAP		g4530327	890	205	2.00E-80	79	30	(AF110494) mitochondrial precursor protein import receptor tom70 [Neurospora crassa]
18827	ENU02621	ANI61C8770:	70-89	623-642	NAP		g1710055	788	148	2.00E-35	44	44	RDS1 protein ; rds1 protein - fission yeast (Schizosaccharomyces pombe) ; (X77328) rds1 [Schizosaccharomyces pombe]
18828	ENU02622	ANI61C293:2	30-50	583-602	NAP		g1929333	120	61	0.000000	26	97	(Z93767) ywrf [Bacillus subtilis] ; (Z99122) ywrf [Bacillus subtilis]
18829	ENU02623	ANI61C5354:	65-83	619-638	NAP		g464725	689	249	2.00E-65	69	91	"40S ribosomal protein S8 (S14) (Y59) (RP19) ; ribosomal protein S8-e, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z26879) ribosomal protein S8 [Saccharomyces cerevisiae] ; (Z35833) ORF YBL072c [Saccharomyces cerevisiae] ; (U18839) Rps8bp: Ribosome protein, small subunit [Saccharomyces cerevisiae] " (U13050) pectate lyase D [Fusarium solani f. sp. pisi]
18830	ENU02624	ANI61C3563:	58-77	611-631	NAP		g1526987	450	183	7.00E-46	54	77	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18831	ENU02625	ANI61C8909:	30-49	582-603	NAP		g2773042	750	105	3.00E-22	41	17	(AF038440) phospholipase D2 [Homo sapiens]
18832	ENU02626	2964..3579 ANI61C1583:	22-45	571-596	NAP		g1723912	78	50	0.00002	33	11	hypothetical 73.5 KD protein in SCS3-SUP44 intergenic region ; hypothetical protein YGL124c - yeast (Saccharomyces cerevisiae) ; (Z72646) ORF YGL124c [Saccharomyces cerevisiae] ; (X94106) G2889 [Saccharomyces cerevisiae]
18833	ENU02627	ANI61C1141	71-97	626-645	NAP		g83699	1733	264	5.00E-70	98	57	[Saccharomyces cerevisiae] dehydratase [Emmericella nidulans] (M77665) dehydratase [Emmericella nidulans] (U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici]
18834	ENU02628	ANI61C915:2	43-62	591-617	NAP		g799150	179	98	7.00E-20	40	14	"signal sequence processing protein SEC11 ; signal peptidase (EC 3.4.99.-) SEC11 - yeast (Saccharomyces cerevisiae) ; (Z38061) sec11, len: 167, CAL: 0.17 SCI11_yeast P15367 signal sequence processing protein [Saccharomyces cerevisiae]"
18835	ENU02629	ANI61C5294:	22-45	576-598	NAP		g730717	400	117	1.00E-31	50	90	[Saccharomyces cerevisiae] "PIM1 protein ; pim1 hypothetical protein - fission yeast (Schizosaccharomyces pombe) hypothetical 24.7 KD protein C3A12.04C in chromosome I ; (Z95395) conserved hypothetical protein [Schizosaccharomyces pombe] hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRPL27 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018 [Saccharomyces cerevisiae]
18836	ENU02630	ANI61C4039:	60-79	610-636	NAP		g132172	699	154	5.00E-37	38	38	
18837	ENU02631	ANI61C3092:	22-53	580-599	NAP		g3219941	318	77	5.00E-25	34	94	
18838	ENU02632	ANI61C6403:	52-82	609-629	NAP		g586394	356	134	4.00E-31			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18839	ENU02633	ANI61C8982: 6024..5404	52-71	610-630	NAP		g3170178	71	5.00E-12				(AF039689) antigen NY-CO-7 [Homo sapiens]
18840	ENU02634	ANI61C3314: 1350..1971	48-67	605-627	NAP		g3004934	801	189	2.00E-47	46	43	(AF036871) annexin XIV [Neurospora crassa]
18841	ENU02635	ANI61C748:1 7..638	38-58	582-617	NAP		g2132293	228	75	3.00E-21	38	53	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae) ; (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325)
18842	ENU02636	ANI61C7556: 2814..3435	41-62	601-620	NAP		g2624417	384	126	1.00E-28	53	88	[Saccharomyces cerevisiae] (AJ002959) Ubiquitin carrier protein [Zea mays]
18843	ENU02637	ANI61C9743: 949..3327	23-42	581-603	NAP		g2492754	518	127	5.00E-29	44	63	sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans]
18844	ENU02638	ANI61C8297: 1068..446	70-89	630-650	NAP		g3327876	189	87	8.00E-17	35	47	(AB016218) unknown: similar to human GA17 protein
18845	ENU02639	ANI61C7885: 124..746	22-53	575-602	NAP		g3738142	459	80	1.00E-45	57	99	[Schizosaccharomyces pombe] (AL031852) u-snmp-associated cyclophilin [Schizosaccharomyces pombe]
18846	ENU02640	ANI61C8732: 3940..4562	22-50	573-602	NAP		g459002	392	118	2.00E-32	42	78	(U00036) R151.6 gene product [Caenorhabditis elegans]
18847	ENU02641	ANI61C1042 3:907..1529	68-87	630-649	NAP		g1730032	250	52	2.00E-14	35	66	2-deoxy-D-glucuronate 3-dehydrogenase (2-keto-3-deoxyglucuronate oxidoreductase) ; (U29581) ORF_f253 [Escherichia coli] ; (AE000368) 2-deoxy-D-glucuronate 3-dehydrogenase [Escherichia coli]
18848	ENU02642	ANI61C5330: 798..174	68-87	631-650	NAP		g2924501	390	43	0.001	30	23	(AL022019) conserved hypothetical protein [Schizosaccharomyces pombe]
18849	ENU02643	ANI61C172:3 1..656	47-71	610-630	NAP		g113701	203	50	4.00E-14	42	27	Acetamidase ; amds protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18850	ENU02644	ANI61C9290:	49-68	611-633	NAP		g549626	261	102	2.00E-21	36	92	hypothetical 22.0 KD protein in LAS1-CCPI intergenic region ; hypothetical protein YKR065c - yeast (Saccharomyces cerevisiae) ; (Z28290) ORF YKR065c [Saccharomyces cerevisiae]
18851	ENU02645	ANI61C5915:	33-53	598-617	NAP		g586521	369	153	9.00E-37	43	26	hypothetical 86.4 KD protein in PHO5-VPS15 intergenic region ; hypothetical protein YBR094w - yeast (Saccharomyces cerevisiae) ; (X78993) hyp. protein [Saccharomyces cerevisiae] ; (Z35963) ORF YBR094w [Saccharomyces cerevisiae] (AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]
18852	ENU02646	ANI61C1650:	23-42	588-607	NAP		g4160346	1532	218	3.00E-56	65	38	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA reductase [Gibberella fujikuroi] quinate permease (quate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
18853	ENU02647	ANI61C995:8	56-75	621-640	NAP		g2495263	743	248	3.00E-65	56	21	7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) - Eubacterium sp. (strain VPI 12708) ; (M58473) 7-alpha-hydroxysteroid dehydrogenase [Eubacterium sp. VPI 12708]
18854	ENU02648	ANI61C3926:	55-74	621-640	NAP		g131761	220	112	3.00E-24	30	38	"hypothetical 42.5 KD protein in TSM1-ARE1 intergenic region ; probable membrane protein YCR044c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR044c, len:357 [Saccharomyces cerevisiae]"
18855	ENU02649	ANI61C5699:	46-69	611-631	NAP		g98747	248	116	2.00E-25	30	78	hypothetical protein YDR140w - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae] (AF010138) transcription factor [Mus musculus]
18856	ENU02650	ANI61C2043:	34-53	600-620	NAP		g140496	284	136	2.00E-31	36	55	
18857	ENU02651	ANI61C7025:	28-50	596-615	NAP		g1077536	260	109	2.00E-23	40	77	
18858	ENU02652	ANI61C2654:	40-59	608-627	NAP		g2281697	434	57	0.000000	28	17	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18859	ENU02653	ANI61C6471: 22-55		590-610	NAP		g4538667	391	126	8.00E-29	65	85	(AL049474) clathrin coat assembly protein [Schizosaccharomyces pombe]
18860	ENU02654	ANI61C2906: 22-53		583-610	NAP		g762850	299	76	2.00E-13	40	100	(L41166) p21 protein [Schizosaccharomyces pombe]; (Z99262) p21 protein; cell cycle regulatory protein; interacts with cdc2 in the control of the M-G1 transition [Schizosaccharomyces pombe]
18861	ENU02655	ANI61C7933: 37-56		606-625	NAP		g1077514	302	114	5.00E-25	46	76	hypothetical protein YDR013w - yeast (Saccharomyces cerevisiae) ; (Z48008) unknown [Saccharomyces cerevisiae]; (X95966) orf:PZA208 [Saccharomyces cerevisiae] ; (Z74309) ORF YDR013w [Saccharomyces cerevisiae]
18862	ENU02656	ANI61C9492: 46-65		616-635	NAP		g1723848	277	89	4.00E-17	46	85	"putative mitochondrial 60S ribosomal protein L7/L12 precursor ; probable ribosomal protein L12, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z72591) ORF YGL068w [Saccharomyces cerevisiae]"
18863	ENU02657	ANI61C6172: 38-57		608-627	NAP		g3169083	279	111	6.00E-24	37	61	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18864	ENU02658	ANI61C6638: 28-52		598-617	NAP		g3915558	169	92	3.00E-18	29	62	hypothetical 36.5 KD protein in GBSA-TLPB intergenic region ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18865	ENU02659	ANI61C1015: 56-77		625-645	NAP		g2131385	270	87	1.00E-16	40	33	hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae) ; (Z50046) unknown [Saccharomyces cerevisiae]
18866	ENU02660	ANI61C1039: 44-63		613-634	NAP		g2104422	323	113	1.00E-24	42	26	(Z95395) putative membrane transport protein [Schizosaccharomyces pombe]
18867	ENU02661	ANI61C7015: 22-42		591-613	NAP		g1078629	1199	309	1.00E-83	97	31	DNA binding protein - Emericella nidulans ; (Z47081) DNA binding protein [Emericella nidulans]
18868	ENU02662	ANI61C3159: 25-44		585-616	NAP		g1749831	731	165	2.00E-40	45	26	(Z56279) beta-xyl-glucoSIDase [Thermoaerobacter brockii]
18869	ENU02663	ANI50C7416: 23-42		596-615	NAP		g1781180	47	0.0001	32	29	(Z83859) hypothetical protein Rv1867 [Mycobacterium tuberculosis]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18870	ENU02664	ANI61C3242:	42-61	604-634	NAP		g1173168	299	139	2.00E-32	40	75	hypothetical 31.5 KD protein ; (U05664) homologous to Swiss-Prot Accession Number P20435:
		178..812											Saccharomyces cerevisiae RNA polymerase subunit RPO26 [Sulfolobus acidocaldarius]
18871	ENU02665	ANI61C4376:	45-66	620-639	NAP		g2347143	660	224	4.00E-58	55	89	(U48234) spU2AF23
		881..1482											[Schizosaccharomyces pombe]
18872	ENU02666	ANI61C9847:	71-96	646-666	NAP		g117619	704	131	4.00E-30	36	34	choline transport protein ; choline transport protein - yeast
		8262..7625											(Saccharomyces cerevisiae) ; (J05603)
													choline transport protein
													[Saccharomyces cerevisiae] ; (Z72599)
													ORF YGL077c [Saccharomyces cerevisiae]
18873	ENU02667	ANI61C6047:	22-45	598-617	NAP		g729998	505	174	6.00E-43	45	49	"MRNA capping enzyme (MRNA guanylyltransferase) (GTP--RNA guanylyltransferase) ; (U16143)
		138..775											GTP:RNA guanylyltransferase
													[Schizosaccharomyces pombe] ; (U18811) GTP--RNA
													guanylyltransferase
													[Schizosaccharomyces pombe] ; (Z97211) mma capping enzyme, mma guanylyltransferase
													[Schizosaccharomyces pombe] "
18874	ENU02668	ANI61C1029	60-86	633-655	NAP		g1708418	1571	354	2.00E-97	86	54	eukaryotic initiation factor 4A (EIF-4A) ; (X80796) translation initiation factor eIF-4A [Schizosaccharomyces pombe] ; (L40627) cell cycle control protein eIF-4A [Schizosaccharomyces pombe]
		4:6013..6650											(Z66499) T01B7.8 [Caenorhabditis elegans]
18875	ENU02669	ANI61C8590:	22-41	593-617	NAP		g3879236		36	0.25			hypothetical protein YOL071w - yeast
		5557..4920											(Saccharomyces cerevisiae) ; (Z74813)
18876	ENU02670	ANI61C352:9	52-75	628-648	NAP		g2132007	181	79	2.00E-14	40	89	ORF YOL071w [Saccharomyces cerevisiae]
		224..9862											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18877	ENU02671	ANI61C1805: 2409..2293	40-64	618-637	NAP		g728904	335	95	5.00E-19	41	15	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase); Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae); (U03060) calcium ATPase [Saccharomyces cerevisiae]; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18878	ENU02672	ANI61C9127: 1359..1998	44-63	622-641	NAP		g2959364	326	146	1.00E-34	39	78	(AL022117) putative o-methyltransferase [Schizosaccharomyces pombe]
18879	ENU02673	ANI61C3023: 1260..621	40-63	617-637	NAP		g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450IIIA [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18880	ENU02674	ANI61C3023: 1260..621	40-63	617-637	NAP		g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450IIIA [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18881	ENU02675	ANI61C8458: 2393..1754	63-85	641-660	NAP		g3885836	51	5.00E-14				(AF091042) putative cercosporin transporter [Cercospora kikuchii]
18882	ENU02676	ANI61C8439: 103..745	68-103	649-668	NAP		g2133270	576	100	5.00E-53	91	78	HAP3 protein - Emericella nidulans; (U35341) HapC [Emericella nidulans]
18883	ENU02677	ANI61C9069: 831..188	27-46	609-628	NAP		g1617552	2322	229	4.00E-78	97	38	(U70043) NsdD [Emericella nidulans]; (U70044) DNA binding protein NsdD [Emericella nidulans]
18884	ENU02678	ANI61C2652: 1432..789	66-87	634-667	NAP		g2956779	556	194	4.00E-49	53	38	(AL022103) histidyl-tRNA synthetase [Schizosaccharomyces pombe]
18885	ENU02679	ANI61C2281: 3007..2364	22-41	604-623	NAP		g127297	124	53	0.000001			MPV17 protein; mpv17 protein - mouse; (M36411) Mpv17 [Mus musculus]
18886	ENU02680	ANI61C1422: 79..722	22-52	604-623	NAP		g1870230	1304	436	e-122	99	81	(AC000133) ORF [Emericella nidulans]
18887	ENU02681	ANI61C1079: 4:2116..1472	62-83	642-664	NAP		g4033573	239	85	5.00E-23	43	88	(Z99262) hypothetical protein [Schizosaccharomyces pombe]
18888	ENU02682	ANI61C843:7 34..90	22-52	603-624	NAP		g4106666	421	171	5.00E-42	44	71	(AL035064) putative ubiquinone biosynthesis protein
18889	ENU02683	ANI61C66:29 64..2320	36-56	611-638	NAP		g2842509	416	101	9.00E-41	44	38	[Schizosaccharomyces pombe] (AL021748) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18890	ENU02684	AN161C2870:	64-84	648-667	NAP	g1723479	377	377	164	4.00E-40	43	89	hypothetical 24.9 KD protein C17G8.07 in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe]
18891	ENU02685	AN161C7394:	68-87	650-673	NAP	g1723879	252	95	5.00E-19	37	73	hypothetical 32.1 KD protein in MAD1-SCY1 intergenic region ; probable membrane protein YGL085w - yeast (Saccharomyces cerevisiae) ; (Z72607) ORF YGL085w [Saccharomyces cerevisiae]	
18892	ENU02686	AN161C7972:	55-75	628-660	NAP	g1351612	274	113	7.00E-28	40	61	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe) probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]	
18893	ENU02687	AN161C1056	22-47	601-627	NAP	g2132491	274	75	1.00E-25	40	61	Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracil phosphoribosyltransferase - Bacillus subtilis ; (Z38002) uracil phosphoribosyltransferase [Bacillus subtilis] ; (Z99122) uracil phosphoribosyltransferase [Bacillus subtilis] ; uracil phosphoribosyltransferase [Bacillus subtilis]	
18894	ENU02688	AN161C5718:	51-74	637-657	NAP	g731073	251	48	0.00006			ubiquitin-like protein 9 - Arabidopsis thaliana (AL049559) riboflavin synthase alpha chain [Schizosaccharomyces pombe] (AE000314) putative racemase [Escherichia coli] ; (D90856) similar to [SwissProt Accession Number P31458] [Escherichia coli]	
18895	ENU02689	AN161C3229:	24-52	611-630	NAP	g1362010	267	117	3.00E-28	70	30	ubiquitin-like protein 9 - Arabidopsis thaliana (AL049559) riboflavin synthase alpha chain [Schizosaccharomyces pombe]	
18896	ENU02690	AN161C1148	69-88	652-676	NAP	g4581523	425	178	3.00E-44	53	87	[Schizosaccharomyces pombe]	
18897	ENU02691	AN161C8540:	71-90	653-679	NAP	g1788580	657	146	9.00E-35	40	52	[Escherichia coli] ; (D90856) similar to [SwissProt Accession Number P31458] [Escherichia coli]	
18898	ENU02692	AN161C7170:	42-62	632-651	NAP	g2865171	478	118	3.00E-38	69	90	(AB010901) ribosomal protein L21 homolog [Schizosaccharomyces pombe]	

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18899	ENU02693	AN150C6324	71-95	661-680	NAP		g465873	63	0.000000	002	25	33	hypothetical 59.1 KD protein F22B7.6 in chromosome III ; f22b7.6 protein - Caenorhabditis elegans ; (L12018) putative [Caenorhabditis elegans] hypothetical 98.3 KD protein C9G1.06C in chromosome I ; (Z98763) hypothetical src homology domain containing protein
18900	ENU02694	AN161C5149:	48-67	639-658	NAP		g3183389	540	153	8.00E-37	39	23	[Schizosaccharomyces pombe] (AC005757) R32611_2 [Homo sapiens] (AL031534) putative asparagine synthase [Schizosaccharomyces pombe]
18901	ENU02695	AN161C8056:	50-69	641-660	NAP		g3688090	189	59	2.00E-13	43	86	PSI protein ; DNAI-like protein homolog - fission yeast (Schizosaccharomyces pombe) ; (L37753) Psi protein [Schizosaccharomyces pombe] ; Dnal-like protein [Schizosaccharomyces pombe]
18902	ENU02696	AN161C5061:	23-42	603-634	NAP		g3560144	370	145	3.00E-34	41	38	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] (AL023634) hypothetical protein [Schizosaccharomyces pombe]
18903	ENU02697	AN161C5317:	29-48	619-642	NAP		g1346878	585	141	3.00E-33	39	51	probable membrane protein YPL264c - yeast (Saccharomyces cerevisiae) ; (Z73620) ORF YPL264c [Saccharomyces cerevisiae] hypothetical 29.3 KD protein C3F10.08C in chromosome I ; (Z69369) hypothetical protein [Schizosaccharomyces pombe]
18904	ENU02698	AN161C2530:	45-64	637-658	NAP		g2492825	298	89	3.00E-17	29	52	
18905	ENU02699	AN161C3258:	38-57	633-652	NAP		g3150262	564	146	1.00E-34	38	61	
18906	ENU02700	AN161C1430:	65-84	660-679	NAP		g2133013	401	93	1.00E-18	34	51	
18907	ENU02701	AN161C6665:	45-67	634-660	NAP		g1723253	130	61	0.000000		01	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18908	ENU02702	AN161C6366:	25-56	619-640	NAP		g1352984	390	132	1.00E-39	46	81	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18909	ENU02703	AN161C718:4	33-55	618-648	NAP		g3150116	754	191	4.00E-48	45	39	(AL023595) amino acid permease [Schizosaccharomyces pombe]
18910	ENU02704	AN161C5178:	40-60	636-655	NAP		g1730641	299	79	3.00E-14	29	30	hypothetical 65.0 KD protein in MET2-SEC2 intergenic region ; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae) ; (Z71551) ORF YNL275w [Saccharomyces cerevisiae]
18911	ENU02705	AN161C6874:	49-69	643-664	NAP		g3043428	670	174	1.00E-66	68	97	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
18912	ENU02706	AN161C1298:	66-86	663-682	NAP		g2492997	438	98	2.00E-33	62	68	probable succinyl-COA:3-ketacid-COenzyme A transferase subunit B (succinyl COA:3-OXOacid COA-transferase) (OXCT B) ; (Z95556) scob [Mycobacterium tuberculosis] (L35053) homolog of retroviral gag genes; putative [Magnaporthe grisea] (Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
18913	ENU02707	AN161C3599:	22-44	620-639	NAP		g522301	535	160	8.00E-39	41	46	"mitochondrial inner membrane protease subunit 2 ; proteinase 2 precursor, mitochondrial inner membrane - yeast (Saccharomyces cerevisiae) ; (Z49213) Imp2p [Saccharomyces cerevisiae] "
18914	ENU02708	AN161C1083	72-92	670-689	NAP		g4150918	302	113	1.00E-24	40	81	(AL033391) conserved hypothetical protein [Candida albicans]
18915	ENU02709	AN161C8998:	31-51	627-648	NAP		g1170551	183	88	7.00E-17	37	96	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18916	ENU02710	AN161C6525:	53-72	651-670	NAP		g3850129	585	166	2.00E-40	56	85	
18917	ENU02711	AN161C7950:	70-89	668-687	NAP		g130117	1210	96	1.00E-54	58	30	

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18918	ENU02712	ANI61C3150:	59-80	658-677	NAP			g2492777	537	155	7.00E-39	55	52	hypothetical ZINC-type alcohol dehydrogenase-like protein in pre-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae] (AB012725) zinc finger protein [Mus musculus]
		993..1653												
18919	ENU02713	ANI61C1022	33-53	629-651	NAP			g3298472		38	0.088			hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product [Saccharomyces cerevisiae]
18920	ENU02714	ANI61C8624:	23-50	619-642	NAP			g731611	247	110	1.00E-23	35	89	hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product [Saccharomyces cerevisiae]
		2360..1699												
18921	ENU02715	ANI61C8624:	23-50	619-642	NAP			g731611	247	110	1.00E-23	35	89	hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product [Saccharomyces cerevisiae]
		2360..1699												
18922	ENU02716	ANI61C8082:	57-76	659-678	NAP			g2144564	606	151	9.00E-61	61	61	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) - yeast (Saccharomyces cerevisiae) ; (M67445) phosphoribosyl-amino-imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ; (L22015) AdelP: phosphoribosyl amino imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ORM1 protein ; probable membrane protein YGR038w - yeast (Saccharomyces cerevisiae) ; (Z72823) ORF YGR038w [Saccharomyces cerevisiae]
		2923..2260												
18923	ENU02717	ANI61C9181:	28-47	622-649	NAP			g1723661	472	169	1.00E-49	59	76	
		6564..5901												

Sequence Annotation

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18924	ENU02718	AN161C2491:	23-49	624-645	NAP		g130880	799	167	6.00E-41			"Proteasome component Y7 (macropain subunit Y7) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex subunit Y7); multicatalytic endopeptidase complex (EC 3.4.99.46) chain Y7 - yeast (Saccharomyces cerevisiae); Chain B, Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution; Chain P, Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution; (X56731) proteasome Y7 subunit [Saccharomyces cerevisiae]; (Z46660) proteasome component Y gene, len: 250, CAl:0.15, PRCX_ yeast P23639 [Saccharomyces cerevisiae]" (AL022244) hypothetical protein [Schizosaccharomyces pombe] L-fucose permease; fucose permease - Escherichia coli; (X15025) fucP ORF (AA 1-438) [Escherichia coli]; (U29581) L-fucose permease [Escherichia coli]; (AE000364) fucose permease [Escherichia coli] (Z98601) mitochondrial 40s ribosomal protein mtp4. [Schizosaccharomyces pombe] Elongation factor 2 (EF-2); (D83975) elongation factor 2 [Schizosaccharomyces pombe]; (D83976) elongation factor 2 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans] (AL035065) protein translation factor sui1. [Schizosaccharomyces pombe]
		4228..3564											
18925	ENU02719	AN150C3665	47-66	649-669	NAP		g2995341		121	5.00E-27	41	39	
		0_1:1418..754											
18926	ENU02720	AN161C3667:	33-56	632-656	NAP		g120593	319	74	8.00E-13			
		646..1311											
18927	ENU02721	AN161C1677:	22-49	626-645	NAP		g4038620	521	186	1.00E-46	51	83	
		5888..5223											
18928	ENU02722	AN161C5936:	72-92	677-696	NAP		g3122054	1121	364	e-100	77	26	
		693..27											
18929	ENU02723	AN161C5502:	27-47	617-652	NAP		g1870209	961	265	e-104	86	40	
		520..1187											
18930	ENU02724	AN161C6250:	54-74	655-679	NAP		g4106682	245	59	7.00E-11	59	82	
		1768..1100											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18931	ENU02725	ANI61C9933:	61-80	666-687	NAP		g1175363	535	198	3.00E-50	44	70	hypothetical protein H11014 ; hypothetical protein H11014 - Haemophilus influenzae (strain Rd KW20) ; (U32782) conserved hypothetical protein [Haemophilus influenzae Rd]
		144..812											
18932	ENU02726	ANI61C8405:	22-43	623-649	NAP		g3925782	333	146	1.00E-34	48	91	(AL034353) putative 60s ribosomal protein [Schizosaccharomyces pombe]
		2151..1485											
18933	ENU02727	ANI61C205:1	45-66	653-672	NAP		g4581877	144	92	3.00E-18	30	40	(AF120278) proline dehydrogenase; PRODH [Homo sapiens]
		473..2142											
18934	ENU02728	ANI61C3750:	33-54	640-660	NAP		g2367392	873	118	4.00E-26	34	30	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]
		1137..468											
18935	ENU02729	ANI61C1118	32-52	641-660	NAP		g488189	367	87	7.00E-22	29	51	(U00063) weakly similar to R. ricketsii protein P34 [Caenorhabditis elegans]
		4:5694..5023											
18936	ENU02730	ANI61C4356:	23-42	632-651	NAP		g1020413	319	145	4.00E-34	34	41	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
		86..756											
18937	ENU02731	ANI61C8178:	66-85	676-695	NAP		g1173334	401	157	9.00E-38	52	82	RAS-like GTP-binding protein RYL2 ; (L06970) ras-like protein [Yarrowia lipolytica]
		1686..1015											
18938	ENU02732	ANI61C9465:	22-52	631-651	NAP		g2226413	148	41	0.00002	43	65	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
		4908..4237											
18939	ENU02733	ANI61C1088	57-77	667-687	NAP		g1706202	656	152	1.00E-61	70	87	Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae]
		5:1706..2378											
18940	ENU02734	ANI61C9472:	44-64	646-674	NAP		g464287	410	145	2.00E-34	56	82	"NADH-ubiquinone oxidoreductase 21 KD subunit (complex 1-21KD) (Cl- 21KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20.9K chain - Neurospora crassa ; (X60829) NADH dehydrogenase, 21 kDa subunit [Neurospora crassa]"
		810..138											
18941	ENU02735	ANI61C4807:	25-47	631-655	NAP		g418596	431	91	3.00E-19	56	93	putative 40S ribosomal protein YHR148W ; hypothetical protein YHR148w - yeast (Saccharomyces cerevisiae) ; (X69480) uORF1 [Saccharomyces cerevisiae] ; (U10397) Yhr148wp [Saccharomyces cerevisiae] (AE000955) 2-nitropropane dioxygenase (necd2) [Archaeoglobus fulgidus]
		3495..2823											
18942	ENU02736	ANI61C11:25	22-53	632-652	NAP		g2648355	318	73	3.00E-17	34	72	
		73..3245											

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18943	ENU02737	ANI61C5118:	71-91	675-702	NAP		g2492756	213	47	0.0001			putative sterigmatocystin biosynthesis ketoreductase STCE ; (U34740)
		756..83											putative ketoreductase [Emericella nidulans]
18944	ENU02738	ANI61C1354:	23-53	635-654	NAP		g729965	467	124	9.00E-39	66	44	"saccharopine dehydrogenase [NAD+, L-lysine forming] (lysine--2-oxoglutarate reductase) (SDH) ; saccharopine dehydrogenase (NAD+, L-lysine-forming) - yeast (Yarrowia lipolytica) (strain W29) ; (M34929)
		82..755											saccharopine dehydrogenase [Yarrowia lipolytica] "
18945	ENU02739	ANI61C3530:	26-45	638-657	NAP		g3420982	502	112	2.00E-24	57	52	(Z97628) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans] ; (Z81080) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans]
		5..678											(AL034382) putative ras-related GTP-binding protein [Schizosaccharomyces pombe]
18946	ENU02740	ANI61C5321:	57-76	663-689	NAP		g3947880	533	120	4.00E-49	62	98	hypothetical protein YDR071c - yeast (Saccharomyces cerevisiae) ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74367) ORF YDR071c
		303..977											[Saccharomyces cerevisiae]
18947	ENU02741	ANI61C566:1	22-40	629-654	NAP		g1077519	163	85	4.00E-16	36	98	hypothetical protein YDR071c - yeast (Saccharomyces cerevisiae) ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74367) ORF YDR071c
		660..986											[Saccharomyces cerevisiae]
18948	ENU02742	ANI61C7088:	22-57	636-655	NAP		g626443	140	68	5.00E-11	32	96	hypothetical protein YLR193c - yeast (Saccharomyces cerevisiae) ; (U14913) Ylr193cp [Saccharomyces cerevisiae]
		2908..3583											(Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI)
18949	ENU02743	ANI61C1134	54-73	668-687	NAP		g3876766	272	104	2.00E-23	45	86	YCAC (SW:YCAC_ECOLI)
		4:2479..1804											[Caenorhabditis elegans]
18950	ENU02744	ANI61C1253:	25-44	637-659	NAP		g2995384	706	242	2.00E-71	83	82	(AJ004810) cytochrome P450 monooxygenase [Zea mays]
		7105..6501											(AL034463) hypothetical protein [Schizosaccharomyces pombe]
18951	ENU02745	ANI61C7538:	22-56	638-657	NAP		g4007800	323	61	3.00E-15	43	92	(K01609) gall [Saccharomyces carlsbergensis]
		242..920											
18952	ENU02746	ANI61C9073:	30-49	634-665	NAP		g171567	338	131	7.00E-34	35	42	
		3923..3246											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18953	ENU02747	AN161C7240:	70-92	686-705	NAP		g3006178	279	89	3.00E-17	32	32	(AL022304) putative mma transport regulator [Schizosaccharomyces pombe]
		3297..2620											
18954	ENU02748	AN161C3687:	61-80	670-697	NAP		g3169083	261	108	4.00E-23	36	66	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
		1121..1799											
18955	ENU02749	AN161C1049	31-51	648-667	NAP		g3041738	1512	81	2.00E-51	61	35	"T-complex protein 1, ETA subunit (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF interacting protein); (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]"
		7:1379..702											
18956	ENU02750	AN161C5629:	40-59	643-676	NAP		g100489	133	72	3.00E-12			transposase Tam3 - garden snapdragon transposon Tam3; (X55078) Tam3-transposase [Antirrhinum majus]; (AB013982) transposase [Antirrhinum majus]; (AB013983) transposase [Antirrhinum majus]; (AB013984) transposase [Antirrhinum majus]; (AB013986) transposase [Antirrhinum majus]; (AB013990) transposase [Antirrhinum majus]; (AB013991) transposase [Antirrhinum majus]; (AB013995) transposase [Antirrhinum majus]; (AB013997) transposase [Antirrhinum majus]
		4616..5294											(AL031740) putative rRNA biogenesis protein; trp5 homolog; multiple S1 ma binding domain protein
18957	ENU02751	AN161C7852:	57-88	664-693	NAP		g3650378	1057	154	5.00E-37	51	10	[Schizosaccharomyces pombe]
		1392..714											(Z99262) putative endosomal Vps protein complex subunit
18958	ENU02752	AN161C5415:	49-70	668-687	NAP		g2414668	256	86	3.00E-16	39	85	[Schizosaccharomyces pombe]
		698..1378											possible apospory-associated protein C; (U13148) possible apospory-associated protein [Pennisetum ciliare] (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]
18959	ENU02753	AN161C7921:	69-88	678-708	NAP		g2501555	296	100	3.00E-24	38	62	
		2564..1883											
18960	ENU02754	AN161C7147:	33-53	639-673	NAP		g4090259	218	83	2.00E-15	37	85	
		5245..5927											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18961	ENU02755	AN161C7273:	22-47	642-662	NAP		g1723256	227	84	2.00E-19	34	93	"hypothetical 23.0 KD protein C3F10.12C in chromosome I ; (Z69369) SPAC3F10.12c, unknown, 201, similar to transcription factors and SW:CBF1_yeast P17106 centromere-binding protei n 1 (39.8% identity in 113 aa overlap), contains PS00038 Myc-type, 'helix-loop-helix' dimerization dom..."
18962	ENU02756	AN161C7786:	25-47	647-666	NAP		g1363314	213	53	2.00E-11	36	19	probable cell division control protein p55CDC - rat ; (U05341) p55CDC [Rattus norvegicus]
18963	ENU02757	AN161C1129	54-75	674-695	NAP		g549750	253	67	1.00E-10	39	71	hypothetical 29.4 KD protein in STE6-LOS1 intergenic region ; hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) ; (Z28207) ORF YKL207w [Saccharomyces cerevisiae]
18964	ENU02758	AN161C566:5	22-50	645-664	NAP		g1679882	1002	279	2.00E-74	61	31	(L35484) acetylglutamate synthase [Neurospora crassa]
18965	ENU02759	AN161C6119:	23-44	647-666	NAP		g3123033	365	90	3.00E-31	37	86	vacuolar protein sorting-associated protein VPS28 ; hypothetical protein YPL065w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe5p [Saccharomyces cerevisiae] ; (U50630) Vps28p [Saccharomyces cerevisiae]
18966	ENU02760	AN161C8915:	46-79	664-690	NAP		g1633466	111	56	0.000000	27	79	"Crystal Structure Of Bacteriorhodopsin In Purple Membrane ; Structure Of Bacteriorhodopsin At 3.0 Angstrom Determined By Electron Crystallography ; Chain A, X-Ray Structure Of The Bacteriorhodopsin Trimerlipid Complex ; Bacteriorhodopsinlipid complex " (AL031743) phosphatidylethanolamine methyltransferase. [Schizosaccharomyces pombe]
18967	ENU02761	AN161C6486:	22-51	638-666	NAP		g3650386	1486	102	3.00E-21	38	20	putative oxidoreductase precursor BLI-4 ; (X89499) bli-4 protein [Neurospora crassa]
18968	ENU02762	AN161C6019:	35-59	662-682	NAP		g3023397	320	160	8.00E-39	41	54	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18969	ENU02763	ANI61C1042	32-51	660-679	NAP		g1730832	258	111	6.00E-24	37	61	hypothetical 31.6 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL232w - yeast
		7:1698..2387											(Saccharomyces cerevisiae) ; (Z69381) N1154 [Saccharomyces cerevisiae] ; (Z71508) ORF YNL232w
18970	ENU02764	ANI61C191:1	22-52	647-670	NAP		g2804298	89	68	5.00E-11	26	40	[Saccharomyces cerevisiae] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
18971	ENU02765	ANI61C8095: 52..743	72-92	702-721	NAP		g731042	398	118	1.00E-32			ubiquitin carboxyl-terminal hydrolase 5 (ubiquitin thiolesterase 5) (ubiquitin-specific processing protease 5) (DEubiquitinating enzyme 5) ; ubiquitin-specific proteinase UBP5 (EC 3.4.-.-) - yeast (Saccharomyces cerevisiae) ; (U10082) ubiquitin-specific protease [Saccharomyces cerevisiae] ; (U18917) Ubp5p: ubiquitin-specific protease [Saccharomyces cerevisiae] (AE000848) ribonuclease PH [Methanobacterium thermoautotrophicum] (Z99165) dehydrogenase [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis]
18972	ENU02766	ANI61C6486: 5121..5812	55-74	675-704	NAP		g2621768	73	40	0.0003	31	72	"Phenylalanyl-TRNA synthetase beta chain cytoplasmic (phenylalanine--TRNA ligase beta chain) ; phenylalanine--TRNA ligase (EC 6.1.1.20) beta chain, cytosolic - yeast (Saccharomyces cerevisiae) ; (D50617) cytoplasmic phenylalanyl-TRNA synthetase beta chain [Saccharomyces cerevisiae] "
18973	ENU02767	ANI61C9140: 81..773	22-55	651-672	NAP		g2408060	306	133	1.00E-30	44	66	
18974	ENU02768	ANI61C1828: 2180..1488	56-76	687-706	NAP		g2635242	347	102	3.00E-21	28	65	
18975	ENU02769	ANI61C8024: 152..844	58-77	680-708	NAP		g1174509	898	315	2.00E-85	71	41	

Seq num	Seq id	Contig	Source	5 pos	Primer	3 pos	Selection	Database	Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18976	ENU02770	ANI61C4361:	67-86	890..197	696-718	NAP	NAP		g586321		47	0.000002				Hypothetical 25.3 KD protein in RIM2-MS11 intergenic region; hypothetical protein YBR193c - yeast (Saccharomyces cerevisiae); (Z21487) unknown product [Saccharomyces cerevisiae]; (Z36062) ORF YBR193c [Saccharomyces cerevisiae] Potential proteasome component C5 (multicatalytic endopeptidase complex subunit C5); multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRS3 - yeast (Saccharomyces cerevisiae); (M34777) proteasome subunit [Saccharomyces cerevisiae]; (D00845) proteasome subunit [Saccharomyces cerevisiae]; (X78214) PRS3 [Saccharomyces cerevisiae]; (Z35802) ORF YBL041w [Saccharomyces cerevisiae] (Y15013) copalyl diphosphate synthase [Gibberella fujikuroi] (AB024617) isochlorogenic acid C-15 hydroxylase [Gibberella zeae] (Z81110) predicted using GeneFinder; cDNA EST EMBL.D76086 comes from this gene; cDNA EST EMBL.C077... (AF063095) SELIL [Mus musculus] (AJ005963) 100 kDa protein [Ajellomyces capsulatus] "hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae); (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae]"
18977	ENU02771	ANI61C3960:	23-58	920..226	646-675	NAP	NAP		g130882		593	259	2.00E-68			
18978	ENU02772	ANI61C7782:	60-79	719..25	690-712	NAP	NAP		g3549899		1287	146	1.00E-34	32	23	
18979	ENU02773	ANI61C548:	69-88	87..93	698-721	NAP	NAP		g4589927		232	52	3.00E-13	32	39	
18980	ENU02774	ANI61C5279:	28-47	94..789	662-681	NAP	NAP		g3879255		261	117	7.00E-26	34	56	
18981	ENU02775	ANI61C6626:	69-88	4422..5118	704-723	NAP	NAP		g4159995		577	93	2.00E-18			
18982	ENU02776	ANI61C4759:	46-65	28..724	680-700	NAP	NAP		g3135013		808	323	1.00E-87	66	25	
18983	ENU02777	ANI61C322:	52-71	962..5264	688-707	NAP	NAP		g586554		160	56	0.000000	32	92	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18984	ENU02778	ANI61C8274:	72-93	708-727	NAP		g1171666	303	70	3.00E-16	51	87	NADH-ubiquinone oxidoreductase 14.8 KD subunit (complex I-14.8KD) (CI-14.8KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) - Neurospora crassa ; (X76344) NADH dehydrogenase (ubiquinone) [Neurospora crassa]
18985	ENU02779	ANI61C7893:	43-62	679-701	NAP		g1708501	245	73	8.00E-22	36	11	Integrin alpha chain-like protein (alpha-INT1) ; (U35070) integrin-like protein alpha Int1p [Candida albicans]
18986	ENU02780	ANI61C301:5	24-43	650-684	NAP		g1064798	256	83	6.00E-20	40	47	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis] ; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]
18987	ENU02781	ANI61C1078	57-82	697-717	NAP		g3152652	365	155	4.00E-37	38	49	"(AF064870) endo-1,3(4)-beta-glucanase [Xanthophyllomyces dendrorhous]"
18988	ENU02782	ANI61C3321:	57-77	698-717	NAP		g1723660	211	76	6.00E-20	33	89	hypothetical 27.6 KD protein in RPL26B-ACB1 intergenic region ; probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae) ; (Z72821) ORF YGR036c [Saccharomyces cerevisiae]
18989	ENU02783	ANI61C301:5	24-43	650-684	NAP		g1064798	256	83	6.00E-20	40	47	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis] ; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]
18990	ENU02784	ANI61C3956:	42-74	677-703	NAP		g3702646	401	66	3.00E-10			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
18991	ENU02785	ANI61C6073:	23-42	659-684	NAP		g2132916	448	136	2.00E-31	43	32	probable membrane protein YOR206w - yeast (Saccharomyces cerevisiae) ; (Z75114) ORF YOR206w [Saccharomyces cerevisiae]
18992	ENU02786	ANI61C2284:	70-90	707-731	NAP		g3766371	328	152	2.00E-36	40	90	(AL031907) hypothetical protein [Schizosaccharomyces pombe]
18993	ENU02787	ANI61C7986:	63-82	705-724	NAP		g3006189	646	81	4.00E-32	63	62	(AL022304) 60s ribosomal protein 17-c. [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18994	ENU02788	AN161C7899: 40-59	40-59	680-702	NAP		g417305	788	113	2.00E-30	42	35	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN(9)-alpha-mannosidase) ; alpha-mannosidase MNS1 (EC 3.2.1.-) - yeast (Saccharomyces cerevisiae) ; (M63598) alpha-mannosidase [Saccharomyces cerevisiae] ; (Z49631) ORF YJR131w [Saccharomyces cerevisiae] "
		4999..4295											probable membrane protein YLR130c - yeast (Saccharomyces cerevisiae) ; (X91258) L3120 [Saccharomyces cerevisiae] ; (U53881) Ylr130cp [Saccharomyces cerevisiae] ; (Z73302) ORF YLR130c [Saccharomyces cerevisiae]
18995	ENU02789	AN161C6615: 72-96	72-96	715-734	NAP		g1363710	345	90	2.00E-17	27	54	(D84656) ORF N118 [Schizosaccharomyces pombe]
		2346..1642											general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae] (AF104986) calmodulin [Magnaporthe grisea]
18996	ENU02790	AN161C8963: 62-81	62-81	706-725	NAP		g1507666	100	38	0.073			choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
		3632..4337											hypothetical 24.0 KD protein in EMP47-SEC53 intergenic region ; probable membrane protein YFL046w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL046W [Saccharomyces cerevisiae]
18997	ENU02791	AN161C7925: 59-82	59-82	699-723	NAP		g1703215	374	77	2.00E-16	31	37	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]
		1866..2573											
18998	ENU02792	AN161C1046: 24-46	24-46	662-688	NAP		g4028590	625	144	3.00E-54	89	99	
		1:848..1554											
18999	ENU02793	AN161C1518: 34-63	34-63	668-698	NAP		g117619		80	2.00E-17			
		2666..1960											
19000	ENU02794	AN161C7112: 66-85	66-85	710-730	NAP		g1175951	328	114	1.00E-25	40	91	
		2765..3471											
19001	ENU02795	AN161C9541: 61-92	61-92	700-726	NAP		g4160573	199	86	3.00E-16	33	24	
		60..767											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
19002	ENU02796	ANI61C7325:	24-43	670-689	NAP		g3417433	411	117	9.00E-26	46	57	(AL031262) putative transcription factor [Schizosaccharomyces pombe]
19003	ENU02797	3090..2383 ANI61C3136:	22-52	668-687	NAP		g3914054	783	256	1.00E-67	53	30	MUTS protein homolog 1 ; (Z98559) dna mismatch repair muts family [Schizosaccharomyces pombe]
19004	ENU02798	1862..1155 ANI61C7529:	22-53	663-687	NAP		g4160343	482	102	8.00E-28	37	69	(AL035216) similar to rat synaptic glycoprotein sc2 [Schizosaccharomyces pombe]
19005	ENU02799	1958..1251 ANI61C7521:	40-59	687-706	NAP		g117093	285	69	4.00E-13	50	86	cytochrome C oxidase polypeptide VI precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Saccharomyces cerevisiae) ; (M10138) cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] ; (U00062) Cox6p: cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] (U16782) chlorophenol monooxygenase [Ralstonia eutropha] (U33115) high copy suppressor of polymerase alpha mutations [Saccharomyces cerevisiae]
19006	ENU02800	898..187 ANI61C1008	34-53	680-700	NAP		g1764155	252	134	5.00E-31	42	39	"lysozyme M1 precursor (1,4-beta-N-acetylmuramidase M1) ; lysozyme (EC 3.2.1.17) M1 precursor - Streptomyces globisporus ; (M30645) N-acetylmuramidase M1 precursor [Streptomyces globisporus]" (U85498) glutamate-cysteine ligase catalytic subunit [Mus musculus] hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae) ; (Z75160) ORF YOR252w [Saccharomyces cerevisiae]
19007	ENU02801	1171..1882 ANI61C4037:	67-87	701-736	NAP		g992654	72	46	9.00E-10	45	8	mitochondrial carrier protein PMT ; mitochondrial uncoupling protein homolog YKL120w - yeast (Saccharomyces cerevisiae) ; (L04948) mitochondrial transporter protein [Saccharomyces cerevisiae] ; (Z28120) ORF YKL120w [Saccharomyces cerevisiae]
19008	ENU02802	82..793 ANI61C2626:	23-45	670-692	NAP		g1945070	727	223	9.00E-58	51	34	
19009	ENU02803	2735..2631 ANI61C3329:	71-91	714-741	NAP		g2132100		75	4.00E-13	30	87	
19010	ENU02804												
19011	ENU02805	108..820 ANI61C8183:	34-53	684-704	NAP		g417500	568	127	6.00E-44	55	62	

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19012	ENU02806	AN161C1120	55-78	704-725	NAP		g2833337	103	73	2.00E-12	30	36	Dihydrofolate reductase / thymidylate synthase (DHFR-TS) ; (U20781)
		5:6686..5974											dihydrofolate reductase-thymidylate synthase [Trypanosoma brucei] (AJ009973) hexokinase [Aspergillus niger]
19013	ENU02807	AN161C2275:	65-86	716-735	NAP		g4140255	2000	401	e-111	83	48	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		1667..955											choline transport protein
19014	ENU02808	AN161C559:8	22-49	664-693	NAP		g117619		37	0.17			[Saccharomyces cerevisiae] ; (Z772599) ORF YGL077c [Saccharomyces cerevisiae]
		37..124											(AF022892) orotidine monophosphate pyrophosphorylase [Coccidioides immitis]
19015	ENU02809	AN161C7117:	27-46	676-698	NAP		g4249578	892	355	2.00E-97	75	97	"(S76267) Snq2 homolog=brf1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa]
		1674..961											[Schizosaccharomyces pombe] "
19016	ENU02810	AN161C414:1	26-51	675-698	NAP		g913016	332	124	3.00E-32	37	14	[Schizosaccharomyces pombe] "
		4..724											(U41625) coded for by C. elegans cDNA yk52e10.5; coded for by C. elegans cDNA yk50f4.3; coded for by C. elegans cDNA yk50f4.5; Similar to acetyl-coenzyme A synthetase. [Caenorhabditis elegans] (AF036871) annexin XIV [Neurospora crassa]
19017	ENU02811	AN161C1124:	22-45	667-694	NAP		g1118129	524	88	4.00E-27	41	25	hypothetical protein YOL135c - yeast (Saccharomyces cerevisiae) ; (Z74877) ORF YOL135c [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
		887..1601											acid proteinase capC precursor - chesnut blight fungus ; (X83997) acid proteinase [Cryphonectria parasitica]
19018	ENU02812	AN161C2113:	71-90	725-744	NAP		g3004934	490	144	6.00E-34	35	49	
		847..132											
19019	ENU02813	AN161C8918:	54-74	697-727	NAP		g2132018	288	96	2.00E-25	36	94	
		643..1358											
19020	ENU02814	AN161C8241:	30-49	673-704	NAP		g2133287	421	189	2.00E-47	43	85	
		1541..2257											

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19021	ENU02815	ANI61C952:1	34-68	683-709	NAP		g130582	173	92	4.00E-18	28	17	Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease; reverse transcriptase; endonuclease]; hypothetical protein - common tobacco; (X13777) ORF [Nicotiana tabacum]
19022	ENU02816	ANI61C9559: 23-58		678-698	NAP		g3913768	102	61	0.000000	28	98	phosphoglycolate phosphatase (PGP); (AE000735) phosphoglycolate phosphatase [Aquifex aeolicus]
19023	ENU02817	ANI61C6527: 66-84		722-741	NAP		g3122361	271	116	2.00E-25	42	86	putative lipote-protein ligase B (lipote biosynthesis protein B); (Z98980) hypothetical protein [Schizosaccharomyces pombe]
19024	ENU02818	ANI50C2369 01_1:30..748	22-43	672-698	NAP		g118126		59	0.000000	36	90	regulatory protein CYS-3; regulatory protein cys-3 - Neurospora crassa; (M26008) cys-3 [Neurospora crassa]
19025	ENU02819	ANI61C1250: 36-55		693-712	NAP		g2499588	1079	248	e-100	98	62	cell division control protein 2 (cyclin-dependent protein kinase); (U07169) protein kinase functional homolog of cdc2 [Emmentella nidulans]
19026	ENU02820	ANI61C1099 9:1170..1888	44-65	689-720	NAP		g2804298	372	85	4.00E-16	32	28	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19027	ENU02821	ANI61C1040 9:1373..655	27-47	684-703	NAP		g2132880	284	83	8.00E-23	27	89	probable membrane protein YOR087w - yeast (Saccharomyces cerevisiae); (Z74995) ORF YOR087w [Saccharomyces cerevisiae]
19028	ENU02822	ANI61C5788: 22-49		678-698	NAP		g131031	328	113	1.00E-29	41	96	putative PRT1 protein; probable PRT1 protein - yeast (Hansenula polymorpha); (X15111) put. PRT1 protein (AA 1-221) (1 is 1st base in codon) [Pichia angusta]
19029	ENU02823	ANI61C1758: 72-92		729-748	NAP		g2497056	214	86	3.00E-16	36	47	putative dioxigenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19030	ENU02824	ANI61C1211: 22-41		680-699	NAP		g3183014	706	150	3.00E-65	65	85	GTP cyclohydrolase I (GTP-CH-I); (Z98849) gtp cyclohydrolase I [Schizosaccharomyces pombe]

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19031	ENU02825	AN161C8770:	47-67	698-724	NAP		g2981719	776	91	1.00E-30	44	30	Crystal Structures Of The Copper-Containing Amine Oxidase From <i>Arthrobacter Globiformis</i> In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone ; Crystal Structures Of The Copper-Containing Amine Oxidase From <i>Arthrobacter Globiformis</i> In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone
		4573..3854											
19032	ENU02826	AN161C6467:	22-47	681-700	NAP		g461926	228	69	5.00E-22	33	95	Haloacetate dehalogenase H-2 ; haloacetate dehalogenase (EC 3.8.1.3) H-2 - <i>Moraxella</i> sp. plasmid pUOI ; (D90423) haloacetate dehalogenase H-2 [<i>Moraxella</i> sp.]
		2814..3534											
19033	ENU02827	AN161C9085:	57-76	716-735	NAP		g2506921	158	45	0.0006	37	55	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [<i>Escherichia coli</i>] ; (U73857) dioxygenase [<i>Escherichia coli</i>] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [<i>Escherichia coli</i>] "
		505..1225											
19034	ENU02828	AN161C3566:	44-65	697-723	NAP		g731439	132	54	0.000001	28	91	hypothetical 25.6 KD protein in NTF2-SRP1 intergenic region ; hypothetical protein YER010c - yeast (<i>Saccharomyces cerevisiae</i>) ; (U18778) Yer010cp [<i>Saccharomyces cerevisiae</i>] (AF051914) C-4 methyl sterol oxidase [<i>Candida albicans</i>] (AL035521) hypothetical protein [<i>Arabidopsis thaliana</i>] (Z98056) putative glyoxylate pathway regulator [<i>Schizosaccharomyces pombe</i>] (Z98600) hypothetical atp-dependent transporter [<i>Schizosaccharomyces pombe</i>]
		3337..4058											
19035	ENU02829	AN161C3532:	27-56	688-706	NAP		g2970627	908	304	4.00E-82	60	71	
		718..3439											
19036	ENU02830	AN161C8203:	23-44	682-702	NAP		g4455171	303	146	1.00E-34	33	27	
		339..760											
19037	ENU02831	AN161C7700:	57-76	717-736	NAP		g2281979	362	131	5.00E-30	46	64	
		3994..3273											
19038	ENU02832	AN161C9556:	26-45	687-706	NAP		g2330757	649	259	4.00E-68	61	86	
		759..37											

Database Description

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19039	ENU02833	ANI61C1110	42-66	703-722	NAP		g585896	267	130	1.00E-29	38	94	"probable mitochondrial 60S ribosomal protein L16 precursor; mitochondrial - yeast (Saccharomyces cerevisiae) ; (X78214) L16 ribosomal protein [Saccharomyces cerevisiae] ; (Z35799) ORF YBL038w [Saccharomyces cerevisiae]"
19040	ENU02834	ANI61C590:8	45-65	707-726	NAP		g549607	409	125	2.00E-36	38	35	hypothetical 74.7 KD TRP-ASP repeats containing protein in DAL80-GAP1 intergenic region ; hypothetical protein YKR036c - yeast (Saccharomyces cerevisiae) ; (Z28261) ORF YKR036c [Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] hypothetical monooxygenase Y4FC ; (AE000072) Y4FC [Rhizobium sp. NGR234] (AL031852) short-chain dehydrogenase [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans] ALP11 protein ; (Z69727) homolog of co-factor B [Schizosaccharomyces pombe] ; (AB008750) Alp11 [Schizosaccharomyces pombe] "hypothetical 29.0 KD protein in PWP2-SUP61 intergenic region ; probable membrane protein YCR059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR059c, len:258 [Saccharomyces cerevisiae]" probable glutamate 5-kinase (gamma-glutamyl kinase) (GK) ; (Z98597) hypothetical glutamate 5-kinase [Schizosaccharomyces pombe]
19041	ENU02835	ANI61C6543: 27-52	690-709	NAP			g2414650	346	93	2.00E-31	69	93	
19042	ENU02836	ANI61C7500: 22-51	684-704	NAP			g3426048	540	167	6.00E-52	51	50	
19043	ENU02837	ANI61C4138: 57-76	719-739	NAP			g2496621	310	118	3.00E-26	50	64	
19044	ENU02838	ANI61C1289: 23-48	685-706	NAP			g3738145	147	90	1.00E-17	31	64	
19045	ENU02839	ANI61C5187: 60-80	721-743	NAP			g1870209	857	132	4.00E-34	38	42	
19046	ENU02840	ANI61C3158: 50-69	715-734	NAP			g1723421	318	87	1.00E-16	34	78	
19047	ENU02841	ANI61C6895: 23-43	688-707	NAP			g140519	120	74	9.00E-13	29	72	
19048	ENU02842	ANI61C5862: 25-49	684-709	NAP			g3183130	554	200	1.00E-50	52	52	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19049	ENNU02843	AN161C3285:	33-52	700-718	NAP		g3850101	378	137	7.00E-32	47	93	(AL033388) putative ma-binding protein [Schizosaccharomyces pombe]
19050	ENNU02844	2094..1367 AN161C459:7	60-79	726-745	NAP		g3135988	652	69	3.00E-19	46	37	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19051	ENNU02845	441..6714 AN161C5557:	56-77	723-742	NAP		g2501603	311	123	9.00E-28	38	31	hypothetical 77.0 KD protein in HES1-SEC63 intergenic region ; hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae) ; (Z75151) ORF YOR243c [Saccharomyces cerevisiae]
19052	ENNU02846	AN161C1617:	23-41	688-709	NAP		g1806234		63	1.00E-16			(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
19053	ENNU02847	47..774 AN161C7616:	64-83	731-750	NAP		g2697132	287	87	3.00E-22	36	84	(AF036580) necrosis and ethylene inducing peptide [Fusarium oxysporum f. sp. erythroxyl]
19054	ENNU02848	1734..1006 AN161C990:2	69-88	735-755	NAP		g1491795	486	201	6.00E-51	38	26	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus]"
19055	ENNU02849	444..1716 AN161C3212:	34-53	699-720	NAP		g585695	232	120	1.00E-26	32	41	Pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]
19056	ENNU02850	AN161C1640:	34-53	699-720	NAP		g3006187	283	134	5.00E-31	35	74	(AL022304) hypothetical protein [Schizosaccharomyces pombe]
19057	ENNU02851	1744..1016 AN161C3047:	56-77	723-742	NAP		g1723441	353	95	6.00E-19	40	51	hypothetical 36.3 KD protein C56F8.09 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe]
19058	ENNU02852	4114..3386 AN161C3602:	47-66	707-733	NAP		g731385	269	63	3.00E-17	39	73	[Schizosaccharomyces pombe] hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae]
19059	ENNU02853	6005..6734 AN161C2954:	48-67	714-735	NAP		g2258125	164	64	0.000000	29	39	(Z83828) AmMst-1 [Armatia muscaria]
19060	ENNU02854	27..756 AN161C8514:	67-87	722-755	NAP		g3287949	418	147	3.00E-39	41	30	hypothetical 79.5 KD protein C17A5.12 in chromosome I ; (Z98849) hypothetical protein [Schizosaccharomyces pombe]

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19061	ENU02855	AN161C943:1	33-52	700-721	NAP		g140459		61	0.000000			"hypothetical 30.7 KD protein in RV5161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"
19062	ENU02856	AN161C7480:1	70-88	735-759	NAP		g3915154	245	102	3.00E-21	33	39	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichoides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichoides] "probable ATP-dependent permease precursor ; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) ; (X59720) YCR011c, len:1049 [Saccharomyces cerevisiae]"
19063	ENU02857	AN161C6213:1	69-100	740-758	NAP		g113449	552	152	2.00E-36	47	21	hypothetical 34.9 KD protein in RPL44-DCL1 intergenic region ; hypothetical protein YHR142w - yeast (Saccharomyces cerevisiae) ; (U10397) Yhr142wp [Saccharomyces cerevisiae] (AB013443) cytochrome P450 [Coprinus cinereus] (AL033503) putative mitochondrial carrier protein [Candida albicans] putative para-hydroxybenzoate—polyprenyltransferase precursor (PHB:polyprenyltransferase) ; (Z69728) unknown [Schizosaccharomyces pombe]
19064	ENU02858	AN161C9775:1	55-75	724-744	NAP		g731723	589	178	5.00E-44	46	68	Tryptophan synthase ; tryptophan synthase (EC 4.2.1.20) - Neurospora crassa ; (J04594) tryptophan synthetase [Neurospora crassa] acetyl-hydrolyase ; (M64783) acetyl-hydrolyase [Streptomyces hygroscopicus] (AL049522) putative phosphatase component [Schizosaccharomyces pombe]
19065	ENU02859	AN161C1733:1	72-99	742-762	NAP		g3721844	296	73	5.00E-25	36	40	
19066	ENU02860	AN161C7086:1	22-41	693-712	NAP		g3859687	527	150	8.00E-36	53	77	
19067	ENU02861	AN161C920:1	46-65	717-737	NAP		g1706003		76	3.00E-13			
19068	ENU02862	AN161C2401:1	40-59	711-731	NAP		g136372	2405	310	e-109	80	34	
19069	ENU02863	AN161C5992:1	69-87	728-760	NAP		g1352065		69	2.00E-11			
19070	ENU02864	AN161C933:1	25-54	695-717	NAP		g4539598	322	76	9.00E-15	33	62	

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19071	ENU02865	AN161C7676:	68-87	728-760	NAP		g3123232	643	152	1.00E-58	53	78	Description general stress protein 39 (GSP39) ; (AB001488) belongs to the insect-type alcohol dehydrogenase / ribitol dehydrogenase family. [Bacillus subtilis] ; (Z99106) similar to alcohol dehydrogenase [Bacillus subtilis] "Chain N, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 2, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "
19072	ENU02866	AN161C8467:	23-48	694-716	NAP		g3114282	484	163	1.00E-39	47	93	
19073	ENU02867	AN161C9642:	40-59	706-735	NAP		g1175965	388	171	5.00E-42	41	99	hypothetical 25.2 KD protein in TH15 5'region and in TH112 5'region ; hypothetical protein YFL061w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL061W [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae] ; (Z71611) ORF YNL335w [Saccharomyces cerevisiae] (Y11113) endoglucanase IV [Hypocrea jecorina] (AL034583) hypothetical protein [Schizosaccharomyces pombe] (D85230) hypothetical protein [Plectonema boryanum] hypothetical 69.8 KD protein in BDF1-SFP1 intergenic region ; hypothetical protein YLR401c - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr401cp [Saccharomyces cerevisiae] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (Z99759) hypothetical protein [Schizosaccharomyces pombe] glutamate synthase (NADH) precursor (NADH-GOGAT) ; glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa ; (L01660) NADH-glutamate synthase [Medicago sativa]
19074	ENU02868	AN161C6810:	22-41	692-717	NAP		g2315274	731	297	5.00E-80	56	70	
19075	ENU02869	AN161C7686:	54-73	730-749	NAP		g4056557	266	107	8.00E-23			
19076	ENU02870	AN161C4371:	33-53	712-731	NAP		g1339949	174	73	2.00E-12	26	91	
19077	ENU02871	AN161C1115	24-44	702-722	NAP		g2833203	515	189	1.00E-47	50	35	
19078	ENU02872	AN161C1748:	64-86	739-762	NAP		g1438947	932	269	2.00E-94	68	46	
19079	ENU02873	AN161C7911	42-71	721-740	NAP		g2467272	867	356	9.00E-98	72	31	
19080	ENU02874	AN161C1719:	40-60	720-739	NAP		g417073	754	302	1.00E-81	58	11	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19081	ENU02875	ANI61C7336	72-92	753-772	NAP		g2808725		57	0.000000			(AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis]
19082	ENU02876	ANI61C280:2	25-45	706-725	NAP		g113589	814	201	4.00E-51	48	65	Allantoinase ; allantoinase (EC 3.5.3.4) - Neurospora crassa ; (J02927)
19083	ENU02877	ANI61C5029	33-53	709-734	NAP		g3183342	248	102	3.00E-21	36	57	allantoinase [Neurospora crassa] hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596)
19084	ENU02878	ANI61C5155	43-62	717-744	NAP		g2132846		79	4.00E-14			hypothetical protein [Schizosaccharomyces pombe] probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]
19085	ENU02879	ANI61C6256	27-47	709-728	NAP		g731773	599	105	2.00E-44	59	69	hypothetical 31.9 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL003w - yeast (Saccharomyces cerevisiae)
19086	ENU02880	ANI61C4645	30-61	713-732	NAP		g2132214	233	98	7.00E-20			hypothetical protein YPL164c - yeast (Saccharomyces cerevisiae) ; (Z73520) ORF YPL164c [Saccharomyces cerevisiae] ; (X96770) P2550 protein [Saccharomyces cerevisiae] (Z83864) hypothetical protein Rv3854c [Mycobacterium tuberculosis]
19087	ENU02881	ANI61C6841	72-96	741-774	NAP		g1781102	552	185	4.00E-46	38	50	"hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region ; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae) ; (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae]"
19088	ENU02882	ANI61C1062	54-74	735-756	NAP		g586554	137	54	0.000001	29	92	(AL022071) fructosyl amine [Schizosaccharomyces pombe] (AL035655) 60s ribosomal protein 136 [Schizosaccharomyces pombe]
19089	ENU02883	ANI61C1146	54-73	737-756	NAP		g2950465	544	144	8.00E-34	37	52	
19090	ENU02884	ANI61C7987	46-74	725-748	NAP		g4490679	180	82	6.00E-15	56	43	

Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19091	ENU02885	ANI61C1043	44-64	728-747	NAP		g231710	779	256	1.00E-67	86	89	cell division control protein 42 homolog (CDC42SP) ; cell division control protein CDC42 - fission yeast (Schizosaccharomyces pombe) ; (M83650) CDC42sp [Schizosaccharomyces pombe] ; (L25677) Cdc42p [Schizosaccharomyces pombe] hypothetical 22.4 KD protein C6G10.10C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] (AE000853) conserved protein [Methanobacterium thermoautotrophicum] acetyl-CoA hydrolase (acetyl-CoA deacylase) (acetyl-CoA acylase) (acetate utilization protein) ; acu-8 protein - Neurospora crassa ; (M31521) acetate permease (acu-8) [Neurospora crassa]
19092	ENU02886	ANI61C4663	22-41	705-725	NAP		g3219969	156	70	2.00E-11	29	96	"phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptonate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae]"
19093	ENU02887	ANI61C7186	30-52	715-734	NAP		g2621836	150	84	9.00E-16	32	92	(AL031853) putative zinc finger protein [Schizosaccharomyces pombe] (AB014595) KIAA0695 protein [Homo sapiens]
19094	ENU02888	ANI61C8897	60-81	741-764	NAP		g113310	1070	193	6.00E-99	79	47	
19095	ENU02889	ANI61C6534	22-45	707-726	NAP		g461540	883	336	9.00E-92			
19096	ENU02890	ANI61C3210	49-68	729-754	NAP		g3738206	215	46	0.0003			
19097	ENU02891	ANI61C4686	30-49	715-737	NAP		g3327204	609	125	8.00E-44	44	31	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19098	ENU02892	ANI61C8599:	47-66	736-755	NAP		g465105	644	174	1.00E-61	54	31	(U04841) lanosterol synthase [Saccharomyces cerevisiae]
19099	ENU02893	2096..1347 ANI61C4266:	45-64	725-755	NAP		g731476	201	81	1.00E-14	42	55	hypothetical 14.4 KD protein in RNRI-ALD3 intergenic region; hypothetical protein YER072w - yeast (Saccharomyces cerevisiae); (U18813) Yer072wp [Saccharomyces cerevisiae] (AF008220) yler [Bacillus subtilis]; (Z99119) similar to hypothetical proteins [Bacillus subtilis] (AF025475) Masc1 [Ascombolus immersus]
19100	ENU02894	ANI61C1600:	43-67	732-753	NAP		g2293194	289	89	4.00E-23			(AE001036) L-carnitine dehydratase (catB-2) [Archaeoglobus fulgidus] (AL049558) putative phosphatidylinositol-kinase [Schizosaccharomyces pombe] (AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
19101	ENU02895	ANI61C9279:	34-53	722-744	NAP		g2558956	343	124	5.00E-34	40	43	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19102	ENU02896	ANI61C9067:	62-86	746-773	NAP		g2649608		60	4.00E-17			ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19103	ENU02897	ANI61C8232:	62-82	752-774	NAP		g4581508	727	190	4.00E-69	63	11	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19104	ENU02898	ANI61C8865:	33-52	726-745	NAP		g4160583	699	281	4.00E-75	53	80	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19105	ENU02899	ANI61C1147:	23-48	714-736	NAP		g731040	531	157	6.00E-38			ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19106	ENU02900	ANI61C1073:	60-80	754-773	NAP		g3024226	547	69	2.00E-23	35	53	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19107	ENU02901	6:1321..566 ANI61C352:7	26-46	719-739	NAP		g1730615	390	107	3.00E-36	48	90	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19108	ENU02902	ANI61C7690:	65-84	751-780	NAP		g2244799	108	62	0.000000	32	69	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];
19109	ENU02903	793..36 ANI61C1026:	22-49	709-737	NAP		g4049528	342	82	1.00E-25	39	70	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5); HUS5 protein - fission yeast (Schizosaccharomyces pombe); (X81846) hus5 [Schizosaccharomyces pombe]; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe];

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19110	ENJU02904	ANI61C5273:	22-52	721-740	NAP		g731758	419	176	1.00E-43	44	37	hypothetical 67.8 KD protein in IK11-ERG9 intergenic region ; hypothetical protein YHR188c - yeast (Saccharomyces cerevisiae) ; (U00030) Yhr188cp [Saccharomyces cerevisiae] (D85777) cysteine dioxygenase [Homo sapiens]
19111	ENJU02905	ANI61C2115:	63-87	750-782	NAP		g1747324	200	68	3.00E-18	47	76	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN50 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Yal061 wp [Saccharomyces cerevisiae]
19112	ENJU02906	ANI61C9458:	48-72	740-767	NAP		g731294	532	108	3.00E-41	39	59	"putative ATP-dependent RNA helicase T26G10.1 in chromosome III ; ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans ; (Z29115) similar to RNA helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon.; cDNA EST yk368a4.3 comes from this gene; cDNA EST yk368a4.5 comes fr..."
19113	ENJU02907	ANI61C9311:	40-60	735-759	NAP		g465975	1254	314	4.00E-85			making-type switching protein SWI10 ; SWI10 protein - fission yeast (Schizosaccharomyces pombe) ; (X61926) SWI10 [Schizosaccharomyces pombe] ; (AL031534) mating-type switching protein swi10. [Schizosaccharomyces pombe]
19114	ENJU02908	ANI61C8348:	22-46	723-743	NAP		g549012	512	216	2.00E-55	44	98	(U89492) arylsulfatase [Neurospora crassa]
19115	ENJU02909	ANI61C3366:	38-57	737-761	NAP		g2873363	346	95	8.00E-40	40	35	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19116	ENJU02910	ANI61C3113:	68-99	772-791	NAP		g2507070	429	39	0.027	32	39	

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19117	ENU02911	ANI61C8607: 2162..1397	65-84	768-788	NAP		g549705	61	0.000000	007			36.1 KD protein in BUD2-MIF2 intergenic region ; SEC14 protein homolog YKL091c - yeast (Saccharomyces cerevisiae) ; (Z28091) ORF YKL091c [Saccharomyces cerevisiae]
19118	ENU02912	ANI61C1114: 0:928..162	53-72	754-777	NAP		g1175102	266	123	2.00E-27	32	85	hypothetical protein H10077 ; hypothetical protein H10077 - Haemophilus influenzae (strain Rd KW20) ; (U32693) H. influenzae predicted coding region H10077 [Haemophilus influenzae Rd] (Z99113) ymaE [Bacillus subtilis]
19119	ENU02913	ANI61C1138: 0:1440..2206	40-61	742-764	NAP		g2634109	235	107	8.00E-23	36	93	(D89119) unnamed protein product [Schizosaccharomyces pombe]
19120	ENU02914	ANI61C4135: 42..808	63-82	767-787	NAP		g1749446	399	153	1.00E-36	53	50	(U04540) flavocytochrome b5 chimeric protein [synthetic construct] ; (L27087) cytochrome b5 [Artificial gene]
19121	ENU02915	ANI61C1442: 992..224	62-81	769-788	NAP		g488428	181	75	6.00E-13	33	33	pseudouridyate synthase 3 (pseudouridine synthase 3) (depressed growth-rate protein DEG1) ; depressed growth-rate protein DEG1 - yeast (Saccharomyces cerevisiae) ; (D50617) depressed growth-rate protein [Saccharomyces cerevisiae] ; (D44600) depressed growth-rate protein DEG1 [Saccharomyces cerevisiae]
19122	ENU02916	ANI61C9241: 2204..1435	45-68	749-772	NAP		g399356	561	171	5.00E-42	49	44	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618) RTM1 gene product [Saccharomyces cerevisiae]
19123	ENU02917	ANI61C4650: 3141..3910	72-91	774-799	NAP		g730689	120	50	0.00001	30	64	quinate permease (quinate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa] (AF088907) clock-controlled gene-8 protein [Neurospora crassa]
19124	ENU02918	ANI61C3926: 848..78	55-74	759-783	NAP		g131761	220	112	3.00E-24	34	38	
19125	ENU02919	ANI61C5774: 818..48	24-43	729-752	NAP		g3746897	178	96	3.00E-19	29	85	

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19126	ENU02920	AN161C3373: 3533..2763	27-60	736-755	NAP		g2133034	475	135	3.00E-31	39	37	probable membrane protein YPR156c - yeast (<i>Saccharomyces cerevisiae</i>) ; (U28371) Similar to <i>S. cerevisiae</i> hypothetical protein Ybr008p (Swiss Prot. accession number P38124) [<i>Saccharomyces cerevisiae</i>]
19127	ENU02921	AN161C6835: 5945..6715	42-61	751-770	NAP		g3130039	414	154	7.00E-37	40	95	(AL023534) hypothetical protein [<i>Schizosaccharomyces pombe</i>]
19128	ENU02922	AN161C1057: 3:1358..2128	59-78	767-787	NAP		g1787246	178	64	9.00E-10	29	91	(AE000202) putative synthetase [<i>Escherichia coli</i>]
19129	ENU02923	AN161C5814: 411..1182	49-68	752-778	NAP		g3130041	640	229	2.00E-59	53	64	(AL023534) hypothetical protein [<i>Schizosaccharomyces pombe</i>] ; (AL031534) homology to longevity assurance protein.
19130	ENU02924	AN161C138:2 054..1283	25-45	732-754	NAP		g1175373	237	80	3.00E-18	31	31	[<i>Schizosaccharomyces pombe</i>] hypothetical 72.5 KD protein C2F7.10 in chromosome I ; hypothetical protein SPAC2F7.10 - fission yeast (<i>Schizosaccharomyces pombe</i>) ; (Z50142) unknown
19131	ENU02925	AN161C8631: 5833..5062	26-47	731-755	NAP		g2290382	1118	441	e-123	78	53	[<i>Schizosaccharomyces pombe</i>] (U89985) serine/threonine protein phosphatase PPT1 [<i>Neurospora crassa</i>] (AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [<i>Schizosaccharomyces pombe</i>] (AL031798) 40s ribosomal protein s20.
19132	ENU02926	AN161C2278: 2096..2868	44-63	755-774	NAP		g2257524	396	159	2.00E-38	41	92	[<i>Schizosaccharomyces pombe</i>] het-c4 protein - <i>Podospira anserina</i> ; (L36210) het-c [<i>Podospira anserina</i>] putative mitochondrial carrier
19133	ENU02927	AN161C8986: 4696..3924	43-62	752-773	NAP		g3687464	320	131	6.00E-30	62	65	YGR257C ; hypothetical protein YGR257c - yeast (<i>Saccharomyces cerevisiae</i>) ; (Z73042) ORF YGR257c [<i>Saccharomyces cerevisiae</i>] ; (X99228) mitochondrial carrier protein [<i>Saccharomyces cerevisiae</i>] (L78243) alternative splice (exon 17) [<i>Homo sapiens</i>]
19134	ENU02928	AN161C1011: 2918..2145	53-72	765-784	NAP		g2133323	588	163	1.00E-39	64	94	
19135	ENU02929	AN161C1071: 5:3566..2793	62-92	773-793	NAP		g1723767	361	137	1.00E-31	40	62	
19136	ENU02930	AN161C8371: 3..777	24-59	736-755	NAP		g1374920	227	86	2.00E-22	33	14	

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19137	ENU02931	AN161C9255: 4223..3449	23-51	735-755	NAP		g2764632	796	217	1.00E-67	71	99	(AJ001520) 19.3KD iron-sulfur subunit of mitochondrial complex I
19138	ENU02932	AN161C9182: 4568..5342	22-45	735-754	NAP		g2808634	860	192	2.00E-48	40	29	[Neurospora crassa] (AJ001909) transcriptional activator [Aspergillus niger]
19139	ENU02933	AN161C9243: 1724..2497	25-44	730-757	NAP		g2493049	303	59	5.00E-19	58	85	"ATP synthase delta chain, mitochondrial precursor ; (Z82020) ATP-synthase delta-subunit [Agaricus bisporus]"
19140	ENU02934	AN161C9220: 11..785	25-58	738-757	NAP		g4586458	113	85	7.00E-16	33	60	(AB025252) reverse transcriptase [Magnaporthe grisea]
19141	ENU02935	AN161C1049: 7:8419..7645	51-72	763-783	NAP		g133892	473	90	2.00E-22	80	82	40S ribosomal protein S26E (CRP5) (13.6 KD ribosomal protein) ; ribosomal protein S26.e - Neurospora crassa ; (X55637) ribosomal protein [Neurospora crassa]
19142	ENU02936	AN161C1059: 9:3190..2415	24-42	738-757	NAP		g1730831	543	214	5.00E-55	44	68	hypothetical 40.7 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL231c - yeast (Saccharomyces cerevisiae) ; (Z69381) Similar to hypothetical yeast protein L3502 [Saccharomyces cerevisiae] ; (Z71507) ORF YNL231c [Saccharomyces cerevisiae]
19143	ENU02937	AN161C6671: 1311..2086	56-76	763-789	NAP		g2281983	809	252	3.00E-66	59	81	(Z98056) hypothetical protein [Schizosaccharomyces pombe]
19144	ENU02938	AN161C8852: 60..836	34-68	734-767	NAP		g2494268	252	64	1.00E-21	37	98	putative sterigmatocystin biosynthesis protein STCT ; (U34740) putative translation elongation factor 1 gamma [Emericella nidulans]
19145	ENU02939	AN161C7170: 3870..3094	22-43	737-756	NAP		g1710780	744	225	1.00E-70	84	99	40S ribosomal protein S9 (S7) ; (X96613) cytoplasmic ribosomal protein S7 [Podospira anserna]
19146	ENU02940	AN161C6870: 1542..2318	24-43	737-758	NAP		g2494700	514	161	6.00E-39	51	77	hypothetical 31.2 KD protein in CYP5-AM1A intergenic region ; (AE000330) putative regulator [Escherichia coli]
19147	ENU02941	AN161C4612: 1762..986	70-92	785-804	NAP		g3080524	1235	75	6.00E-13	38	34	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
19148	ENU02942	AN161C7417: 2566..1791	66-86	774-800	NAP		g2842510	211	115	5.00E-25	36	26	(AL021748) hypothetical protein [Schizosaccharomyces pombe]

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19149	ENU02943	AN161C17:10	61-80	777-796	NAP		g1723966	355	152	2.00E-36	43	77	hypothetical 32.0 KD protein in GOG5-NIF3 intergenic region ; hypothetical protein YGL224c - yeast (Saccharomyces cerevisiae) ; (Z72746) ORF YGL224c [Saccharomyces cerevisiae]
19150	ENU02944	AN161C9622: 56-75		769-791	NAP		g2132860	366	107	2.00E-29	41	99	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae) ; (Z74904) ORF YOL162w [Saccharomyces cerevisiae]
19151	ENU02945	AN161C8718: 22-44		737-757	NAP		g2654181	1289	195	1.00E-99	75	55	(AF034963) calmodulin-dependent protein kinase; CgCMK [Glomerella cingulata]
19152	ENU02946	AN161C8415: 24-52		741-760	NAP		g2494268	342	123	2.00E-27	38	97	putative sterigmatocystin biosynthesis protein STCT ; (U34740) putative translation elongation factor 1 gamma [Emicella nidulans]
19153	ENU02947	AN161C1835: 56-75		772-794	NAP		g4140255	1017	153	2.00E-36	43	43	(AJ009973) hexokinase [Aspergillus niger]
19154	ENU02948	AN161C9772: 24-53		741-762	NAP		g4586977	2840	272	3.00E-72	47	10	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]
19155	ENU02949	AN161C1091 42-65		762-781	NAP		g1346290	1048	216	5.00E-63	49	47	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluveromyces fragilis]
19156	ENU02950	AN161C3316: 70-89		790-809	NAP		g4106687	480	178	4.00E-44	39	64	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]
19157	ENU02951	AN161C6374: 22-55		741-762	NAP		g731752	432	178	3.00E-44	46	94	hypothetical 26.3 KD protein in OYE2-GND1 intergenic region ; hypothetical protein YHR181w - yeast (Saccharomyces cerevisiae) ; (U00028) Yhr181wp [Saccharomyces cerevisiae]
19158	ENU02952	AN161C1159: 61-81		776-801	NAP		g929862	648	141	7.00E-33	35	51	(X83502) J0916 [Saccharomyces cerevisiae]
19159	ENU02953	AN161C5218: 47-66		768-787	NAP		g3650379	811	250	1.00E-65	77	95	(AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19160	ENU02954	AN161C9551: 3908..4690	22-42	738-762	NAP		g730589	347	153	1.00E-36	41	99	"mitochondrial 60S ribosomal protein L6 precursor (YML6) ; ribosomal protein L6 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (U10397) MRPL6p: Mitochondrial ribosomal protein L6 [Saccharomyces cerevisiae]"
19161	ENU02955	AN161C1209: 3642..4425	25-46	740-766	NAP		g1168402	689	273	7.00E-73	69	99	minor allergen ALT A 7 (ALT A VII) ; minor allergen - Alternaria alternata ; (X78225) minor allergen [Alternaria alternata]
19162	ENU02956	AN161C1656: 210..993	42-61	764-783	NAP		g3929362	202	53	3.00E-20	34	35	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVII]
19163	ENU02957	AN161C1095: 1452..668	61-80	781-803	NAP		g2828147	486	86	4.00E-34	54	88	(AF042384) BC-2 protein [Homo sapiens]
19164	ENU02958	AN150C6268: _1:785..6	55-76	762-797	NAP		g586551		76	3.00E-13	27	73	hypothetical 33.5 KD protein in MRPS9-YSW1 intergenic region ; probable membrane protein YBR147w - yeast (Saccharomyces cerevisiae) ; (Z36016) ORF YBR147w [Saccharomyces cerevisiae]
19165	ENU02959	AN161C1064: 9:1676..891	22-51	745-765	NAP		g1429204	568	208	3.00E-53	56	98	(X99215) leucine zipper [Aspergillus niger]
19166	ENU02960	AN161C1050: 5:88..873	25-44	747-768	NAP		g114971	456	109	6.00E-45	50	23	beta-glucosidase precursor (gentiobiase) (beta-D-glucoside glucosylhydrolase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast (Kluyveromyces marxianus var. marxianus) ; (X05918) beta-glucosidase (AA 1 - 845) [Kluyveromyces marxianus]
19167	ENU02961	AN150C1_19: 01:889..103	26-46	751-770	NAP		g1706333		343	7.00E-94	61	45	pyruvate decarboxylase ; (U00967) pyruvate decarboxylase [Aspergillus parasiticus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19168	ENU02962	ANI61C7922:	72-91	796-816	NAP		g1176153	290	131	6.00E-30	35	86	"hypothetical 27.4 KD protein in RNPB-SOHA intergenic region (ORF 1) ; (U18997) ORF_f256 [Escherichia coli] ; (AE000394) orf, hypothetical protein [Escherichia coli]"
		3045..2259											
19169	ENU02963	ANI61C1099	42-73	768-787	NAP		g1723499	448	171	7.00E-42	52	47	hypothetical 46.7 KD protein C19G10.05 in chromosome 1 ; (Z69909) putative proteasome regulatory subunit
		8:8746..7959											[Schizosaccharomyces pombe] (Z81035) predicted using GeneFinder. Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from...
19170	ENU02964	ANI61C9746:	72-91	799-818	NAP		g3874345		51	0.00001			(AC005106) T25N20.15 [Arabidopsis thaliana]
		1406..2194											"probable citrate synthase, mitochondrial precursor "
19171	ENU02965	ANI61C7857:	25-44	753-772	NAP		g3935151	377	133	9.00E-44	43	94	(Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis]
		2128..2917											26S proteasome regulatory subunit MTS3 ; (X92682) 26S protease regulatory subunit
19172	ENU02966	ANI61C8794:	62-81	791-810	NAP		g1705884	725	98	1.00E-57	58	50	[Schizosaccharomyces pombe] ; 26S protease subunit [Schizosaccharomyces pombe]
		1258..469											probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae) ; (Z74904) ORF YOL162w [Saccharomyces cerevisiae]
19173	ENU02967	ANI61C6439:	54-73	783-802	NAP		g2370322	173	55	2.00E-11	32	40	(U56245) kynurenine 3-monoxygenase [Drosophila melanogaster]
		871..81											
19174	ENU02968	ANI61C1076	63-82	792-813	NAP		g1709170	263	112	3.00E-24	35	82	
		5:866..1658											
19175	ENU02969	ANI61C4271:	32-55	762-782	NAP		g2132860	453	124	7.00E-30	46	93	
		2897..2105											
19176	ENU02970	ANI61C9024:	34-54	756-784	NAP		g1336011	548	180	1.00E-44	42	47	
		4502..5294											

Table 1

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19177	ENU02971	ANI61C832:	25-44	745-776	NAP		g731651	1143	205	2.00E-52	41	38	hypothetical aldehyde-dehydrogenase like protein in PUT2-SRB2 intergenic region ; hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) ; (U00062) Yhr039cp [Saccharomyces cerevisiae]
19178	ENU02972	ANI61C9335:	23-44	756-776	NAP		g465506	334	162	3.00E-39	43	97	HTP reductase ; RIB7 protein - yeast (Saccharomyces cerevisiae) ; (X71329) YBR 12.03 [Saccharomyces cerevisiae] ; (Z36022) ORF YBR153w [Saccharomyces cerevisiae] ; (Z21622) HTP reductase [Saccharomyces cerevisiae]
19179	ENU02973	ANI61C8182:	47-67	774-800	NAP		g417454	823	309	1.00E-83	63	94	proliferating cell nuclear antigen (PCNA) ; proliferating cell nuclear antigen - fission yeast (Schizosaccharomyces pombe) ; (X54857) proliferating cell nuclear antigen [Schizosaccharomyces pombe] ; (AL035637) proliferating cell nuclear antigen [Schizosaccharomyces pombe] (AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]
19180	ENU02974	ANI61C3990:	72-91	802-825	NAP		g4007792	716	287	6.00E-77	60	20	"40S ribosomal protein S6 ; ribosomal protein S6.e, cytosolic - fission yeast (Schizosaccharomyces pombe) ; (M36382) ribosomal protein S6 (rps6) precursor [Schizosaccharomyces pombe] ; (Z54308) 40S ribosomal protein [Schizosaccharomyces pombe]
19181	ENU02975	ANI61C2420:	44-63	778-797	NAP		g133980	591	136	2.00E-31	75	64	
19182	ENU02976	ANI61C5533:	64-88	788-818	NAP		g3901117	570	122	2.00E-27	37	30	(AJ012752) maltose permease [Saccharomyces cerevisiae]
19183	ENU02977	ANI61C3559:	24-47	751-779	NAP		g2258125	526	190	9.00E-51	49	47	(Z83828) ArnMst-1 [Amanita muscaria]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19184	ENU02978	AN161C4093:	56-75	792-811	NAP		g3929361	758	167	2.00E-67	75	94	NADH-ubiquinone oxidoreductase 23 KD subunit precursor (complex I-23KD) (CI-23KD) ; (X95547)
		748..1548											ferredoxin-like iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
19185	ENU02979	AN161C7409:	55-75	793-812	NAP		g1679597		37	0.15			(Z50095) mannosidase [Agaricus bisporus]
19186	ENU02980	AN161C3696:	54-73	793-812	NAP		g2996620	207	83	2.00E-15	32	91	(AF009224) beta-ketoadipate enol-lactone hydrolase [Acinetobacter sp. ADP1] ; beta-ketoadipate enol-lactone hydrolase [Acinetobacter calcoaceticus]
		1569..769											(U80063) lipase LipA [Streptomyces cinnamomeus]
19187	ENU02981	AN161C8073:	22-46	761-780	NAP		g2435400	162	71	9.00E-12	34	55	vacuolar ATP synthase 16 KD
		6666..5866											proteolipid subunit (V-ATPase C-subunit) ; (AF008924) V-ATPase C-subunit [Aedes aegypti]
19188	ENU02982	AN150C8867	50-69	787-808	NAP		g3334403		69	3.00E-11	53	99	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
		_3:902..102											mucin - rhesus macaque (fragment) ; (U00483) mucin [Macaca mulatta]
19189	ENU02983	AN161C8446:	47-68	783-806	NAP		g1654074	217	52	0.000005	35	53	GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gen20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae]
		6996..6195											"(AF069298) similar to ATPases associated with various cellular activities (Pfam: AAA_hmm, score: 230.91) [Arabidopsis thaliana]"
19190	ENU02984	AN161C4168:	53-76	793-812	NAP		g2134574	200	35	0.74	37	95	"cytochrome P450 52L9 (CYPLIA9) (alkane-inducible P450-ALK5-A) ; cytochrome P450 ALK5-A, alkane-inducible - yeast (Candida maltosa) ; (D12717) n-alkane inducible cytochrome P-450 [Candida maltosa]"
		1493..234											(AJ010475) RNA helicase [Arabidopsis thaliana]
19191	ENU02985	AN161C1026	56-79	796-816	NAP		g1169871	956	211	2.00E-81	65	33	
		3:1614..811											
19192	ENU02986	AN161C7203:	38-57	779-798	NAP		g3193292	520	116	1.00E-25	42	66	
		17..819											
19193	ENU02987	AN161C1049	37-58	778-798	NAP		g3913326	467	99	7.00E-22	41	42	
		1:851..48											
19194	ENU02988	AN161C6305:	23-42	766-784	NAP		g3776027	624	107	6.00E-38	45	31	
		82..885											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
19195	ENJU02989	ANI61C8325:	23-45	766-785	NAP		g4455301	337	88	7.00E-22	45	87	(AL035528) putative protein [Arabidopsis thaliana]
19196	ENJU02990	2398..1594 ANI61C2426:	22-41	765-784	NAP		g1723231	229	114	7.00E-25	36	92	hypothetical 27.1 KD protein CID4.09C in chromosome I ; (Z69239) unknown [Schizosaccharomyces pombe]
19197	ENJU02991	ANI61C1087:	52-71	790-814	NAP		g1764133	346	115	4.00E-25	36	94	(U81790) PIG8 [Uromyces fabae]
19198	ENJU02992	793..1597 ANI61C3686:	64-83	807-827	NAP		g126066	230	83	3.00E-15	35	52	L-lactate dehydrogenase (LDH) ; L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize ; (Z11754) lactate dehydrogenase [Zea mays]
19199	ENJU02993	558..848 ANI61C9004:	56-75	798-820	NAP		g2507431	967	266	2.00E-70	48	55	"phenylalanyl-TRNA synthetase mitochondrial precursor (phenylalanine--TRNA ligase) (PHERS) ; phenylalanine--tRNA ligase (EC 6.1.1.20) alpha chain precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49219) MstIp [Saccharomyces cerevisiae] ; (Z71235) MstIp [Saccharomyces cerevisiae]"
19200	ENJU02994	1905..2711 ANI61C9827:	37-57	766-801	NAP		g2245570	205	84	5.00E-16	36	23	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda]"
19201	ENJU02995	104..910 ANI61C1114:	63-87	808-828	NAP		g2959376	980	203	1.00E-51	56	68	(AL022117) hypothetical protein [Schizosaccharomyces pombe]
19202	ENJU02996	686..1493 ANI61C8366:	35-54	782-801	NAP		g4220472	301	73	2.00E-23	34	98	(AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]
19203	ENJU02997	1075..1883 ANI61C1234:	49-68	786-815	NAP		g2497056	586	123	1.00E-27	41	56	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19204	ENJU02998	3091..2283 ANI61C5032:	37-58	778-804	NAP		g1633572	115	47	0.0002			"(U52064) Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] ; (U75698) ORF 73; extensive acidic domains, potential leucine zipper; immediate early protein homolog [Kaposi's sarcoma-associated herpesvirus]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19205	ENU02999	ANI61C8256:	41-60	790-809	NAP		g2497179	145	57	0.000000	28	18	hypothetical 113.2 KD protein in SSO2-HSC82 intergenic region ;
		855..45											hypothetical protein YMR185w - yeast (Saccharomyces cerevisiae) ; (Z49808)
19206	ENU03000	ANI61C45:26	33-53	782-801	NAP		g125886	657	181	5.00E-45	41	67	unknown [Saccharomyces cerevisiae] lactate 2-monoxygenase (lactate oxidase) ; lactate 2-monoxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis]
		82..3492											
19207	ENU03001	ANI61C6754:	22-52	769-790	NAP		g1723578	652	266	2.00E-70	49	83	probable oxidoreductase C26F1.07 in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe]
		4137..4947											
19208	ENU03002	ANI61C6415:	58-77	809-828	NAP		g4376408	384	96	1.00E-30	36	64	(AE001600) Hypothetical Protein [Chlamydia pneumoniae]
		841..1654											
19209	ENU03003	ANI61C1054	29-50	780-799	NAP		g2648302	290	108	4.00E-32	46	79	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hnpE-2) [Archaeoglobus fulgidus]"
		0:6432..6207											
19210	ENU03004	ANI61C6496:	24-57	776-795	NAP		g4557817	1234	250	7.00E-66	54	48	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor ; succinyl-CoA:3-ketoacid-coenzyme A transferase precursor (succinyl CoA:3-oxoacid CoA-transferase) (OXCCT) ; (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]
		9172..9986											
19211	ENU03005	ANI61C4798:	41-62	793-812	NAP		g2388907	606	50	0.00002			(Z98974) hypothetical protein [Schizosaccharomyces pombe]
		1015..1828											
19212	ENU03006	ANI61C9801:	59-78	812-831	NAP		g416589	445	207	7.00E-53	42	49	AFG1 protein ; AFG1 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Afg1p [Saccharomyces cerevisiae] (AF003835) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Rattus norvegicus]
		4737..3923											
19213	ENU03007	ANI61C9149:	42-65	794-814	NAP		g2253701	524	90	1.00E-45	53	89	alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) (AL049498) rho1 gdp-gtp exchange protein 1 [Schizosaccharomyces pombe]
		1260..2074											
19214	ENU03008	ANI61C7738:	65-91	810-837	NAP		g2146821	107	48	0.000000	29	32	
		2704..1890											
19215	ENU03009	ANI61C2364:	23-50	772-796	NAP		g4539279	867	259	2.00E-75	55	18	
		513..1328											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19216	ENU03010	ANI61C1752:	55-74	809-828	NAP		g1723371	1081	406	e-113	63	51	hypothetical protein in CRTE 3'region (ORF2) ; (M87280) ORF2 [Erwinia herbicola]
		1711..896											(X92509) crg1 [Ustilago maydis]
19217	ENU03011	ANI61C3291:	25-55	778-799	NAP		g1514667	331	104	1.00E-26	36	63	"(AF068712) similar to cytochrome P450 (Pfam: p450.hmm, score: 265.98) [Caenorhabditis elegans]"
19218	ENU03012	ANI61C6315:	46-75	801-820	NAP		g3168924		64	9.00E-10			microfibrillar-associated protein 1 ; microfibrillar protein MFAP1 - human ; (U04209) associated microfibrillar protein [Homo sapiens] (U78597) kinesin light chain [Plectonema boryanum]
19219	ENU03013	ANI61C7472:	55-72	813-832	NAP		g1709012	253	59	0.000000	34	55	GAR1 protein ; GAR1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe] ; (AB000537) snoRNP protein GAR1 [Schizosaccharomyces pombe] ; (Z95397) Gar1p [Schizosaccharomyces pombe] ; (AL021747) gar1 protein; small nucleolar rnp required for pre-mrna for pre-mrna processing [Schizosaccharomyces pombe]
19220	ENU03014	ANI61C9978:	40-59	794-818	NAP		g2645229	488	199	3.00E-50	40	55	"5-formyltetrahydrofolate cyclo-ligase (5,10-methenyl-tetrahydrofolate synthetase) (methenyl-THF synthetase) (MTHFS) ; indoleacetate-lysine synthetase (EC 6.3.2.20) - human ; (L38928) 5,10-methenyltetrahydrofolate synthetase [Homo sapiens]"
19221	ENU03015	ANI61C3973:	51-70	810-829	NAP		g544370	439	82	1.00E-30			hypothetical 39.6 KD protein in MTD1-NUP133 intergenic region ; hypothetical protein YKR081c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR401 [Saccharomyces cerevisiae] ; (Z28306) ORF YKR081c [Saccharomyces cerevisiae]
19222	ENU03016	ANI61C1000	22-41	777-800	NAP		g1706921	173	81	1.00E-14	36	99	
		4:4568..3748											
19223	ENU03017	ANI61C406:9	39-58	798-818	NAP		g549638	500	171	4.00E-42	38	77	
		57..136											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19224	ENU03018	ANI61C8156:	67-86	826-846	NAP		g452120		64	2.00E-15			(L28112) complete cds [Rattus norvegicus]
19225	ENU03019	ANI61C6265:	25-46	785-805	NAP		g2326188	622	182	4.00E-49	43	79	(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum]
19226	ENU03020	ANI61C8257:	40-59	799-820	NAP		g1175386	245	77	2.00E-13	30	78	hypothetical 37.7 KD protein C18B11.06 in chromosome 1; hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe) ; (Z50728) hypothetical protein [Schizosaccharomyces pombe]
19227	ENU03021	ANI61C8772:	43-62	796-823	NAP		g1208451	347	129	2.00E-29	32	67	(D64004) hypothetical protein [Synechocystis sp.]
19228	ENU03022	ANI61C7523:	22-41	784-803	NAP		g1078634	1309	281	e-130	98	36	sepB protein - Emeritella nidulans ; sepB protein - Emeritella nidulans ; (X86399) sepB [Emeritella nidulans] probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz11p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana] (X78712) glycerol kinase [Homo sapiens]
19229	ENU03023	ANI61C5260:	22-50	770-804	NAP		g1362406	531	131	8.00E-30	46	65	(AF020040) xylose reductase [Pichia guilliermondii] (Z93941) YuxA [Bacillus subtilis] ; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]
19230	ENU03024	ANI61C1027:	22-50	786-805	NAP		g3318617	537	140	3.00E-52	64	71	ribulose-phosphate 3-epimerase (pentose-5-phosphate 3-epimerase) (PPE) (RPE) ; POS18 protein - yeast (Saccharomyces cerevisiae) ; (X83571) Ribulose-5-Phosphate-Epimerase [Saccharomyces cerevisiae] ; (Z49396) ORF YJL121c [Saccharomyces cerevisiae]
19231	ENU03025	ANI61C1491:	40-61	806-825	NAP		g516124	1027	109	2.00E-32	43	43	(AC004218) unknown protein [Arabidopsis thaliana]
19232	ENU03026	ANI61C7207:	62-81	828-847	NAP		g4103055	827	146	1.00E-73	59	80	
19233	ENU03027	ANI61C1024:	31-52	798-817	NAP		g2624002	213	101	7.00E-21	31	85	
19234	ENU03028	ANI61C9660:	67-86	834-853	NAP		g1173139	546	105	1.00E-50	55	86	
19235	ENU03029	ANI61C2864:	70-89	836-856	NAP		g3355474	359	148	3.00E-35	32	65	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19236	ENU03030	ANI61C1875:	54-74	822-841	NAP		g4539944	218	76	1.00E-20	38	61	(AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
19237	ENU03031	33..862 ANI61C819:2	23-53	790-810	NAP		g1477466	612	128	2.00E-57	50	44	(U35246) vacuolar protein sorting homolog h-vps45 [Homo sapiens]
19238	ENU03032	..831 ANI61C1128	22-51	792-811	NAP		g2047309		71	1.00E-11			(U44750) NAD-dependent 15- hydroxyprostaglandin dehydrogenase [Rattus norvegicus]
19239	ENU03033	ANI61C3329:	27-55	786-816	NAP		g3184115	646	111	5.00E-24	29	52	(AL023780) DNA binding protein [Schizosaccharomyces pombe]
19240	ENU03034	1435..604 ANI61C3763:	43-62	811-833	NAP		g1351714	297	71	1.00E-11	31	50	putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe]
19241	ENU03035	ANI61C3280:	22-41	786-813	NAP		g603587	1340	404	e-112	70	58	(X83512) Yna1p [Saccharomyces cerevisiae]
19242	ENU03036	1255..2088 ANI61C7044:	64-83	835-855	NAP		g731638	1109	380	e-105	65	50	"asparaginyl--TRNA synthetase, cytoplasmic (asparagine--TRNA ligase) (ASNRS) ; hypothetical protein YHR019c - yeast (Saccharomyces cerevisiae) ; (U10399) Ded81p: Asparaginyl-tRNA synthetase [Saccharomyces cerevisiae]" (AB000704) ribosomal protein S11 homolog [Schizosaccharomyces pombe]
19243	ENU03037	ANI61C1058	46-66	818-838	NAP		g1813337	491	159	2.00E-38	82	71	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI] (U59215) cyclin-dependent protein kinase PHOA(M1) [Emmericella nidulans]
19244	ENU03038	ANI61C7997:	22-53	792-815	NAP		g3929362	292	114	7.00E-25	40	36	36.7 KD protein in CBR5-NOT3 intergenic region ; hypothetical protein YIL041w - yeast (Saccharomyces cerevisiae) ; (Z46861) unknown [Saccharomyces cerevisiae] (AL035339) putative protein [Arabidopsis thaliana] (AC002340) hypothetical protein [Arabidopsis thaliana]
19245	ENU03039	ANI61C1048	35-56	808-829	NAP		g3643644	1098	194	9.00E-82	70	59	
19246	ENU03040	ANI61C566:1	50-69	823-844	NAP		g731801	269	66	4.00E-25	32	80	
19247	ENU03041	ANI61C6225:	30-49	802-825	NAP		g4539334		36	0.27			
19248	ENU03042	995..1832 ANI61C2571:	45-64	821-840	NAP		g2880049	251	126	2.00E-28	35	54	

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19249	ENU03043	AN150C346_1:3130..2293	65-87	835-860	NAP		g731285	66	4.00E-10	35	81		hypothetical 27.1 KD protein in ACS1-GCV3 intergenic region ; hypothetical protein YAL049c - yeast (Saccharomyces cerevisiae) ; (U12980) Yal049cp [Saccharomyces cerevisiae] probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (AL035216) probable involvement in ergosterol biosynthesis
19250	ENU03044	AN161C3044: 852..14	40-60	816-835	NAP		g2132957	310	66	4.00E-10	29	47	[Saccharomyces cerevisiae] (AL035216) probable involvement in ergosterol biosynthesis
19251	ENU03045	AN161C8498: 45..883	43-62	806-839	NAP		g4160344	682	264	5.00E-70	48	54	[Schizosaccharomyces pombe] DNA-binding protein amda - Emricella nidulans ; (L28810) regulatory protein [Emricella nidulans]
19252	ENU03046	AN161C7244: 133..972	62-81	830-858	NAP		g2133268	575	112	4.00E-49	41	31	hypothetical 35.9 KD protein C56F8.08 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19253	ENU03047	AN161C1118: 6:3..842	23-58	801-820	NAP		g1723440	608	204	8.00E-52	50	74	hypothetical 35.9 KD protein C56F8.08 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19254	ENU03048	AN161C4142: 923..84	22-56	788-819	NAP		g2370322	220	87	1.00E-16	32	70	hypothetical 35.9 KD protein C56F8.08 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19255	ENU03049	AN161C9321: 3703..2864	33-52	811-830	NAP		g732372	202	97	1.00E-19	33	66	hypothetical 35.9 KD protein C56F8.08 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19256	ENU03050	AN161C1077: 6:2216..3055	48-72	826-845	NAP		g1235752	1535	215	2.00E-69	65	38	(D63916) protein phosphatase 2A 65kD regulatory subunit (A subunit) [Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19257	ENU03051	AN161C4209: 3767..2927	64-83	842-862	NAP		g3560142	454	160	1.00E-38	32	45	[Schizosaccharomyces pombe] putative cytochrome C1 heme lyase (CC1HL) ; (Z98601) cytochrome c1 heme lyase [Schizosaccharomyces pombe]
19258	ENU03052	AN161C2329: 3142..2302	42-61	814-840	NAP		g3183375	284	161	8.00E-39	47	95	[Schizosaccharomyces pombe] putative cytochrome C1 heme lyase (CC1HL) ; (Z98601) cytochrome c1 heme lyase [Schizosaccharomyces pombe]

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19259	ENU03053	ANIS0C1079_1:92..931	32-51	811-830	NAP		g134966	153	1.00E-36	37	27		"STE6 protein ; ste6 protein - fission yeast (Schizosaccharomyces pombe) ; (X53254) ste6 [Schizosaccharomyces pombe] ; (AL049559) guanine-nucleotide releasing factor, Ste6p [Schizosaccharomyces pombe] ; ste6 gene [Schizosaccharomyces pombe]"
19260	ENU03054	ANIS0C7943: 2176..1335	28-47	799-827	NAP		g632081	103	1.00E-21				hypothetical protein 4 - Xanthobacter sp. ; (X79863) orf4 [Xanthobacter sp. Py2]
19261	ENU03055	ANIS0C8446: 6996..6155	47-68	823-846	NAP		g1654074	217	52	0.000005	34	55	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19262	ENU03056	ANIS0C4954: 5249..4407	39-59	820-839	NAP		g2497056	327	105	8.00E-24	31	60	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19263	ENU03057	ANIS0C2666: 4935..4092	45-64	826-845	NAP		g130971	531	193	1.00E-48	47	93	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (strain PAO) ; (M33557) delta-1-pyrroline-5-carboxylate reductase (EC 1.5.1.2) [Pseudomonas aeruginosa] ; (D30688) cytochrome P-450 17 alpha-hydroxylase/C17,20-lyase [Equus caballus]"
19264	ENU03058	ANIS0C4625_4_1:1..844	22-53	796-823	NAP		g1132477	50	9.00E-10				(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19265	ENU03059	ANIS0C3373: 1622..2465	66-87	848-867	NAP		g1654074	1763	246	e-100	78	54	"(Z99113) endo-1,4-beta-xylanase (xylanase D) [Bacillus subtilis]"
19266	ENU03060	ANIS0C9674: 2561..3405	22-49	799-824	NAP		g2634199	426	174	7.00E-43	38	53	lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
19267	ENU03061	ANIS0C45:26 48..3492	62-81	845-864	NAP		g125886	657	183	1.00E-45	40	70	(AL023634) cyclin [Schizosaccharomyces pombe]
19268	ENU03062	ANIS0C3172: 1727..881	33-54	818-837	NAP		g3150260	169	67	1.00E-10	28	71	

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19269	ENU03063	ANI61C2645:	22-49	805-826	NAP		g2132011	501	208	5.00E-53	42	94	hypothetical protein YOL080c - yeast (Saccharomyces cerevisiae) ; (Z74822)
		314..1160											ORF YOL080c [Saccharomyces cerevisiae]
19270	ENU03064	ANI61C1036	58-80	838-864	NAP		g3334212	1108	235	5.00E-97	65	82	delta-aminolevulinic acid dehydratase (porphobilinogen synthase) (ALADH) ; (AF038566) porphobilinogen synthase [Candida glabrata]
		2:2974..3822											(AL032639) predicted using GeneFinder; similar to Iron-containing alcohol dehydrogenases; cDNA EST yk372c11.5 comes from this gene; cDNA EST yk304d8.3 comes from this gene; cDNA EST yk304d8.5 comes from this gene; cDNA EST yk26...
19271	ENU03065	ANI61C6401:	22-54	809-829	NAP		g3880867	728	217	1.00E-55	56	56	UTR2 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Utr2p [Saccharomyces cerevisiae]
19272	ENU03066	ANI61C5735:	22-46	807-829	NAP		g320712	418	159	2.00E-38	31	60	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region ; hypothetical protein YHR112c - yeast (Saccharomyces cerevisiae) ; (U00059) Yhr112cp [Saccharomyces cerevisiae]
19273	ENU03067	ANI61C8613:	27-47	800-834	NAP		g731700	817	252	3.00E-66	47	71	"mitogen-activated protein kinase HOG1 (MAP kinase HOG1) (osmosensing protein HOG1) ; protein kinase HOG1 (EC 2.7.1.-), mitogen-activated - yeast (Saccharomyces cerevisiae) ; (X89514) mitogen-activated protein kinase [Saccharomyces cerevisiae] ; (Z73285) ORF YLR113w [Saccharomyces cerevisiae]"
19274	ENU03068	ANI61C8213:	23-54	805-830	NAP		g2507192	584	158	5.00E-38	63	47	hypothetical 36.7 KD protein C2F7.14C in chromosome I ; hypothetical protein SPAC2F7.14c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe]
19275	ENU03069	ANI61C8076:	36-55	817-845	NAP		g1175376	475	184	6.00E-46	54	67	
		852..1											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19276	ENU03070	AN161C1075	59-78	851-870	NAP		g285211	366	128	4.00E-29	40	51	"[3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase (EC 2.7.1.115) - rat ; branched-chain alpha-ketoacid dehydrogenase kinase 44 kda isoform [rats, lung, heart, Peptide Mitochondrial, 412 aa] ; (M93271) branched-chain alpha-ketoacid dehydrogenase kinase [Rattus norvegicus] "
19277	ENU03071	AN161C1018	52-71	842-864	NAP		g4007783	320	85	7.00E-26	37	72	"(X72850) hydroxyquinol 1,2-dioxygenase [Sphingomonas sp.] "
19278	ENU03072	AN161C5164: 48..903	5:1671..817	834-853	NAP		g1169885	966	314	7.00E-85	65	25	putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein) ; hypothetical protein SPAC13G6.06c - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative glycine dehydrogenase (decarboxylase) [Schizosaccharomyces pombe] (Z64354) unknown
19279	ENU03073	AN161C8668: 2770..3625	58-77	849-871	NAP		g4160354	274	119	3.00E-26	31	93	[Schizosaccharomyces pombe]
19280	ENU03074	AN161C1132: 9650..8794	24-43	819-838	NAP		g2190516	224	99	3.00E-20	34	91	(Y13635) Vip1 protein [Schizosaccharomyces pombe] ; (AL009197) hypothetical protein [Schizosaccharomyces pombe]
19281	ENU03075	AN161C1081 6:1297..2153	37-56	832-851	NAP		g632081	285	87	2.00E-23	41	84	[Schizosaccharomyces pombe] hypothetical protein 4 - Xanthobacter sp. ; (X79863) orf4 [Xanthobacter sp. Py2]
19282	ENU03076	AN161C3713: 943..87	53-72	846-867	NAP		g1894771	362	135	3.00E-31	31	57	(Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]
19283	ENU03077	AN161C539:2 464..2568	28-47	823-842	NAP		g3183310	235	112	3.00E-24	46	95	hypothetical 23.2 KD protein C5D6.06C in chromosome I ; (Z98056) putative osmotolerance protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19284	ENU03078	ANI61C1029:	51-70	838-866	NAP		g1175915	189	64	7.00E-14	44	44	hypothetical 28.8 KD protein in SMC1-SEC4 intergenic region ; probable membrane protein YFL006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL006W [Saccharomyces cerevisiae] ; (D44604) unknown [Saccharomyces cerevisiae]
		1179..322											
19285	ENU03079	ANI61C3377:	22-49	816-837	NAP		g3192044	226	86	3.00E-16	36	80	(AL023796) hypothetical protein [Schizosaccharomyces pombe]
		1390..2247											
19286	ENU03080	ANI61C683:1	22-51	814-837	NAP		g134777	248	128	6.00E-29	29	84	stage V sporulation protein K ; spo VJ protein - Bacillus subtilis ; (X59412) spo VJ [Bacillus subtilis]
		456..599											(Y13623) multifunctional protein2 [Cavia porcellus]
19287	ENU03081	ANI61C1140	43-63	840-859	NAP		g3005897	338	175	4.00E-43	34	38	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
		7:1618..2476											ubiquinol-cytochrome C reductase
19288	ENU03082	ANI61C7321:	61-80	858-878	NAP		g1654074	240	118	5.00E-26	29	57	iron-sulfur subunit precursor (Riske iron-sulfur protein) (RISP) ; ubiquinol-cytochrome-c reductase (EC 1.10.2.2)
		2751..1892											iron-sulfur protein - Neurospora crassa ; (X02472) cytochrome c reductase
19289	ENU03083	ANI61C9902:	70-89	869-888	NAP		g136704	666	162	1.00E-47	66	85	iron-sulfur subunit [Neurospora crassa]
		639..475											branched-chain amino acid aminotransferase (BCAT) ; (AE000647) branched-chain-amino-acid aminotransferase (ilvE) [Helicobacter pylori 26695]
19290	ENU03084	ANI61C7849:	33-54	819-852	NAP		g3024012	404	184	6.00E-46	36	82	acid aminotransferase (ilvE) (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
		1987..1126											probable adenosine deaminase (adenosine aminohydrolase) ; adenosine deaminase homolog YNL141w - yeast (Saccharomyces cerevisiae) ; (Z46843) adenosine deaminase (putative) [Saccharomyces cerevisiae] ; (Z71417) ORF YNL141w [Saccharomyces cerevisiae]
19291	ENU03085	ANI61C1875:	54-74	854-873	NAP		g4539944	218	76	1.00E-20	37	65	
		33..894											
19292	ENU03086	ANI61C8984:	23-42	821-843	NAP		g1703166	704	218	4.00E-56	45	80	
		1974..1112											

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19293	ENU03087	AN161C229:3	59-83	857-880	NAP		g549723	738	282	2.00E-75	54	39	hypothetical 75.5 KD protein in SDH1-CIM5/YTA3 intergenic region ; hypothetical protein YKL146w - yeast (Saccharomyces cerevisiae) ; (Z28146) ORF YKL146w [Saccharomyces cerevisiae]
		436..2573											
19294	ENU03088	AN161C6709: 3506..2643	58-76	853-879	NAP		g2104455	456	98	8.00E-38	48	77	(Z95397) unknown [Schizosaccharomyces pombe]
19295	ENU03089	AN161C9444: 1599..735	22-49	825-844	NAP		g1542843	397	162	4.00E-39	34	94	(D87681) acetylsterase [Aspergillus awamori]
19296	ENU03090	AN161C2926: 4377..3210	67-86	867-890	NAP		g2645229	457	129	3.00E-43	37	58	(U78597) kinesin light chain [Plectonema boryanum]
19297	ENU03091	AN161C5745: 29..894	50-72	854-873	NAP		g1078626	1501	413	e-114	99	19	bimD protein - Emericella nidulans ; (L03200) bimD [Emericella nidulans]
19298	ENU03092	AN161C9795: 3152..2286	24-55	829-848	NAP		g2388966	1410	294	4.00E-79	52	27	(Z98979) putative phosphatidylserine decarboxylase proenzyme [Schizosaccharomyces pombe]
19299	ENU03093	AN161C3270: 1954..2821	22-43	828-847	NAP		g1363743	1110	168	6.00E-41	42	35	probable membrane protein YLR241w - yeast (Saccharomyces cerevisiae) ; (U20865) YIR241wp [Saccharomyces cerevisiae]
19300	ENU03094	AN161C7067: 928..61	55-74	861-880	NAP		g2494101	628	237	9.00E-62	41	74	mannitol-1-phosphate 5-dehydrogenase ; (U18943) mannitol-1-phosphate dehydrogenase [Bacillus stearothermophilus]
19301	ENU03095	AN161C3705: 2000..1133	53-72	852-878	NAP		g2649289		103	2.00E-21			(AE001015) acyl-CoA dehydrogenase (acid-9) [Archaeoglobus fulgidus]
19302	ENU03096	AN161C1705: 3803..4670	27-52	825-852	NAP		g1546072	1002	112	4.00E-24	31	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
19303	ENU03097	AN161C322:1	26-45	834-853	NAP		g2507070	1257	299	2.00E-80	62	57	N amino acid transport system protein (methyl/tryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19304	ENU03098	AN161C1188: 9136..8271	24-48	832-852	NAP		g4539455	365	154	6.00E-37	40	69	(AL049500) TSC23.70 [Arabidopsis thaliana]

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19305	ENU03099	ANI61C9049:	22-52	827-850	NAP		g2500006	708	287	5.00E-77	52	99	formyltetrahydrofolate D-formylase (formyl-FH(4) hydrolase); formyltetrahydrofolate deformylase (EC 3.5.1.10) - Corynebacterium sp.; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.]; (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]; (AL022197) putative protein [Arabidopsis thaliana]; (AF034260) protein kinase NRC-2 [Neurospora crassa]; "ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae); (U19729) Ylr406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae]" (AL022304) eukaryotic translation initiation factor 3 ma-binding subunit [Schizosaccharomyces pombe]; vacuolar protein sorting-associated protein VPS16; vacuolar protein sorting-associated protein VPS16 - yeast (Saccharomyces cerevisiae); (U44030) Vsp16p: Vacuolar sorting protein [Saccharomyces cerevisiae] (AE000715) chorisimate mutase/prephenate dehydratase [Aquifex aeolicus] hypothetical 36.4 KD protein in SMP1-MBA1 intergenic region; probable membrane protein YBR183w - yeast (Saccharomyces cerevisiae); (Z36052) ORF YBR183w [Saccharomyces cerevisiae]; (U02073) unknown [Saccharomyces cerevisiae] (AL022072) arginine n-methyltransferase [Schizosaccharomyces pombe] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa]
		1749..879											
19306	ENU03100	ANI61C2649:	64-86	869-892	NAP		g3184098	307	142	4.00E-33	33	53	
		91..961											
19307	ENU03101	ANI61C1190:	25-44	825-853	NAP		g2980795	379	90	3.00E-40	45	97	
		7048..6177											
19308	ENU03102	ANI61C3127:	40-72	849-869	NAP		g2654106	1056	228	e-111	79	41	
		1166..295											
19309	ENU03103	ANI61C1713:	31-49	840-860	NAP		g1084846	321	96	2.00E-19	68	40	
		253..1124											
19310	ENU03104	ANI61C2402:	68-90	870-898	NAP		g3006180	545	121	8.00E-41	45	90	
		47..918											
19311	ENU03105	ANI61C5793:	33-57	843-863	NAP		g2507153	123	57	2.00E-10	24	33	
		1062..190											
19312	ENU03106	ANI61C212:2	22-53	833-852	NAP		g2983461		139	2.00E-32			
		78..1150											
19313	ENU03107	ANI61C1730:	39-59	851-870	NAP		g586314	199	47	3.00E-12	30	66	
		1945..1072											
19314	ENU03108	ANI61C8793:	24-51	836-855	NAP		g4008547	745	145	3.00E-47	42	55	
		1536..662											
19315	ENU03109	ANI61C6738:	22-49	832-854	NAP		g2970667	293	101	6.00E-21	35	73	
		6151..7026											

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19316	ENU03110	ANI61C6877: 22-46		827-854	NAP		g3724291	64	8.00E-16				(AB011417) phosphate permease [Gibberella zeae]
19317	ENU03111	1..875 ANI61C9103: 23-46		836-855	NAP		g2951785	248	66	3.00E-11	41	95	(AB011822) clathrin light chain [Schizosaccharomyces pombe]
19318	ENU03112	120..995 ANI61C1065 24-46		837-856	NAP		g3881189	413	103	1.00E-21	52	98	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...
19319	ENU03113	ANI61C4534: 59-78 2584..3459		865-892	NAP		g4164400	574	93	2.00E-18	36	41	(AL035248) putative cell surface protein by similarity [Schizosaccharomyces pombe]
19320	ENU03114	ANI61C9963: 22-46 1350..2225		834-855	NAP		g585956	397	108	5.00E-28	34	95	"probable mitochondrial 40S ribosomal protein S9 precursor; ribosomal protein S9 precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (Z36015) ORF YBR146w [Saccharomyces cerevisiae]"
19321	ENU03115	ANI61C2000: 43-70 422..1297		841-876	NAP		g585695	70	2.00E-11				pisatin demethylase (cytochrome P450 57A2); pisatin demethylase - fungus (Nectria haematococca); (X73145) pisatin demethylase [Nectria haematococca]

Gene Ontology

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19322	ENU03116	AN150C5234	28-50	843-862	NAP		g1170012		334	6.00E-91			UDP-N-acetylglucosamine--dolichyl-phosphate N-
		_1:1735..859											acetylglucosaminophosphotransferase (GPT) (G1PT) (N-acetylglucosamine-1-phosphate transferase) (GLCNAC-1-P transferase) ; UDP-N-
													acetylglucosamine--dolichyl-phosphate N-
													acetylglucosaminophosphotransferase (EC 2.7.8.15) - fission yeast
													(Schizosaccharomyces pombe) ;
													(U09454) UDP-N-acetylglucosamine: dolichyl phosphate N-
													acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe] ; (AL031349) N-
													acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe]
19323	ENU03117	AN161C9036:	22-50	837-856	NAP		g2132491	210	78	2.00E-24	33	81	probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ;
		1040..164											(U51031) Ydr284cp [Saccharomyces cerevisiae]
19324	ENU03118	AN161C1093	22-51	835-856	NAP		g286165	498	217	6.00E-56	41	96	"(D14846) endo alpha-1,4
		0:921..1797											polygalactosaminidase precursor [Pseudomonas sp.] "
19325	ENU03119	AN161C2150:	70-89	881-904	NAP		g1723784	264	75	7.00E-13	38	88	hypothetical 31.3 KD protein in TAF145-YOR1 intergenic region ;
		1557..1733											hypothetical protein YGR280c - yeast (Saccharomyces cerevisiae) ; (Z73065) ORF YGR280c [Saccharomyces cerevisiae]
19326	ENU03120	AN161C8019:	66-85	874-903	NAP		g4154817	955	300	4.00E-87	61	86	(AE001466) putative [Helicobacter pylori J99]
19327	ENU03121	AN161C5895:	23-46	841-860	NAP		g4490676	643	121	6.00E-63	68	98	(AL035655) ras-related protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19328	ENU03122	AN161C538.3	45-65	864-883	NAP		g2132846	476	175	5.00E-43	32	55	probable membrane protein YOL119c-yeast [Saccharomyces cerevisiae] ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]
		38..1218											protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) form II - bovine
19329	ENU03123	AN161C1077	22-47	837-860	NAP		g482365	426	175	4.00E-43	51	97	proteasome component C7-alpha (macropain subunit C7-alpha) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex C7) (component Y8) (SCL1 suppressor protein) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain YC7-alpha - yeast [Saccharomyces cerevisiae] ; (M63641) proteasome Y8 [Saccharomyces cerevisiae] ; (M55440) yeast proteasome subunit YC7-alpha [Saccharomyces cerevisiae] ; (X56732) proteasome Y8 subunit [Saccharomyces cerevisiae] ; (Z72533) ORF YGL011c [Saccharomyces cerevisiae] ; (S58126) Unknown [Saccharomyces cerevisiae] ; proteasome PRS2 [Saccharomyces cerevisiae]
19330	ENU03124	AN161C8.219	56-78	876-895	NAP		g130858	650	201	2.00E-59			
		0..1309											
19331	ENU03125	AN161C1097	72-91	887-911	NAP		g1086919		84	1.00E-15			(U41279) similar to E. coli acyl-CoA thioesterase II (SP:P23911) [Caenorhabditis elegans]
19332	ENU03126	AN161C8922.	63-82	881-904	NAP		g2499790	1425	388	e-107	98	94	antigen 1 precursor (ASPND1) ; (Z50175) Aspergillus nidulans antigen 1 [Emmericella nidulans] (X98252) HA Vcr-1 protein [Chlorococcus aethiops]
		1914..2797											
19333	ENU03127	AN150C6641	40-59	862-881	NAP		g1526574		46	0.0002			
		1_1:889..6											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19334	ENU03128	ANI61C8587: 4021..3138	22-47	841-863	NAP		g731865	313	96	4.00E-19	26	50	hypothetical 59.6 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL121w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
19335	ENU03129	ANI61C905:2 334..3218	22-50	843-864	NAP		g4336889	961	189	2.00E-78	97	92	(AF107254) cyclophilin B; CYPB [Emeticella nidulans]
19336	ENU03130	ANI61C6956: 112..996	53-76	865-895	NAP		g1710852	786	189	2.00E-55	93	94	GTP-binding protein SARA ; (Z67742) sara [Aspergillus niger]
19337	ENU03131	ANI61C8618: 1156..2040	43-62	860-885	NAP		g4038630	523	122	1.00E-47	58	99	(AL032684) ER lumen protein retaining receptor protein [Schizosaccharomyces pombe]
19338	ENU03132	ANI61C1162: 1273..2157	71-90	882-913	NAP		g3702646	625	105	5.00E-25	34	47	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19339	ENU03133	ANI61C9958: 948..63	47-66	871-890	NAP		g730502	721	277	1.00E-73			activator 1 41 KD subunit (replication factor C 41 KD subunit) ; replication factor C chain RFC2 - yeast (Saccharomyces cerevisiae) ; (D28499) Rfc2 protein [Saccharomyces cerevisiae] ; (U26028) Rfc2p [Saccharomyces cerevisiae] ; (Z49568) ORF YJR068w [Saccharomyces cerevisiae] ; (L47993) ORF YJR068w [Saccharomyces cerevisiae]
19340	ENU03134	ANI61C7904: 526..1411	22-46	846-865	NAP		g585304	596	188	5.00E-47			[Saccharomyces cerevisiae] eukaryotic translation initiation factor 5 (EIF-5) ; translation initiation factor eIF-5 - yeast (Saccharomyces cerevisiae) ; (Z68111) Tif5p [Saccharomyces cerevisiae] ; (Z71255) Tif5p [Saccharomyces cerevisiae] ; (Z73616) eukaryotic translation initiation factor 5 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 843-870	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19341	ENU03135	ANI61C873:2	26-45			NAP		g1350594	699	136	5.00E-70	79	95	RHO1 protein ; Rho1 protein - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC1F7.04 - fission yeast (Schizosaccharomyces pombe) ; (D38180) Rho1 [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe] (U19882) F1bD [Emmericella nidulans] ; Myb-like DNA-binding protein [Emmericella nidulans] (AL034583) putative exonuclease [Schizosaccharomyces pombe] "putative D-3-phosphoglycerate dehydrogenase YIL074W (PGDH) ; hypothetical protein YIL074c - yeast (Saccharomyces cerevisiae) ; (Z37997) orf, len: 469, CAl: 0.23, similar to SERA_ECOLI P08328 D-3-phosphoglycerate dehydrogenase [Saccharomyces cerevisiae] " (D87444) Similar to S.cerevisiae EMP70 protein precursor (S25110) [Homo sapiens] haloacetate dehalogenase H-1 ; haloacetate dehalogenase (EC 3.8.1.3) H-1 - Moraxella sp. plasmid PUOI ; (D90422) haloacetate dehalogenase H-1 [Moraxella sp.] ribonucleoside-Diphosphate reductase M2 chain (ribonucleotide reductase) ; ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M2 - mouse ; Protein R2 Of Ribonucleotide Reductase From Mouse ; (X15666) M2 ribonucleotide reductase [Mus musculus] ; (M14223) ribonucleotide reductase subunit M2 [Mus musculus]
		274..1388												
19342	ENU03136	ANI61C9705:45-64				NAP		g642577	1691	592	e-169	99	94	
		4099..3213												
19343	ENU03137	ANI61C4397:50-71				NAP		g4056553	514	145	3.00E-34	42	43	
		29..917												
19344	ENU03138	ANI61C7016:38-61				NAP		g731830	1371	277	1.00E-81	66	51	
		1144..2032												
19345	ENU03139	ANI61C7328:43-63				NAP		g1665777	884	166	1.00E-48	44	41	
		1520..2409												
19346	ENU03140	ANI61C8058:72-91				NAP		g461925	408	188	4.00E-47	38	95	
		439..1327												
19347	ENU03141	ANI61C8183:25-50				NAP		g132626	877	182	2.00E-70			
		2180..3069												

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19348	ENU03142	ANI61C6083:	63-83	892-911	NAP		g131771	473	179	4.00E-45	36	53	"probable metabolite transport protein GIT1 ; probable membrane protein YCR098c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR098c, len:518 [Saccharomyces cerevisiae] "
		1014..124											putative transporter C11D3.18C ; (Z68166) unknown
19349	ENU03143	ANI61C6144:	43-70	870-892	NAP		g1351714		134	8.00E-31			[Schizosaccharomyces pombe] (AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
		24..915											probable stergmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740) putative p450 monooxygenase [Emenccella nidulans]
19350	ENU03144	ANI61C7133:	35-54	865-884	NAP		g4104775	177	95	6.00E-19	28	70	TRNA-splicing endonuclease subunit SEN2 (TRNA-intron endonuclease) ; tRNA-splicing endonuclease beta chain - yeast (Saccharomyces cerevisiae) ; (M32336) tRNA splicing endonuclease beta-subunit [Saccharomyces cerevisiae] ; (U53876) Sen2p: tRNA-splicing endonuclease beta-subunit [Saccharomyces cerevisiae] ; (Z73277) ORF YLR105c [Saccharomyces cerevisiae]
		2531..3422											(Y16834) hexose transporter [Candida albicans]
19351	ENU03145	ANI61C5627:	53-80	882-902	NAP		g2493389	313	48	5.00E-13	30	45	"(AL031228) dl1033B10.9 (Short-chain alcohol dehydrogenase family member (HKE6, RING2)) [Homo sapiens] "
		952..61											(L07734) DNA polymerase delta [Schizosaccharomyces pombe] (AL021839) topoisomerase ii associated protein [Schizosaccharomyces pombe] (U78319) chitinase [Entamoeba histolytica]
19352	ENU03146	ANI61C1479:	53-75	879-903	NAP		g134427	269	87	1.00E-16			
		1081..189											
19353	ENU03147	ANI61C7638:	64-84	886-915	NAP		g3336839	365	108	8.00E-23	28	44	
		647..1540											
19354	ENU03148	ANI61C5168:	26-45	857-878	NAP		g3820984	239	103	2.00E-21	36	91	
		2742..1848											
19355	ENU03149	ANI61C7755:	63-87	895-916	NAP		g173384	1021	185	3.00E-94	66	25	
		123..1018											
19356	ENU03150	ANI61C363:	32-51	864-885	NAP		g2894266	759	159	4.00E-41	35	35	
		154..4049											
19357	ENU03151	ANI61C9942:	50-70	880-903	NAP		g1685362	459	179	3.00E-44	32	57	
		55..950											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19358	ENU03152	ANI61C7955:	57-76	893-912	NAP		g544276	1444	291	e-110	76	70	glutathione-dependent FORMaldehyde dehydrogenase (FDH) (FALDH); FDH1 protein - yeast (Candida maltosa) ; (M58332) encoding formaldehyde resistance [Candida maltosa]
19359	ENU03153	ANI61C9825:	64-83	900-919	NAP		g3023753	328	138	7.00E-32	35	94	potential formate transporter ; (U52681) FdhC [Methanobacterium thermoformicum]
19360	ENU03154	ANI61C1073	43-62	879-898	NAP		g416643	770	153	1.00E-70	63	69	"aristolochene synthase (sesquiterpene cyclase) (AS) ; sesquiterpene cyclase, aristolochene synthase, AS - Penicillium roqueforti ; (L05193) aristolochene synthase [Penicillium roqueforti] "
19361	ENU03155	ANI61C5905:	61-85	890-916	NAP		g1730741	392	60	0.000000	25	47	hypothetical 65.3 KDa protein in SUN4-MAS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141) membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w [Saccharomyces cerevisiae]
19362	ENU03156	ANI61C1640:	49-68	883-904	NAP		g2583218	594	212	2.00E-54	51	21	[Saccharomyces cerevisiae] (AF029913) beta glucosidase homolog [Cochliobolus heterostrophus]
19363	ENU03157	ANI61C7916:	72-93	910-929	NAP		g2132851	225	91	9.00E-18	29	55	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae]
19364	ENU03158	ANI61C9393:	22-45	861-880	NAP		g1706221	106	55	0.000000	25	66	[Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] cytochrome B5 ; cytochrome b5 - yeast (Saccharomyces cerevisiae) ; (Z69382) Cytochrome B5 [Saccharomyces cerevisiae] ; (Z71387) ORF YNL111c [Saccharomyces cerevisiae]
19365	ENU03159	ANI61C6658:	22-50	847-880	NAP		g2257554	806	210	3.00E-81	57	34	(AB004538) probable membrane protein YOL130w [Schizosaccharomyces pombe] ; (AL021766) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19366	ENU03160	ANI61C7097:	69-88	909-928	NAP		g1363775	295	136	2.00E-31	40	90	hypothetical protein YDR041w - yeast (Saccharomyces cerevisiae) ; (Z54075) unknown [Saccharomyces cerevisiae]
		1027..126											
19367	ENU03161	ANI61C5156:	53-72	894-913	NAP		g3133108	648	182	4.00E-45	64	93	(AL023554) 40s ribosomal protein s3. [Schizosaccharomyces pombe]
		49..951											
19368	ENU03162	ANI61C7054:	22-49	864-883	NAP		g1749716	1313	367	e-101	60	58	"(D89254) similar to Saccharomyces cerevisiae dihydroxy-acid dehydratase precursor, SWISS-PROT Accession Number P39522 [Schizosaccharomyces pombe]"
		1789..886											
19369	ENU03163	ANI61C7052:	47-68	888-911	NAP		g4587302	1541	226	2.00E-73	54	35	(AB016896) Pcu1 [Schizosaccharomyces pombe]
		3943..3037											
19370	ENU03164	ANI61C1092	46-69	876-911	NAP		g131768	178	62	3.00E-14	28	33	quinate permease (quinate transporter) ; quinate transport protein - Emeritella nidulans ; (X13525) quinate permease [Emeritella nidulans]
		5:1380..474											
19371	ENU03165	ANI61C2278:	22-43	868-887	NAP		g2257524	396	161	5.00E-39	40	95	(AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe]
		1961..2868											
19372	ENU03166	ANI61C9199:	43-62	882-909	NAP		g730753	863	235	7.00E-83			chromosome segregation protein SMC2 (DA-BOX protein SMC2) ; chromosome segregation protein SMC2p [Saccharomyces cerevisiae] ; - yeast (Saccharomyces cerevisiae) ; (U05820) Smc2p [Saccharomyces cerevisiae] ; (D50617) chromosome segregation protein SMC2p [Saccharomyces cerevisiae] ; (D44602) DA-box protein Smc2p [Saccharomyces cerevisiae] (Z98979) hypothetical protein [Schizosaccharomyces pombe]
		1466..557											
19373	ENU03167	ANI61C1000	22-45	865-888	NAP		g2388953	350	113	3.00E-37	42	96	
		4:4856..5763											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19374	ENU03168	AN161C6610:	24-59	869-890	NAP		g464862	503	498	e-140			26S protease regulatory subunit 7 homolog (CIM5 protein) (TAT-binding homolog 3) ; tat-binding protein homolog YTA3 - yeast
		1659..1842											(Saccharomyces cerevisiae) ; (X73571)
													26S proteasome subunit Rpt1 [Saccharomyces cerevisiae] ; (Z22817)
													putative ATPase [Saccharomyces cerevisiae] ; (Z28145) ORF YKL145w [Saccharomyces cerevisiae] ; 26S
													protease [Saccharomyces cerevisiae] (AL033502) uroporphyrinogen-III synthase [Candida albicans]
19375	ENU03169	AN161C9449:	53-72	901-920	NAP		g3859663	70	5.00E-16				hydroxymethylglutaryl-CoA synthase (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) ; hydroxymethylglutaryl-CoA synthase - fission yeast (Schizosaccharomyces pombe) ; (U32187) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Schizosaccharomyces pombe] ; (Z98530) irt1; myo-inositol transporter [Schizosaccharomyces pombe]
19376	ENU03170	AN161C1038	22-56	866-889	NAP		g1708240	1190	379	e-104			cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C lactate ferrihydride oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] (AL031525) mitochondrial carrier protein [Schizosaccharomyces pombe]
19377	ENU03171	AN161C7185:	36-56	884-904	NAP		g117803	635	169	2.00E-41	38	47	hypothetical 81.2 KD protein in MES1-FOL2 intergenic region ; probable membrane protein YGR266w - yeast (Saccharomyces cerevisiae) ; (Z73051) ORF YGR266w [Saccharomyces cerevisiae] ; (Y07893) ORF YGR266w [Saccharomyces cerevisiae]
		648..1558											
19378	ENU03172	AN161C7334:	22-49	871-890	NAP		g3560163	925	201	8.00E-96	67	89	
		1694..784											
19379	ENU03173	AN161C5271:	22-56	872-891	NAP		g1723773	128	59	0.000000	23	28	
		67..978											

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 875-894	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19380	ENU03174	ANI61C4304:	25-44			NAP		g3169083	282	116	2.00E-25	34	79	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
19381	ENU03175	ANI61C8225:	22-52			NAP		g4587575	220	77	1.00E-20	28	96	"(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb AA585719, gb AA728503 and gb T22272 come from this gene. [Arabidopsis thaliana]"
19382	ENU03176	ANI61C1734:	22-50			NAP		g1351729	388	87	1.00E-17	43	73	MAL3 protein ; (Z68198) putative chromosome segregation protein [Schizosaccharomyces pombe] ; (Y09518) MAL3 protein [Schizosaccharomyces pombe] (AE000705) hypothetical protein [Aquifex aeolicus] (X91837) G1315 [Saccharomyces cerevisiae]
19383	ENU03177	ANI61C1699:	24-55			NAP		g2983324	578	201	4.00E-51	43	89	hypothetical oxidoreductase in MRP144-MTF1 intergenic region ; hypothetical protein YMR226c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
19384	ENU03178	ANI61C379:6	23-42			NAP		g1177632	187	91	9.00E-18	32	79	cytochrome P450 51 (CYP11) (P450-L1A1) (sterol 14-alpha demethylase) (eburicol 14-alpha-demethylase) (P450-14DM) ; lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 51 - Penicillium italicum ; (Z49750) cytochrome P-450 [Penicillium italicum]
19385	ENU03179	ANI61C499:5	40-59			NAP		g2492763	572	112	1.00E-44	54	94	Phosphatidylinositol-Specific Phospholipase C In Complex With Glucosamine-(Alpha-1-6)-Myo-Inositol
19386	ENU03180	ANI61C9494:	59-78			NAP		g2493386	1608	337	7.00E-92	58	57	Phosphatidylinositol-Specific Phospholipase C In Complex With Myo-Inositol ; Phosphatidylinositol-Specific Phospholipase C ; Phosphatidylinositol-Specific Phospholipase C In Complex With Glucosamine-(Alpha-1-6)-Myo-Inositol
19387	ENU03181	ANI61C8220:	44-64			NAP		g1633139	95	82	6.00E-15	29	91	

Seq num	Seq id	Contig	Source	5 pos	Primer 3 pos	Primer 5 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
19388	ENU03182	ANI61C674	9	31-54	887-906		NAP		g1723510	446	108	2.00E-43	37	76	hypothetical 42.4 KD protein C1F12.05 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (AL031787) putative heavy metal transport protein [Schizosaccharomyces pombe]
19389	ENU03183	ANI61C776	1	67-86	911-943		NAP		g3687489	432	69	4.00E-30	49	93	"40S ribosomal protein RP10 ; ribosomal protein 50.e.B, cytosolic - yeast (Candida albicans) ; (X82017) ribosomal protein 10 [Candida albicans]"
19390	ENU03184	ANI61C3974	42-62		892-919		NAP		g730655	923	280	8.00E-89	76	97	hypothetical 50.4 KD protein C1F8.04C in chromosome I ; (Z81312) unknown [Schizosaccharomyces pombe]
19391	ENU03185	ANI61C8192	34-53		893-912		NAP		g2842689	733	258	4.00E-68	53	59	(AL033339) hypothetical membrane protein [Candida albicans] (AB015511) Avicelase III [Aspergillus aculeatus]
19392	ENU03186	ANI61C3842	38-57		890-917		NAP		g3850125	399	161	5.00E-39	32	60	(AL049495) conserved phosphatase-like hypothetical protein [Schizosaccharomyces pombe]
19393	ENU03187	ANI61C2363	48-67		900-927		NAP		g3242655	2990	316	1.00E-85	58	35	(Z99753) rho protein [Schizosaccharomyces pombe]
19394	ENU03188	ANI61C1084	68-87		923-947		NAP		g4539262	321	73	5.00E-22	38	92	[Schizosaccharomyces pombe]
19395	ENU03189	ANI61C6527	62-81		923-942		NAP		g2465150	419	86	4.00E-38	61	88	(Z99753) rho protein [Schizosaccharomyces pombe]
19396	ENU03190	ANI61C1037	22-51		883-905		NAP		g2494084	335	134	9.00E-31	37	87	glycerate dehydrogenase (NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) (hydroxypyruvate dehydrogenase) (glyoxylate reductase) (HPR-A)
19397	ENU03191	ANI61C1103	24-47		883-908		NAP		g731385	329	73	2.00E-12	39	79	hypothetical 33.7 KD protein in ISC10 3region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae]
19398	ENU03192	ANI61C9880	60-80		920-944		NAP		g3116131	60	48	0.00007	27	32	(AL023288) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	art Score	Blast Score	Blast Prob	%id	cvrg	%	Description
19410	ENU03204	ANI61S911:1	38-67	914-933	NAP	g1363737	g4512354	216	98	1.00E-19	29	91	98	probable membrane protein YLR247c - yeast (Saccharomyces cerevisiae); (U20865) Yhr247cp [Saccharomyces cerevisiae]
19411	ENU03205	ANI61C3367: 46-65	922-941	NAP	g2133310	551	139	8.00E-59	46	93	91	98	halodurans] 32.0k protein - Neurospora crassa; (L40806) open reading frame [Neurospora crassa]	
19412	ENU03206	ANI61C8472: 27-49	901-922	NAP	g2492767	58	4.00E-23	35	98	98	98	98	ORF [Neurospora crassa] putative short-chain type dehydrogenase/reductase Y4mp; (Rhizobium sp. NGR234)	
19413	ENU03207	ANI50346_1: 49-68	927-946	NAP	g728797	797	405	e-133	80	77	77	77	actin-like protein (centractin); actin-related protein ro-4 - Neurospora crassa; (L31505) centractin [Neurospora crassa]	
19414	ENU03208	ANI61C6286: 59-79	934-957	NAP	g3914053	1151	438	e-122	72	33	33	33	DNA mismatch repair protein MSH2; DNA mismatch repair protein [Neurospora crassa] (AF030634)	
19415	ENU03209	ANI61C1109	939-964	NAP	g2408039	785	196	2.00E-80	56	42	42	42	protein [Neurospora crassa] (Z99163) putative beta-glucan synthetase-associated protein [Schizosaccharomyces pombe]	
19416	ENU03210	ANI61C8920: 65-84	921-956	NAP	g131768	232	74	2.00E-12	25	54	54	54	synthetase (quininate transporter), quinate permease protein - Emericella nidulans; (X13525) quinate permease quinate transporter [Emericella nidulans]	
19417	ENU03211	ANI61C1682: 56-76	914-933	NAP	g4008461	108	6.00E-23						from this gene [Caenorhabditis elegans]	
19418	ENU03212	ANI61C5444: 32-51	909-931	NAP	g2980819	226	96	4.00E-19	43	57	57	57	(A1224865) IgE-binding protein [Aspergillus fumigatus]	
19419	ENU03213	ANI61C4081: 30-49	943-962	NAP	g3647337	268	100	2.00E-20	35	73	73	73	endonuclease subunit [Schizosaccharomyces pombe]	
19420	ENU03214	ANI61C5488: 61-81												

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19421	ENU03215	ANI61C7354:	59-78	938-960	NAP		g2769696	318	143	2.00E-33	33	80	(AC003982) unknown function; 60% similar to Z50177 (PID:g27403) (PID:g27402) [Homo sapiens]
19422	ENU03216	ANI61C1019	63-82	947-966	NAP		g2501598	411	120	2.00E-26	40	89	hypothetical 28.3 KD protein in PPR1-SNF7 intergenic region ; hypothetical protein YLR022c - yeast (Saccharomyces cerevisiae) ; (Z73194) ORF YLR022c [Saccharomyces cerevisiae]
19423	ENU03217	ANI61C5194:	37-56	922-941	NAP		g133961	801	128	2.00E-56	74	90	40S ribosomal protein S4 (omnipotent suppressor protein SUP44) (RP12) (S2E) ; ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) ; (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] ; (Z72645) ORF YGL123w [Saccharomyces cerevisiae] ; (X94106) SUP44 [Saccharomyces cerevisiae] (AL033503) transcription regulatory protein [Candida albicans] (L39639) kievitone hydratase [Fusarium solani] esterase D ; (AF112219) esterase D [Homo sapiens] (Z97204) hypothetical protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] ; (D13712) protein phosphatase [Schizosaccharomyces pombe] ; (AL031540) serine-threonine protein phosphatase [Schizosaccharomyces pombe]
19424	ENU03218	ANI61C152:	26-47	912-931	NAP		g3859681	446	198	7.00E-50	34	94	
19425	ENU03219	ANI61C8982:	22-46	898-928	NAP		g755011	263	134	1.00E-30	34	81	
19426	ENU03220	ANI61C7190:	49-67	937-956	NAP		g544254	688	212	3.00E-68	55	95	
19427	ENU03221	ANI61C8388:	22-43	908-929	NAP		g2226414	258	74	9.00E-16	43	99	
19428	ENU03222	ANI61C4017:	30-49	918-938	NAP		g548584	793	228	4.00E-59			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19429	ENU03223	ANI61C7183:	25-56	912-933	NAP		g2498438	58	48	0.00007	18	48	transcriptional coactivator HF11/ADA1 ; HF11 protein - yeast (Saccharomyces cerevisiae) ; (Z67751) putative protein [Saccharomyces cerevisiae] ; (Z73610) ORF YPL254w [Saccharomyces cerevisiae] ; (U76735) putative transcriptional coactivator [Saccharomyces cerevisiae] (AF063095) SEL1L [Mus musculus]
		1667..2617											
19430	ENU03224	ANI61C6626:	72-92	963-982	NAP		g4159995	577	130	2.00E-29	36	29	hypothetical 57.6 KD protein C3OD10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] hypothetical 44.9 KD protein in URA10-NRC1 intergenic region ; probable membrane protein YMR272c - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae] (U85909) hydroxylase [Aureobasidium pullulans] (U68040) polyketide synthase [Cochliobolus heterostrophus] (U09358) Rcal1p [Saccharomyces cerevisiae] "(S83228) beta-isopropylmalate dehydrogenase [Aspergillus niger, strain A733, Peptide, 363 aa] [Aspergillus niger] ; (U51130) beta-isopropylmalate dehydrogenase [Aspergillus niger]" sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans] (AL033385) transketolase [Schizosaccharomyces pombe] (AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana]
		5169..6121											
19431	ENU03225	ANI61C1070:	22-50	916-935	NAP		g3219924	276	52	0.000005	29	34	
		6:6101..5146											
19432	ENU03226	ANI61C6762:	70-91	956-984	NAP		g2493967	854	151	2.00E-75	53	72	
		994..1950											
19433	ENU03227	ANI61C8592:	40-59	934-954	NAP		g4099311	604	165	5.00E-40	44	62	
		19..976											
19434	ENU03228	ANI61C2749:	24-46	921-940	NAP		g1546072	373	173	2.00E-42	35	12	
		1407..449											
19435	ENU03229	ANI61C4206:	50-70	944-966	NAP		g508233	1246	191	e-106	67	35	
		76..1034											
19436	ENU03230	ANI61C4920:	51-77	949-969	NAP		g1911741	1223	326	e-121	82	82	
		1744..784											
19437	ENU03231	ANI61C9581:	24-46	925-944	NAP		g2492754	354	111	4.00E-33	38	87	
		3857..4819											
19438	ENU03232	ANI61C4572:	59-78	961-980	NAP		g3850070	1235	434	e-121	63	46	
		3699..2735											
19439	ENU03233	ANI61C1071:	29-48	916-951	NAP		g3763927	329	99	2.00E-41	39	58	
		8:1060..96											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19440	ENU03234	ANI61C8700:	32-49	927-955	NAP		g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
19441	ENU03235	ANI61C8700:	32-49	927-955	NAP		g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
19442	ENU03236	ANI61C8861:	50-69	959-978	NAP		g2131729	702	189	7.00E-66	50	36	hypothetical protein YLL029w - yeast (Saccharomyces cerevisiae) ; (Z73134) ORF YLL029w [Saccharomyces cerevisiae]
19443	ENU03237	ANI61C4087:	40-59	949-968	NAP		g464435	1346	507	e-143	69	77	acid phosphatase precursor ; acid phosphatase (EC 3.1.3.2) - Aspergillus ficuum ; (L20566) acid phosphatase [Aspergillus niger] (Z83867) fadB4 [Mycobacterium tuberculosis] hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19444	ENU03238	ANI61C9249:	22-52	932-952	NAP		g1781226	345	138	8.00E-32	34	92	hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19445	ENU03239	ANI61C1997:	23-44	933-954	NAP		g3183237	1374	244	8.00E-64	45	34	hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19446	ENU03240	ANI61C1025	25-46	921-956	NAP		g1351660	526	222	4.00E-57	45	78	endonuclease III homolog (DNA- (apurinic or apyrimidinic site) lyase) ; endonuclease III (EC 3.1.-.-) - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC30D11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) endonuclease III homolog [Schizosaccharomyces pombe]
19447	ENU03241	ANI61C6477:	41-60	951-972	NAP		g3169050	118	68	8.00E-11	32	64	(AL023702) hypothetical protein SC1C3.24 [Streptomyces coelicolor]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19448	ENU03242	ANI61C9181:	51-70	961-983	NAP		g2497056	183	52	6.00E-12			putative dioxxygenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae] hypothetical protein C17H9.20 in chromosome I; (Z98597) hypothetical protein [Schizosaccharomyces pombe] (D87681) acetyltransferase [Aspergillus awamori]
19449	ENU03243	ANI61C8589:	24-44	926-956	NAP		g3183360	411	155	4.00E-37	27	57	[Saccharomyces cerevisiae] hypothetical protein C17H9.20 in chromosome I; (Z98597) hypothetical protein [Schizosaccharomyces pombe] (D87681) acetyltransferase [Aspergillus awamori]
19450	ENU03244	ANI61C8537:	22-51	934-954	NAP		g1542843	1046	206	e-105	66	94	"DNA polymerase beta; Dna Polymerase Beta (Beta Polymerase) (E.C.2.7.7.7) (Apo, Full Protein); Rattus norvegicus; Rattus norvegicus; Rattus norvegicus"
19451	ENU03245	ANI61C266:	41-60	955-974	NAP		g585064	296	146	2.00E-34	28	95	(U59376) N-carbamoyl-D-amino acid amidohydrolase [Agrobacterium radiobacter]
19452	ENU03246	ANI61C9849:	47-67	950-982	NAP		g1401216	471	145	6.00E-34	41	95	"hypothetical 29.7 KD protein in HRP-A-ALDA intergenic region; (D90780) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli]; (D90781) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli]; (AE000239) orf. hypothetical protein [Escherichia coli]"
19453	ENU03247	ANI61C4859:	22-46	931-960	NAP		g2506663	339	162	3.00E-39	38	99	(AB017112) mCAC [Mus musculus] hypothetical GTP-binding protein in POP2-HOL1 intergenic region; hypothetical protein YNR053c - yeast (Saccharomyces cerevisiae); (Z71668) ORF YNR053c [Saccharomyces cerevisiae]
19454	ENU03248	ANI61C1038:	32-58	942-971	NAP		g4239974		68	1.00E-10			(AB017112) mCAC [Mus musculus] hypothetical GTP-binding protein in POP2-HOL1 intergenic region; hypothetical protein YNR053c - yeast (Saccharomyces cerevisiae); (Z71668) ORF YNR053c [Saccharomyces cerevisiae]
19455	ENU03249	ANI61C7390:	22-39	942-961	NAP		g1730685	1466	270	8.00E-72	67	44	(AB017112) mCAC [Mus musculus] hypothetical GTP-binding protein in POP2-HOL1 intergenic region; hypothetical protein YNR053c - yeast (Saccharomyces cerevisiae); (Z71668) ORF YNR053c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19456	ENU03250	ANI61C7332:	29-48	933-968	NAP		g3122261	843	164	2.00E-84	74	99	eukaryotic translation initiation factor 6 (EIF-6) ; hypothetical protein YPR016c - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz15p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AL033391) hypothetical membrane protein [Candida albicans] (Z98944) hypothetical protein [Schizosaccharomyces pombe] (AB010465) lactonohydrolase [Fusarium oxysporum] "hypothetical 67.7 KD protein C23C11.03 in chromosome 1 ; (Z98559) SPAC23C11.03; len:598aa, similar eg. to YJR002W, YJX2 yeast, P47083, hypothetical 67.0 kd protein, (593aa), fasta scores, opt:855, E(0):0, (33.0% identity in 610 aa overlap) [Schizosaccharomyces pombe]"
19457	ENU03251	ANI61C8252:	58-77	977-997	NAP		g3850125	624	199	3.00E-50	35	63	tubulin alpha-2 chain ; tubulin alpha-2 chain - Emeritella nidulans (AL035570) putative nitrilase homolog [Schizosaccharomyces pombe] (AF002660) aflatoxin [Aspergillus parasiticus] probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) ; (Z75170) ORF YOR262w [Saccharomyces cerevisiae] "2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase - Escherichia coli ; (Z47799) 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [Escherichia coli] ; (Z37980) hypothetical 2,4-dihydroxy-hepta-2-ene-1,7-dioate aldolase [Escherichia coli]"
19458	ENU03252	ANI61C1118	31-53	946-971	NAP		g2370496	354	173	1.00E-42	33	35	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19459	ENU03253	ANI61C9343:	60-79	973-1001	NAP		g3810873	478	150	1.00E-35	41	76	
19460	ENU03254	ANI61C9255:	48-78	969-989	NAP		g3183346	559	215	5.00E-55	38	53	
19461	ENU03255	ANI61C3731:	32-51	954-973	NAP		g135407	1617	590	e-168	97	67	
19462	ENU03256	ANI61C1106	31-50	942-977	NAP		g4467274	575	206	2.00E-52	48	97	
19463	ENU03257	ANI61C6325:	45-65	970-991	NAP		g2738309	408	73	1.00E-27	31	70	
19464	ENU03258	ANI61C4666:	51-73	980-998	NAP		g2132930	814	222	3.00E-57	47	83	
19465	ENU03259	ANI61C4278:	42-61	955-990	NAP		g1073302	269	126	3.00E-28	30	100	
19466	ENU03260	ANI61C1072	29-50	955-977	NAP		g2879890	503	220	1.00E-56	37	99	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19467	ENU03261	AN161C9659:	72-98	1002-1021	NAP		g1723239	784	314	6.00E-85	55	93	hypothetical 35.7 KD protein C26A3.11 in chromosome I ; (Z69240)
		1464..473											putative amidohydrolase
													[Schizosaccharomyces pombe]
													GTP-binding nuclear protein
													GSP1/CNR1 ; GTP-binding protein
													GSP1 - yeast (Saccharomyces cerevisiae) ; (L08690) GTP-binding protein [Saccharomyces cerevisiae] ; (X71945) CNR2 [Saccharomyces cerevisiae] ; (U17243) GTP-binding nuclear protein. Highly similar to GSP2_yeast. Belongs to the Ran family of Ras proteins [Saccharomyces cerevisiae]
19468	ENU03262	AN161C7455:	65-84		995-1014	NAP	g417090	878	138	2.00E-84			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
		6773..7764											(AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]
19470	ENU03264	AN161C7232:	22-52		949-972	NAP	g3647335	145	67	2.00E-10	25	74	hypothetical 33.5 KD protein C1D4.02C in chromosome I ; (Z69239) unknown [Schizosaccharomyces pombe]
		5559..4567											cytochrome C PEROxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae) ; (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae] ; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]
19471	ENU03265	AN161C3420:	22-46		940-972	NAP	g1723224	302	96	5.00E-19	32	99	hypothetical 32.6 KD protein in DAL5-TH11 intergenic region ; aryl-alcohol dehydrogenase homolog YJR155w - yeast (Saccharomyces cerevisiae) ; (Z49655) ORF YJR155w [Saccharomyces cerevisiae]
		1758..2750											
19472	ENU03266	AN161C9030:	66-85		997-1016	NAP	g543969	478	217	7.00E-56	44	74	
		2449..3441											
19473	ENU03267	AN161C2045:	58-78		989-1008	NAP	g1352946	411	73	2.00E-21	42	94	
		3325..2331											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19474	ENU03268	ANI61C1109	22-57	953-973	NAP		g1293655	783	249	3.00E-65	44	49	(U51327) versicolorin B synthase [Aspergillus parasiticus]; (U51328) versicolorin B synthase [Aspergillus parasiticus]
		0:630..1622											
19475	ENU03269	ANI61C9633:	38-57	970-989	NAP		g3668160	203	59	0.000000	23	47	(AL031764) hexose transporter. [Schizosaccharomyces pombe]; (AF098076) ght6p [Schizosaccharomyces pombe] (U42349) 39 kDa encoded by N33 [Homo sapiens]
		3640..3430								04			putative thiosulfate sulfoxidase; hypothetical protein YOR251c - yeast (Saccharomyces cerevisiae); (Z75159) ORF YOR251c [Saccharomyces cerevisiae]
19476	ENU03270	ANI61C7613:	22-45	950-974	NAP		g1353673	151	62	2.00E-17	30	75	UDP-glucose--glycoprotein glucosyltransferase (EC 2.7.8.19) - fission yeast (Schizosaccharomyces pombe); (U38417) UDP-Glc:Glycoprotein Glucosyltransferase [Schizosaccharomyces pombe]
		205..1199											
19477	ENU03271	ANI61C1373:	24-43	949-977	NAP		g3122964	432	129	3.00E-50	41	94	
		141..1136											
19478	ENU03272	ANI61C7897:	43-62	976-996	NAP		g2131132	1110	444	e-124	66	22	
		22..1017											
19479	ENU03273	ANI61C1083	22-46	957-976	NAP		g1708467	333	148	4.00E-35	35	82	
		7:1059..63											
													[Schizosaccharomyces pombe] branched-chain amino acid aminotransferase (transaminase B) (BCAT); branched-chain-amino-acid transaminase homolog - Haemophilus influenzae (strain Rd KW20); (U32798) branched-chain-amino-acid transaminase (ilvE) [Haemophilus influenzae Rd] lactose permease; lactose permease - yeast [Kluyveromyces marxianus var. lactis]; (X06997) lactose permease (AA1-587) [Kluyveromyces lactis] (AL023780) DNA binding protein [Schizosaccharomyces pombe] (AB010442) PMR1 [Penicillium digitatum] (AF010494) sorbitol dehydrogenase [Callitrix sp.]
19480	ENU03274	ANI61C5227:	46-65	973-1000	NAP		g125935	578	76	2.00E-35	36	46	
		997..1											
19481	ENU03275	ANI61C9068:	26-48	951-981	NAP		g3184115	377	166	3.00E-40	30	63	
		9..1006											
19482	ENU03276	ANI61C4858:	54-74	981-1009	NAP		g3288709	1234	458	e-128	68	22	
		43..1040											
19483	ENU03277	ANI61C1942:	45-65	975-1001	NAP		g2352843	715	104	5.00E-36	42	80	
		3132..2133											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19484	ENU03278	ANI61C9666:	33-53	965-990	NAP		g2132925	517	263	2.00E-69	41	77	probable membrane protein YOR245c - yeast (Saccharomyces cerevisiae) ; (Z75153) ORF YOR245c
		4320..3321											[Saccharomyces cerevisiae]
19485	ENU03279	ANI61C4960:	53-72	988-1010	NAP		g729534	739	146	1.00E-75	51	58	UTR1 protein (unknown transcript 1 protein) ; UTR1 protein - yeast (Saccharomyces cerevisiae) ; (L26347) orf gIE530 [Saccharomyces cerevisiae] ; (Z49549) ORF YJR049c
		3192..2193											[Saccharomyces cerevisiae] ; (L36344) ORF, putative [Saccharomyces cerevisiae]
19486	ENU03280	ANI61C6471:	42-61	973-1000	NAP		g547648	949	280	2.00E-92			histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase) ; his 3 protein - fission yeast (Schizosaccharomyces pombe) ; (L19523) imidazoleglycerol-phosphate dehydratase [Schizosaccharomyces pombe] ; (L19524) imidazoleglycerol-phosphate dehydratase
		11749..10749											[Schizosaccharomyces pombe] ; (AB004534) histidinol-phosphate aminotransferase
19487	ENU03281	ANI61C7553:	40-59	979-998	NAP		g2633013	351	145	1.00E-38	30	93	[Schizosaccharomyces pombe] (Z99107) similar to hypothetical proteins [Bacillus subtilis]
		299..1299											phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
19488	ENU03282	ANI61C1037	49-72	989-1008	NAP		g130117	869	214	7.00E-55	35	56	(AF052688) putative transmembrane transporter Liz1p
		3:5272..6273											[Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p
19489	ENU03283	ANI61C1131:	34-53	964-994	NAP		g2981103		107	2.00E-22	39	21	[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
		1000..250											
19490	ENU03284	ANI61C7525:	23-47	964-983	NAP		g3169097	190	74	1.00E-12	28	85	
		7424..8426											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19491	ENU03285	AN150C202_3:1765..2767	23-42	950-983	NAP		g2239196	257	6.00E-68	45	98	98	(Z97209) hypothetical protein [Schizosaccharomyces pombe]
19492	ENU03286	AN161C836:3785..4788	38-60	966-999	NAP		g135407	823	341	5.00E-93	60	62	tubulin alpha-2 chain - Emmericella nidulans
19493	ENU03287	AN150C721_1:3356..2353	25-50	967-986	NAP		g116929	272	3.00E-75	49	63	63	hexaprenyl pyrophosphate synthetase precursor (HPS) ; trans-pentaprenyltransferase (EC 2.5.1.33) precursor - yeast (Saccharomyces cerevisiae) ; (J05547) hexaprenyl pyrophosphate synthetase (COQ1) [Saccharomyces cerevisiae] ; (Z35872) ORF YBR003w [Saccharomyces cerevisiae]
19494	ENU03288	AN161C1055:7:3124..4127	34-53	976-995	NAP		g549725	332	126	8.00E-31			"NADH-cytochrome B5 reductase precursor (P34/P32) ; cytochrome-b5 reductase (EC 1.6.2.2), mitochondrial outer membrane form - yeast (Saccharomyces cerevisiae) ; (Z26877) unknown [Saccharomyces cerevisiae] ; (Z28150) ORF YKL150w [Saccharomyces cerevisiae] ; (X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] "
19495	ENU03289	AN161C562:1854..850	22-48	964-984	NAP		g1346485	889	182	3.00E-54	41	53	malate oxidoreductase (malic enzyme) (ME) (NADP-dependent malic enzyme) (NADP-ME) ; (X56233) malic enzyme [Populus balsamifera subsp. trichocarpa] (M96667) proteosome-related protein [Saccharomyces cerevisiae]
19496	ENU03290	AN161C30:3623..2618	23-52	967-986	NAP		g172260	721	111	6.00E-38	67	52	hypothetical 55.1 KD protein in FABI-PE54 intergenic region ; probable membrane protein YFR021w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR021W [Saccharomyces cerevisiae] (Z99126) hypothetical oxidoreductase [Schizosaccharomyces pombe]
19497	ENU03291	AN161C8552:8701..9708	72-94	1018-1037	NAP		g1176002	452	164	7.00E-40	32	60	probable serine/threonine-protein kinase C29A4.16 ; (Z97210) protein kinase [Schizosaccharomyces pombe]
19498	ENU03292	AN161C1658:3373..2365	22-44	968-988	NAP		g2398818	192	61	1.00E-23	36	73	
19499	ENU03293	AN161C1649:2056..1048	36-55	976-1002	NAP		g3183055	461	216	2.00E-55	41	47	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19500	ENU03294	ANI61C1183:	28-47	976-995	NAP		g418391	589	236	1.00E-61	39	88	"ZRT1" protein ; zinc transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (X67787) ORF1 [Saccharomyces cerevisiae] ; (X94357) ORF NRC376; EMBL:SCFZF1;X67787; PIR:DEBY4;S07614 [Saccharomyces cerevisiae] ; (Z72777) ORF YGL255w [Saccharomyces cerevisiae]" (Z98597) hypothetical nadh-cytochrome reductase
19501	ENU03295	ANI61C6843:	46-65	994-1013	NAP		g2330719	105	73	2.00E-12	32	93	[Schizosaccharomyces pombe] ubiquitin--protein ligase RSP5 ; hypothetical protein YER125w - yeast (Saccharomyces cerevisiae) ; (U18916) Rsp5p [Saccharomyces cerevisiae] (AB016895) Pop3 [Schizosaccharomyces pombe] glycerol-3-phosphate dehydrogenase (NAD+) 1 ; glycerol-3-phosphate dehydrogenase (NAD+) (EC 1.1.1.8) precursor - yeast (Saccharomyces cerevisiae) ; (Z24454) glycerol 3-phosphate dehydrogenase [Saccharomyces cerevisiae] ; (U04621) dihydroxyacetone phosphate reductase [Saccharomyces cerevisiae] ; (X76859) glycerol-3-phosphate dehydrogenase (NAD+) [Saccharomyces cerevisiae] ; (Z48432) glycerol-3-phosphate dehydrogenase (NAD+) (X76859) [Saccharomyces cerevisiae] ; (Z74071) ORF YDL022w [Saccharomyces cerevisiae] (AF092576) translation initiation factor eIF3 p40 subunit; eIF3p40 [Homo sapiens] (AB000703) phosphomannomutase [Schizosaccharomyces pombe] (AL023533) hypothetical protein [Schizosaccharomyces pombe]
19502	ENU03296	ANI61C9202:	22-48	968-990	NAP		g730684	2522	226	e-113	73	35	
19503	ENU03297	ANI61C6531:	22-55	971-990	NAP		g3434986	778	255	1.00E-85	62	81	
19504	ENU03298	ANI61C1100	25-45	973-993	NAP		g462197	726	223	6.00E-59			
19505	ENU03299	ANI61C4362:	31-51	980-1000	NAP		g3986482	414	99	2.00E-40	37	80	
19506	ENU03300	ANI61C7112:	31-51	967-1000	NAP		g1813335	721	176	2.00E-75	63	99	
19507	ENU03301	ANI61C1095:	34-55	985-1004	NAP		g3130060	914	115	5.00E-25	32	37	

Sequence Description

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19508	ENU03302	AN150C66_1	22-51	966-993	NAP		g2879890		245	e-101	70	91	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19509	ENU03303	AN161C9775	33-61	985-1004	NAP		g3873958	194	103	2.00E-21	26	95	(Z81458) similar to transposable element [Caenorhabditis elegans]
19510	ENU03304	AN161C8634	22-51	971-994	NAP		g538066	181	62	0.000000	25	96	(M77661) putative gag protein [Magnaporthe grisea]
19511	ENU03305	AN161C8943	55-80	997-1027	NAP		g3426039	273	127	9.00E-29	49	25	(AC005168) unknown protein [Arabidopsis thaliana]
19512	ENU03306	AN161C1622	29-48	974-1001	NAP		g549739	163	101	9.00E-21	34	37	hypothetical 55.4 KD protein in STE3-GIN10 intergenic region ; hypothetical protein YKL175w - yeast
19513	ENU03307	AN161C9973	38-57	992-1011	NAP		g2318125	316	82	4.00E-18	38	75	(Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28175) ORF YKL175w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] (AF014404) HIV-Nef associated acyl CoA thioesterase [Homo sapiens] ; (AL008726) dJ337O18.3.1 (Thioesterase II) (isoform 1) [Homo sapiens]
19514	ENU03308	AN161C1292	59-78	1014-1034	NAP		g2271503		64	7.00E-17			(AF009672) unknown [Acinetobacter sp. ADP1]
19515	ENU03309	AN161C1011	22-56	978-997	NAP		g2924499	331	124	8.00E-28	35	91	(AL022019) putative 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase(3beta-hsd) [Schizosaccharomyces pombe]
19516	ENU03310	AN161C1143	68-91	1022-1044	NAP		g3687478	1534	414	e-115	60	61	(AL031786) putative delta-1-pyrroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe]
19517	ENU03311	AN161C541	23-49	971-999	NAP		g2267603	246	121	9.00E-27	35	54	(AF009418) trichothecene biosynthesis transcription factor [Myrothecium roridum]
19518	ENU03312	AN161C7921	24-58	970-1001	NAP		g2879861	148	84	1.00E-17	25	97	(AL021815) hypothetical protein [Schizosaccharomyces pombe] ; (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe]
19519	ENU03313	AN161C8093	33-52	992-1011	NAP		g3282211	1131	211	e-117	70	69	(U68714) isocitrate lyase 1 [Botryotinia fuckeliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19520	ENU03314	ANI61C1147	36-55	1000-	NAP		g3318897	337	161	8.00E-39	30	48	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum "
		4:3071..2048		1017									(AL023634) hypothetical protein [Schizosaccharomyces pombe]
19521	ENU03315	ANI61C1118:	58-78	1020-	NAP		g3150262	713	178	4.00E-44	42	85	[Schizosaccharomyces pombe]
		5506..6530		1040									uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
19522	ENU03316	ANI61C7162:	24-44	984-1006	NAP		g2492816		74	3.00E-24			permease [Schizosaccharomyces pombe]
		1316..291											spermidine synthase (putrescine aminopropyltransferase) (SPDSY) ; (Z54140) putrescine aminopropyltransferase
19523	ENU03317	ANI61C4572:	38-71	1002-	NAP		g1174417	970	129	5.00E-42	71	65	[Schizosaccharomyces pombe]
		1170..2195		1021									hypothetical 37.4 KD protein in SEC27-SSM1B intergenic region ; hypothetical protein YGL136c - yeast (Saccharomyces cerevisiae) ; (X92670) G2830 [Saccharomyces cerevisiae] ; (Z72658) ORF YGL136c [Saccharomyces cerevisiae]
19524	ENU03318	ANI61C6048:	49-71	1013-	NAP		g1723920	355	134	1.00E-31	40	77	thiazole biosynthetic enzyme (stress-inducible protein STI35) ; stress-inducible protein sti35 - fungus (Fusarium oxysporum) ; (M33643) STI35 protein [Fusarium oxysporum]
		28..1055		1034									hypothetical 33.9 KD protein C14C4.12C in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
19525	ENU03319	ANI61C1082	27-46	993-1012	NAP		g1351122	1143	324	e-122	74	98	plasma membrane Ca2+-ATPase isoform 4 - rat ; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus]
		6:2111..1083											Pectin Lyase A
19526	ENU03320	ANI61C1026	55-79	1012-	NAP		g3183345	259	127	1.00E-28	36	61	
		5:1499..471		1041									
19527	ENU03321	ANI61C7819:	25-44	993-1012	NAP		g1083757	781	156	4.00E-55	44	25	
		5645..4616											
19528	ENU03322	ANI61C1019	22-47	991-1010	NAP		g2624697	1322	155	e-101	73	75	
		3:1386..356											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
19529	ENU03323	AN161C7349:	62-80	1032-1052	NAP	g1657510	628	175	8.00E-62	39	70		(U73857) betaine-aldehyde dehydrogenase [Escherichia coli]
19530	ENU03324	274..1306 AN161C1834:	54-73	1024-1044	NAP	g2500755	486	173	2.00E-47	57	31		response regulator MCS4 (mitotic catastrophe suppressor 4); (Y11927)
		4387..3355											Mcs4 protein [Schizosaccharomyces pombe]; (AF004694) Msc4 [Schizosaccharomyces pombe]; (AL033388) response regulator mcs4 [Schizosaccharomyces pombe]
19531	ENU03325	AN161C9207:	53-75	1021-1043	NAP	g2894293	822	284	9.00E-76	43	65		(AL021837) hypothetical protein [Schizosaccharomyces pombe]
19532	ENU03326	94..1126 AN161C3172:	38-58	1004-1029	NAP	g1653791	159	104	1.00E-23	32	97		(D90916) hypothetical protein [Synechocystis sp.]
19533	ENU03327	3489..2456 AN161C1086	70-93	1033-1061	NAP	g3738189	314	131	6.00E-30	27	69		(AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe]
19534	ENU03328	5:3495..2461 AN161C8189:	71-101	1043-1062	NAP	g462023	715	129	4.00E-29	65	62		C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus; C-8 sterol isomerase - rice blast fungus; (Z22775) C-8 sterol isomerase [Magnaporthe grisea]
19535	ENU03329	AN161C9130:	51-71	1022-1043	NAP	g399766	100	78	7.00E-14	29	59		gluconolactonase precursor (D-glucono-delta-lactone lactonohydrolase); gluconolactonase (EC 3.1.1.17) precursor - Zymomonas mobilis; (X67189) gluconolactonase [Zymomonas mobilis]
19536	ENU03330	AN161C9354:	24-49	987-1016	NAP	g1770301	196	71	7.00E-14	36	94		(X95074) Translin [Gallus gallus]
19537	ENU03331	1135..101 AN161C139:	40-62	1011-1032	NAP	g731893	1070	128	9.00E-56	47	54		putative transporter YIL166C; probable membrane protein YIL166C - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
19538	ENU03332	AN161C1034	72-91	1030-1065	NAP	g2370487	1901	444	e-124	65	48		(Z98849) glutaryl-tma synthetase [Schizosaccharomyces pombe]

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19539	ENU03333	AN161C4602:	49-75	1023-1042	NAP		g1723769	269	55	3.00E-11			putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
19540	ENU03334	AN161C7359:	28-47	1002-1021	NAP		g3925755	533	246	2.00E-64	39	65	(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [Schizosaccharomyces pombe]
19541	ENU03335	AN161C1897:	24-51	999-1018	NAP		g3434937	503	158	5.00E-38	61	94	(AB000281) krev-1 [Neurospora crassa]
19542	ENU03336	AN161C8156:	69-89	1043-1064	NAP		g3551511	910	320	9.00E-87	47	83	(AB016807) flavohemoglobin [Fusarium oxysporum]
19543	ENU03337	AN161C6276:	31-56	1007-1026	NAP		g129781	355	175	4.00E-43	32	87	Pepsinogen II-2/3 precursor (pepsinogen A) ; (M59235) pepsinogen [Oryctolagus cuniculus]
19544	ENU03338	AN161C7530:	22-48	993-1018	NAP		g4008577	348	111	8.00E-24	32	98	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]
19545	ENU03339	AN161C5932:	59-78	1033-1055	NAP		g4512354	224	83	5.00E-20			(AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
19546	ENU03340	AN161C8268:	32-67	1010-1029	NAP		g2879890	782	185	4.00E-77	52	98	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19547	ENU03341	AN161C1048:	27-47	1005-1024	NAP		g3915140	678	89	2.00E-46	36	63	Isotrichoderm C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichoderm C-15 hydroxylase [Fusarium sporotrichioides]
19548	ENU03342	AN161C8858:	22-41	996-1020	NAP		g2293194	303	152	3.00E-36	28	89	(AF008220) yreK [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19549	ENU03343	AN161C2233:	24-46	1003-1022	NAP		g585542	541	223	1.00E-57			putative NADH-cytochrome B5 reductase (P35) ; cytochrome-b5 reductase (EC 1.6.2.2) - yeast (Saccharomyces cerevisiae) ; (Z28365)
		3..1043											cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861)
													cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861)
													cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861)
													cytochrome b reductase [Saccharomyces cerevisiae]
19550	ENU03344	AN161C3401:	22-52	998-1021	NAP		g2131525	108	39	0.01	25	94	[Saccharomyces cerevisiae] hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae) ; (U33050) Ydr489wp; CAL: 0.16 [Saccharomyces cerevisiae]
		493..1534											(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] (AL022071) hypothetical protein [Schizosaccharomyces pombe]
19551	ENU03345	AN161C9825:	47-66	1028-1047	NAP		g3850084	230	63	5.00E-17	29	90	Heat shock protein HSP1 (65 KD IGE-binding protein) ; (U92465) heat shock protein [Aspergillus fumigatus]
19552	ENU03346	AN161C1042	51-77	1032-1051	NAP		g2950464	1087	312	e-102	67	58	glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase) ; glucosamine-6-phosphate deaminase protein (nagB) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32700) glucosamine-6-phosphate isomerase (nagB) [Haemophilus influenzae Rd]
19553	ENU03347	AN161C5619:	65-84	1046-1065	NAP		g2851483	1706	493	e-138	93	78	protein transport protein SEC13 ; SEC13 protein - yeast (Saccharomyces cerevisiae) ; (L05929) Sec13p [Saccharomyces cerevisiae] ; (U14913) Sec13p [Saccharomyces cerevisiae] (AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe] (L39639) kievitone hydratase [Fusarium solani]
		2226..1184											
19554	ENU03348	AN161C41:20	44-64	1025-1044	NAP		g1171641	795	316	1.00E-85	59	96	
		88..1046											
19555	ENU03349	AN161C7807:	64-84	1044-1065	NAP		g417748	807	150	4.00E-77	62	90	
		1969..3013											
19556	ENU03350	AN161C4411:	37-56	1014-1038	NAP		g4056558	130	74	2.00E-12	35	18	
		1439..396											
19557	ENU03351	AN161C3627:	53-73	1032-1054	NAP		g755011	496	217	1.00E-55	36	92	
		6985..5942											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19558	ENU03352	ANI61C5159:	22-47	1008-1027	NAP	g1171024	542	169	9.00E-49	46	87	"mitochondrial RNA splicing protein MRS3 ; splicing protein MRS3, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X56445) MRS3 protein [Saccharomyces cerevisiae] ; (X87371) mitochondrial splicing unit [Saccharomyces cerevisiae] ; (Z49408) ORF YJL133w [Saccharomyces cerevisiae] "	
19559	ENU03353	ANI61C1040	23-45	1009-1028	NAP	g3024013	949	203	6.00E-57	66	94	eukaryotic translation initiation factor 2 alpha subunit (EIF-2-alpha) ; (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]	
19560	ENU03354	ANI61C2163:	53-72	1027-1060	NAP	g1523784	140	83	1.00E-25	32	38	(Z79750) acid phosphatase [Emmericella nidulans]	
19561	ENU03355	ANI61C766:1	22-49	1008-1030	NAP	g2414631	65	61	0.000000	28	48	(Z99260) hypothetical protein [Schizosaccharomyces pombe]	
19562	ENU03356	ANI61C8382:	64-83	1052-1072	NAP	g3135990	765	167	2.00E-50	41	64	(AL023589) membrane transporter [Schizosaccharomyces pombe]	
19563	ENU03357	ANI61C9268:	22-55	1011-1031	NAP	g1351310	1415	514	e-145	83	96	Thioredoxin reductase ; 72k broad-range disulfide reductase (NADPH) (EC 1.-.-.-) - Penicillium chrysogenum ; (X76119) thioredoxin reductase [Penicillium chrysogenum]	
19564	ENU03358	ANI61C6529:	22-47	1012-1031	NAP	g127112	758	204	6.00E-57	56	97	MAK16 protein ; MAK16 protein - yeast (Saccharomyces cerevisiae) ; (J03852) MAK16 protein [Saccharomyces cerevisiae] ; (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]	
19565	ENU03359	ANI61C3092:	23-42	1014-1034	NAP	g125271	1258	389	e-107	72	94	"Casein kinase II, alpha chain (CK II) (CK2-alpha) ; casein kinase II (EC 2.7.1.-) alpha chain - maize ; Protein Kinase CK2 (Catalytic Subunit) From Zea Mays ; (X61387) casein kinase II alpha subunit [Zea mays] "	

Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19566	ENU03360	ANI61C8693:	59-91	1048-1070	NAP	g1170603	1038	375	e-103	53	32	probable serine/threonine-protein C2F7.03C ; hypothetical protein SPAC2F7.03c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) protein kinase [Schizosaccharomyces pombe] (L35487) mannanase [Aspergillus aculeatus]
		76..1129										
19567	ENU03361	ANI61C51:26	47-68	1040-1059	NAP	g558311	1144	254	e-118	65	82	(AF054824) delta 5 microsomal desaturase [Mortierella alpina]
		..1080										
19568	ENU03362	ANI61C980:5	22-57	1001-1034	NAP	g3342268	95	57	0.000000	38	14	GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228)
		747..4693							2			
19569	ENU03363	ANI61C5185:	22-47	1020-1039	NAP	g121087	556	217	5.00E-57			GCY protein (AA 1-312) [Saccharomyces cerevisiae] ; (X90518) ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w [Saccharomyces cerevisiae] ; (X96740) GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w [Saccharomyces cerevisiae]
		1040..2099										
19570	ENU03364	ANI61C1024	65-84	1052-1083	NAP	g417431	604	254	1.00E-66			NADPH dehydrogenase 1 (old yellow enzyme 1) : NADPH dehydrogenase (EC 1.6.99.1) chain OYE1 - yeast (Saccharomyces cerevisiae) ; Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1) Complexed With P-Hydroxybenzaldehyde ; Old Yellow Enzyme (Reduced) (Oye) (E.C.1.6.99.1) ; Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1) ; (X53597) NADPH dehydrogenase [Saccharomyces pastorianus] (Z11701) putative protein kinase [Saccharomyces cerevisiae] (Y14766) alk8 [Candida albicans]
		9:1587..527										
19571	ENU03365	ANI61C8885:	32-51	1024-1050	NAP	g3836	697	186	2.00E-76	47	29	
		3652..2592										
19572	ENU03366	ANI61C8063:	22-50	1013-1041	NAP	g3395458	212	56	1.00E-22	39	35	
		1..1062										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19573	ENU03367	ANI61C5331	36-56	1027-1056	NAP	g117178	2183	640	0	85	68		Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19574	ENU03368	ANI61C9104	49-68	1049-1070	NAP	g3183387	608	109	3.00E-37	40	71		Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19575	ENU03369	ANI61C2888	24-42	1029-1048	NAP	g1077195	884	136	3.00E-31	34	56		Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19576	ENU03370	ANI61C2922	22-53	1020-1047	NAP	g2276350	899	290	1.00E-77	56	99		Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19577	ENU03371	ANI61C6515	38-57	1032-1064	NAP	g1346660	77	4.00E-22					Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19578	ENU03372	ANI61C9024	29-61	1034-1055	NAP	g3130036	1225	299	e-115	61	87		Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19579	ENU03373	ANI61C6515	44-63	1038-1070	NAP	g1346660	77	4.00E-22					Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19580	ENU03374	ANI61C8602	27-46	1036-1055	NAP	g1078613	1726	301	e-171	88	74		Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19581	ENU03375	ANI61C6203:	25-45	1031-	NAP		g4503653	590	211	8.00E-54	40	52	"fatty-acid-Coenzyme A ligase, very long-chain 1 ; very-long-chain acyl-CoA synthetase (very-long-chain-fatty-acid-CoA ligase) ; (D88308) very-long-chain acyl-CoA synthetase [Homo sapiens] ; (AF096290) very long-chain acyl-CoA synthetase [Homo sapiens]"
		3521..2451		1053									(AL033497) transport protein [Candida albicans]
19582	ENU03376	ANI61C5100:	70-90	1077-	NAP		g3859693		75	7.00E-13			hypothetical 35.1 K D protein in NAM8-GAR1 intergenic region ; hypothetical protein YHR088w - yeast (Saccharomyces cerevisiae) ; (U000060) Yhr088wp [Saccharomyces cerevisiae] (U62917) glucose transporter TGTTP2 [T. acnia solium]
		1151..81		1098									(AB011211) pectin methyl-esterase [Aspergillus oryzae]
19583	ENU03377	ANI61C3804:	50-69	1052-	NAP		g731684	590	192	2.00E-52	42	98	hypothetical 37.0 K D protein in SPOIIR-GLYC intergenic region ; SUA5 homolog ipc-29d - Bacillus subtilis ; (Z38002) Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis] ; (Z99122) alternate gene name: ipc-29d, similar to hypothetical proteins [Bacillus subtilis] ; ipc-29d gene [Bacillus subtilis]
		3421..4492		1079									"proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 ; (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]"
19584	ENU03378	ANI61C9031:	63-82	1072-	NAP		g1480799		37	0.000000			(AJ001732) rAsp f 4 [Aspergillus fumigatus]
		342..579		1093									probable calcium-transporting ATPase 9 ; probable membrane protein YOR291w - yeast (Saccharomyces cerevisiae) ; (Z75199) ORF YOR291w [Saccharomyces cerevisiae] (AC000133) ORF [Emmericella nidulans]
19585	ENU03379	ANI61C3234:	52-71	1063-	NAP		g4514622	469	107	4.00E-44	41	89	
		725..1797		1082									
19586	ENU03380	ANI61C8984:	59-81	1054-	NAP		g732384	519	107	8.00E-41			
		3629..2556		1089									
19587	ENU03381	ANI61C1139	65-84	1079-	NAP		g4506223	545	205	5.00E-52	36	84	
		7:730..1805		1098									
19588	ENU03382	ANI61C7637:	50-72	1060-	NAP		g3005839	410	110	1.00E-23	45	31	
		1107..2184		1084									
19589	ENU03383	ANI61C7016:	63-83	1068-	NAP		g2493012	538	99	5.00E-34	41	17	
		6581..5505		1097									
19590	ENU03384	ANI61C567:3	26-48	1029-	NAP		g1870209		46	0.0004			
		434..4511		1061									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19591	ENU03385	ANI61C8963:	26-45	1044-1063	NAP		g2132210	665	268	4.00E-71	41	98	hypothetical protein YPL152w - yeast (Saccharomyces cerevisiae) ; (Z73508) ORF YPL152w [Saccharomyces cerevisiae] ; (X96770) P2591 protein [Saccharomyces cerevisiae]
19592	ENU03386	ANI61C4714:	40-61	1053-1077	NAP		g1836161	530	212	1.00E-56	38	64	"(S83194) Ca2+/calmodulin-dependent protein kinase IV kinase isoform, CaM-kinase kinase alpha [rats, brain, Peptide, 505 aa] [Rattus sp.] ; (AB023658) Calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha [Rattus norvegicus]
19593	ENU03387	ANI61C129:3	29-48	1036-1066	NAP		g2340046	2589	326	e-105	79	42	(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]
19594	ENU03388	ANI61C5996:	22-42	1031-1059	NAP		g2650534	128	74	2.00E-12	29	54	(AE001098) conserved hypothetical protein [Archaeoglobus fulgidus]
19595	ENU03389	ANI61C7595:	23-51	1039-1060	NAP		g2131398	463	120	2.00E-45	37	92	hypothetical protein YDR214w - yeast (Saccharomyces cerevisiae) ; (Z68195) unknown [Saccharomyces cerevisiae] ; (Z68194) unknown [Saccharomyces cerevisiae]
19596	ENU03390	ANI61C1118	47-66	1063-1084	NAP		g1723555		83	2.00E-15			hypothetical 27.0 KD protein C12B10.13 in chromosome I ; (Z70721) conserved hypothetical protein. [Schizosaccharomyces pombe] (AL049522) putative dolichol kinase [Schizosaccharomyces pombe]
19597	ENU03391	ANI61C8085:	52-71	1074-1093	NAP		g4539603	263	91	1.00E-17	36	37	2-nitropropane dioxygenase precursor (nitroalkane oxidase) (2-NPD) ; (U22530) 2-nitropropane dioxygenase precursor [Neurospora crassa]
19598	ENU03392	ANI61C1118:	22-53	1043-1065	NAP		g2498094	348	162	4.00E-39	34	93	hypothetical 48.0 KD protein C4G8.06C in chromosome I ; hypothetical protein SPAC4G8.06c - fission yeast (Schizosaccharomyces pombe) ; (Z56276) hypothetical protein [Schizosaccharomyces pombe]
19599	ENU03393	ANI61C4327:	27-47	1047-1071	NAP		g1351597	376	203	2.00E-51	40	72	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19600	ENU03394	ANI61C238:1	22-49	1047-1066	NAP		g3135988	201	89	1.00E-19	35	36	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19601	ENU03395	ANI61C7744:	33-54	1058-7338..6252	NAP		g130684	910	314	7.00E-85	66	93	Outer mitochondrial membrane protein porin ; porin - Neurospora crassa ; (X05824) major protein (AA 1-283) [Neurospora crassa]
19602	ENU03396	ANI61C3311:	24-55	1050-1021..2108	NAP		g4581517	83	3.00E-33				(AL049559) putative d-amino acid oxidase [Schizosaccharomyces pombe]
19603	ENU03397	ANI61C2398:	58-77	1084-1506..418	NAP		g113712	600	147	6.00E-40	35	61	Amidase ; amidase (EC 3.5.1.4) - Brevibacterium sp. (strain R312) ; amidase - Rhodococcus sp. (strain N-774) ; (X54074) amidase [Rhodococcus sp.] ; (M60264) enantiomer-selective amidase [Brevibacterium sp.] ; (AB016078) amidase [Rhodococcus sp. N-771] "putative 38.2 KD phosphatase 2C in chromosome I ; (Z98762)
19604	ENU03398	ANI61C7272:	24-43	1046-1840..2929	NAP		g3183379	405	144	9.00E-34	36	83	SPAC4A8.03c, putative protein phosphatase, len:339aa, similar eg. to P2C1_SCHPO, P40371, protein phosphatase 2c homolog 1, (347aa), fasta scores, opt:276, E0):3.2e-11, (29.4% identity in 282 aa overlap), also simi...."
19605	ENU03399	ANI61C1068	50-70	1079-8:1439..2529	NAP		g4507713	505	203	4.00E-51	36	69	tetratricopeptide repeat domain 2 ; (U46571) tetratricopeptide repeat protein [Homo sapiens]
19606	ENU03400	ANI61C6636:	23-42	1051-268..1358	NAP		g2213547	476	183	1.00E-48	52	59	(Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe]
19607	ENU03401	ANI61C8531:	38-58	1068-1173..79	NAP		g2879890	627	264	7.00E-70	46	89	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19608	ENU03402	ANI61C6472:	69-88	1090-5222..4127	NAP		g3914593	236	132	4.00E-30	39	91	putative ribokinase ; (AL023554) ribokinase [Schizosaccharomyces pombe]
19609	ENU03403	ANI61C2203:	48-67	1083-1130..34	NAP		g1352904	296	69	1.00E-24	34	84	hypothetical 37.5 KD protein in YUH1-URA8 intergenic region ; hypothetical protein YJR100c - yeast (Saccharomyces cerevisiae) ; (Z49600) ORF YJR100c [Saccharomyces cerevisiae]

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19610	ENU03404	ANI61C9708:	58-77	1095-1114	NAP	g1168269	1196	222	e-118	72	95	"Arabitan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]"
		3952..5050										(AC006569) hypothetical protein [Arabidopsis thaliana]
19611	ENU03405	ANI61C9805:	42-61	1079-1098	NAP	g4512702	567	70	3.00E-11	35	24	hypothetical 42.4 KD protein in ENO2-STB5 intergenic region; hypothetical protein YHR176w - yeast (Saccharomyces cerevisiae); (U00027) Yhr176wp [Saccharomyces cerevisiae]
		1380..282										hypothetical zinc-type alcohol dehydrogenase-like protein in AHPF-RNK intergenic region; (U82598) FadH homolog [Escherichia coli]; (AE000166) putative oxidoreductase [Escherichia coli]; (D90701) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]; (D90702) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]
19612	ENU03406	ANI61C1031	63-82	1096-1119	NAP	g731746	302	130	2.00E-29	36	80	hypothetical protein YHR176w - yeast (Saccharomyces cerevisiae); (U00027) Yhr176wp [Saccharomyces cerevisiae]
		6:2340..3438										hypothetical 42.4 KD protein in ENO2-STB5 intergenic region; hypothetical protein YHR176w - yeast (Saccharomyces cerevisiae); (U00027) Yhr176wp [Saccharomyces cerevisiae]
19613	ENU03407	ANI61C1067:	69-88	1104-1125	NAP	g3024986	129	59	1.00E-10			hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]
		1112..2210										"Leucyl-TRNA synthetase, mitochondrial precursor (leucine--TRNA ligase) (LEURS); leucine--TRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa; (M30472) leucyl-tRNA synthetase [Neurospora crassa]"
19614	ENU03408	ANI50C1743	37-64	1060-1093	NAP	g2132293	157	1.00E-37	32	90		hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]
		6_1:16..1114										"Leucyl-TRNA synthetase, mitochondrial precursor (leucine--TRNA ligase) (LEURS); leucine--TRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa; (M30472) leucyl-tRNA synthetase [Neurospora crassa]"
19615	ENU03409	ANI61C7138:	45-65	1082-1102	NAP	g135142	1945	270	9.00E-72	44	36	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]
		1323..2422										"Leucyl-TRNA synthetase, mitochondrial precursor (leucine--TRNA ligase) (LEURS); leucine--TRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa; (M30472) leucyl-tRNA synthetase [Neurospora crassa]"

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19616	ENU03410	ANI61C7147:	56-83	1093-1114	NAP	g128847	1614	603	e-173	90	69	NADH-ubiquinone oxidoreductase 49 KD subunit precursor (complex I-49KD) (CI-49KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 49K chain - Neurospora crassa ; (X54508) NADH dehydrogenase 49 kD subunit [Neurospora crassa]	
19617	ENU03411	ANI61C9007:	22-51	1061-1080	NAP	g3976	198	71	1.00E-11	31	59	(X53840) mitochondrial ribosomal protein Yml20 [Saccharomyces cerevisiae]	
19618	ENU03412	ANI61C6616:	43-61	1081-1102	NAP	g1708464	1270	222	e-108	67	56	"putative dihydroxy-acid dehydratase precursor (DAD) (2,3-Dihydroxy acid hydrolyase) ; (Z69795) unknown [Schizosaccharomyces pombe]"	
19619	ENU03413	ANI61C953:2	55-74	1093-1115	NAP	g584806	1920	661	0	88	66	"ATP synthase alpha chain, mitochondrial precursor ; H ⁺ -transporting ATP synthase (EC 3.6.1.34) alpha chain - Neurospora crassa ; (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa]"	
19620	ENU03414	ANI61C1699:	27-47	1065-1087	NAP	g2808634	3172	522	e-147	80	39	(AJ001909) transcriptional activator [Aspergillus niger]	
19621	ENU03415	ANI61C8652:	34-54	1080-1099	NAP	g2499716	226	77	2.00E-13	29	67	"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (X99795) exopolysaccharuronase [Aspergillus tubingensis]"	
19622	ENU03416	ANI61C1106	33-52	1082-1101	NAP	g549759	630	185	5.00E-58	31	78	"hypothetical 52.3 KD protein in FRE2 5'region ; hypothetical protein YKL221w - yeast (Saccharomyces cerevisiae) ; (X75950) ORF4, B473 [Saccharomyces cerevisiae] ; (Z28221) ORF YKL221w [Saccharomyces cerevisiae] ; ORF 4 [Saccharomyces cerevisiae]"	
19623	ENU03417	ANI61C5477:	22-48	1068-1090	NAP	g1834342	750	190	3.00E-78	48	21	(Z68905) ATP-binding cassette multidrug transporter [Emmericella nidulans]	

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19624	ENU03418	ANI61C7673:	64-89	1108-1133	NAP	g4495126	1033	1033	269	3.00E-71	37	35	(AL035583) putative helicase [Schizosaccharomyces pombe]
19625	ENU03419	ANI61C8010:	22-51	1056-1091	NAP	g1173405	733	169	2.00E-71				"protein phosphatases PP1 regulatory subunit SDS22 ; protein suppressor sds22 - fission yeast (Schizosaccharomyces pombe) ; (Z98762) SPAC4A8.12c, sds22; protein phosphatases ppl regulat ory subunit, len:332aa, identical to SD22_SCHPO, P22194, (3 32aa), similar eg. to yeast Q15435, SDS22 homolog, (360aa), fasta scores, opt:837, E0:0, (47,6% identi..." (Z99531) ubiquitin system protein [Schizosaccharomyces pombe] (D90917) hypothetical protein [Synechocystis sp.] "uracil-DNA glycosylase precursor (UDG) ; uracil-DNA glycosylase (EC 3.2.2.-) - yeast (Saccharomyces cerevisiae) ; (J04470) uracil-DNA-glycosylase [Saccharomyces cerevisiae] ; (Z46659) UNG1 gene, len: 359, CAl: 0.12, uracil-DNA glycosylase [Saccharomyces cerevisiae]" (AL033503) peptide transport protein [Candida albicans] (AL023592) acetamidase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
19626	ENU03420	ANI61C8479:	62-82	1111-1132	NAP	g2440180	1508	542	e-153	69	11		
19627	ENU03421	ANI61C9176:	22-51	1072-1092	NAP	g1653915	415	203	2.00E-51	32	96		
19628	ENU03422	ANI61C1899:	47-66	1098-1117	NAP	g137043	489	149	4.00E-53	44	84		
19629	ENU03423	ANI61C8616:	22-47	1066-1093	NAP	g3859684	404	140	1.00E-42	32	53		
19630	ENU03424	ANI61C4044:	23-42	1073-1095	NAP	g3136052	320	147	2.00E-36	33	61		
19631	ENU03425	ANI61C1103	68-88	1122-1140	NAP	g2132651	664	80	2.00E-33	30	61		
19632	ENU03426	ANI61C6686:	34-56	1085-1106	NAP	g1351714	288	90	3.00E-17	25	68		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19633	ENU03427	ANI61C1032	22-50	1076-1096	NAP	g126918	310	92	9.00E-32	36	95		Mono- and diacylglycerol lipase precursor (MDGL) ; mono- and diacylglycerol lipase (EC 3.1.1.-) precursor - <i>Penicillium camembertii</i> ; (D90315) MDGL precursor [Penicillium camembertii]
19634	ENU03428	ANI61C2335	57-75	1111-1132	NAP	g1346703	1482	468	e-142	78	96		Polygalacturonase precursor (pectinase) (PGL) ; polygalacturonase (EC 3.2.1.15) precursor - <i>Aspergillus parasiticus</i> ; (U17167) polygalacturonase precursor [Aspergillus parasiticus] ; (L23523) [Aspergillus parasiticus] ; (L23523) polygalacturonase [Aspergillus parasiticus]
19635	ENU03429	ANI61C6897	66-97	1108-1141	NAP	g3646379	657	161	2.00E-59	41	60		(AJ001540) phenylacetyl-CoA ligase [Penicillium chrysogenum]
19636	ENU03430	ANI61C2091	39-58	1087-1114	NAP	g4454019	62	2.00E-12					(AL035396) SRG1-like protein [Arabidopsis thaliana]
19637	ENU03431	ANI61C6093	28-51	1077-1104	NAP	g4107289	467	192	2.00E-50	35	66		(AL035076) putative carboxylesterase-lipase family member
19638	ENU03432	ANI61C9179	35-54	1091-1112	NAP	g1077295	175	102	4.00E-21	31	92		[Schizosaccharomyces pombe] probable membrane protein YOL107w - yeast (Saccharomyces cerevisiae) ; (Z48149) similarity with P. tetraurelia cytochrome C oxidase [Saccharomyces cerevisiae] ; (Z74849) ORF YOL107w [Saccharomyces cerevisiae]
19639	ENU03433	ANI61C7538	22-46	1081-1100	NAP	g730272	625	238	3.00E-77	43	92		Peroxisomal targeting signal 2 receptor (PTS2 receptor) (peroxisome import protein PAS7) (peroxin-7) ; PAS7 protein - yeast (Saccharomyces cerevisiae) ; (X81424) Pas7p [Saccharomyces cerevisiae] ; (X83704) Peb1 [Saccharomyces cerevisiae] (AL022103) deoxycytidylate deaminase [Schizosaccharomyces pombe]
19640	ENU03434	ANI61C6107	62-82	1122-1141	NAP	g2956780	608	108	1.00E-57	46	90		(D45893) act-2 [Neurospora crassa]
19641	ENU03435	ANI61C9017	71-91	1133-1151	NAP	g1754596	398	97	2.00E-19	31	54		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19642	ENU03436	AN161C9774:	65-85	1127-	NAP		g549443	8521	690	0	99	18	Conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866)
		3928..5051		1146									putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans] (AJ005253) C1pP protease [Mus musculus] ; (AJ012249) C1pP protease [Mus musculus]
19643	ENU03437	AN161C1695:	22-52	1069-	NAP		g3559935	425	141	5.00E-47	55	54	"NMT1 protein homolog ; nmt1 protein - Aspergillus parasiticus ; (U15196) the expression of this gene has been shown to be completely inhibited by thiamine as was observed for the Schizosaccharomyces pombe nmt1, Swiss-Prot Accession Number P36597 [Aspergillus parasiticus] ; nmt1 gene [Aspergillus parasiticus]"
		1352..1600		1103									cytochrome C PEROxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae) ; (X62422)
19644	ENU03438	AN161C6466:	22-57	1085-	NAP		g1171741	1602	512	e-144	92	99	Cytochrome c peroxidase [Saccharomyces cerevisiae] ; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]
		615..1739		1104									chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens] (U59214) MAP protein kinase MPKA [Emericella nidulans] (U26463) NADPH-dependent aldehyde reductase [Sporidiobolus salmonicolor] (U41278) contains similarity to G beta repeats (PROsite:PS00670) of the beta-transducin family [Caenorhabditis elegans]
19645	ENU03439	AN161C1045	70-89	1124-	NAP		g543969	593	135	5.00E-61	42	95	probable membrane protein YOR380w - yeast (Saccharomyces cerevisiae) ; (Z75288) ORF YOR380w [Saccharomyces cerevisiae]
		1:4390..3264		1154									
19646	ENU03440	AN161C7019:	64-83	1128-	NAP		g4502497	280	71	1.00E-11	38	89	
		5621..4493		1149									
19647	ENU03441	AN161C3212:	38-58	1104-	NAP		g4580577	2092	412	0	97	81	
		2345..1218		1123									
19648	ENU03442	AN161C1118	46-65	1114-	NAP		g1142698	719	120	3.00E-50	57	94	
		2:2717..3848		1135									
19649	ENU03443	AN161C8239:	22-52	1090-	NAP		g1086900	178	59	9.00E-12	31	39	
		1151..20		1111									
19650	ENU03444	AN161C1097	60-79	1131-	NAP		g2132958	353	153	1.00E-36	30	65	
		9:7353..6221		1150									

Sequence Selection

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19651	ENU03445	ANI61C8387:	72-92	1139-1163	NAP		g3560241	373	85	4.00E-21	40	26	(AL031532) putative amino acid permease [Schizosaccharomyces pombe]
19652	ENU03446	ANI61C5168:	25-52	1088-1116	NAP		g1171946	615	183	1.00E-71	41	93	NADPH dehydrogenase 3 (old yellow enzyme 3) ; NADPH dehydrogenase (EC 1.6.99.1) OYE3 - yeast (Saccharomyces cerevisiae) ; (L29279) NADPH dehydrogenase [Saccharomyces cerevisiae] ; (Z73527) ORF YPL171c [Saccharomyces cerevisiae]
19653	ENU03447	ANI61C1113	46-65	1110-1139	NAP		g1730251	724	192	4.00E-84	56	91	GTP cyclohydrolase II ; GTP-cyclohydrolase - Pichia guilliermondii ; GTP-cyclohydrolase - Pichia guilliermondii ; (Z49093) GTP-cyclohydrolase [Pichia guilliermondii] Triosephosphate isomerase (TIM) ; triose-phosphate isomerase (EC 5.3.1.1) - Emericella nidulans ; (D10019) triosephosphate isomerase [Emericella nidulans]
19654	ENU03448	ANI61C2332:	27-50	1094-1120	NAP		g136053	1099	187	e-111	98	99	hypothetical 30.0 K D protein C13F4.14 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (AL031322) conserved hypothetical protein [Schizosaccharomyces pombe]
19655	ENU03449	ANI61C6376:	58-77	1131-1151	NAP		g1723274	275	96	4.00E-19	36	94	[Schizosaccharomyces pombe] hypothetical 51.6 K D protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae) ; (X78898) (Saccharomyces cerevisiae) ; possibly expressed during the late G1 /S phase; homology with the SS RP proteins [Saccharomyces cerevisiae] ; (Z71482) ORF YNL206c [Saccharomyces cerevisiae]
19656	ENU03450	ANI61C2623:	71-89	1145-1164	NAP		g732190		81	6.00E-16			(AF031376) LIM-domain binding factor 2; LDB2 [Danio rerio]
19657	ENU03451	ANI61C9329:	69-88	1142-1162	NAP		g3078001		36	0.66			Hexokinase ; (L04480) hexokinase [Schistosoma mansoni]
19658	ENU03452	ANI61C3576:	55-75	1120-1150	NAP		g2833327		76	4.00E-13			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19659	ENU03453	ANI61C4140:	43-63	1116-1139	NAP		g1705465	1079	414	e-119	58	88	Biotin synthetase (biotin synthetase); biotin synthetase - yeast (Saccharomyces cerevisiae); (Z73071) ORF YGR286c [Saccharomyces cerevisiae]
19660	ENU03454	ANI61C9438:	31-50	1100-1127	NAP		g3929362	362	174	9.00E-43	32	70	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpVI]
19661	ENU03455	ANI61C6611:	30-57	1105-1127	NAP		g2492777	604	220	1.00E-56	47	88	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5-FET4 intergenic region; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae); (Z54141) unknown [Saccharomyces cerevisiae]
19662	ENU03456	ANI61C7326:	23-45	1093-1122	NAP		g585668	807	192	5.00E-48	49	90	Polygalacturonase precursor (PG) (pectinase); (L02239) endopolylgalacturonase [Gibberella fujikuroi]
19663	ENU03457	ANI61C5335:	22-41	1103-1125	NAP		g2501210	1300	420	e-135	69	99	putative disulfide isomerase TIGA precursor; (X98748) tlgA [Aspergillus niger]
19664	ENU03458	ANI61C2777:	52-71	1137-1156	NAP		g1408294	565	220	1.00E-56	39	94	(U61983) benzyl alcohol dehydrogenase [Acinetobacter calcoaceticus]
19665	ENU03459	ANI61C4098:	72-91	1154-1176	NAP		g1199853	292	140	2.00E-32	36	90	(X95720) O6357 [Saccharomyces cerevisiae]
19666	ENU03460	ANI61C3743:	67-86	1152-1171	NAP		g3914390	685	150	2.00E-35	45	91	Pectin lyase precursor; (L22857) pectin lyase [Colletotrichum gloeosporioides]
19667	ENU03461	ANI61C1756:	50-79	1134-1156	NAP		g113792	1500	466	e-130	63	59	"glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosyltransferase); glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus sp; (D10460) glucoamylase [Aspergillus shirousami]"
19668	ENU03462	ANI61C9390:	67-94	1149-1175	NAP		g3915606	251	86	1.00E-24	30	52	Aminic acid oxidase [flavin-containing] (monoamine oxidase) (MAO)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19669	ENU03463	AN161C348:2	23-58	1109-1133	NAP		g3493591	647	279	3.00E-74	44	56	(AF063231) cytoplasmic dynein intermediate chain 2 [Mus musculus]
19670	ENU03464	..1154 AN161C323:2	25-44	1118-1136	NAP		g140479	785	148	9.00E-35	36	37	"probable transporter FEN2; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR028c, len:512 [Saccharomyces cerevisiae]"
19671	ENU03465	AN161C1037	29-50	1121-1140	NAP		g66290	554	217	9.00E-56	34	59	laccase (EC 1.10.3.2) I - Emericella nidulans
19672	ENU03466	2:81..1234 AN161C843:3	23-46	1111-1134	NAP		g3913072	143	86	5.00E-16	39	24	probable 2-dehydropanioate 2-reductase (ketopantoate reductase) (KPA reductase) ; (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus]
19673	ENU03467	768..2614 AN161C843:3	41-64	1129-1152	NAP		g3913072	143	86	5.00E-16	39	24	probable 2-dehydropanioate 2-reductase (ketopantoate reductase) (KPA reductase) ; (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus]
19674	ENU03468	45..1198 AN161C9542:2	28-53	1120-1139	NAP		g3183308	392	143	2.00E-33	37	38	hypothetical 49.6 KD protein C5D6.04 in chromosome I ; (Z98056) hypothetical protein
19675	ENU03469	1884..728 AN161C6702:2	36-60	1129-1150	NAP		g2132851	146	53	9.00E-12	29	44	[Schizosaccharomyces pombe] probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w
19676	ENU03470	1289..133 AN161C9502:2	55-74	1150-1169	NAP		g3323397	1563	518	e-163	83	92	[Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanylyltransferase [Hypocrea jecorina]
19677	ENU03471	4..1171 AN161C546:1	35-55	1129-1150	NAP		g2499517	578	181	3.00E-66	41	56	hypothetical 71.1 KD protein in DSK2-CAT8 intergenic region; hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae) ; (Z49704) unknown [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19678	ENU03472	ANI61C11:71	67-87	1163-	NAP		g1730840	935	190	1.00E-47	36	45	putative cysteinyl-TRNA synthetase C29E6.00C (cysteine--TRNA ligase) (CYSR5) ; probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19679	ENU03473	ANI61C8853: 29-48		1114-	NAP		g1730193	703	291	5.00E-78			UDP-glucose 4-epimerase (galactowaldenase) (UDP-GALactose 4-epimerase) ; (X99339) UDP-glucose 4-epimerase [Bacillus subtilis] ; (D83026) highly homologous to UDP-glucose 4-epimerases (SwissProt:GALE_HAEIN and GALE_ECOLI); hypothetical [Bacillus subtilis] ; (Z99123) UDP-glucose 4-epimerase [Bacillus subtilis] (M11621) putative [Saccharomyces cerevisiae]
19680	ENU03474	ANI61C676:4 44-65		1145-	NAP		g806323	295	93	2.00E-27	39	58	"(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]"
19681	ENU03475	ANI61C9629: 22-43		1124-	NAP		g4006818	832	135	9.00E-80	55	96	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
19682	ENU03476	ANI61C1097 49-68		1152-	NAP		g2132942		112	4.00E-24			
19683	ENU03477	ANI50C1823 27-46		1128-	NAP		g2191179		72	6.00E-12	31	72	[Saccharomyces cerevisiae] (AF007270) contains similarity to syntaxin [Arabidopsis thaliana]
19684	ENU03478	ANI61C5073: 39-58		1143-	NAP		g3859696	361	123	4.00E-38	34	78	(AL033497) unknown hypothetical protein [Candida albicans]
19685	ENU03479	ANI61C4357: 53-73		1159-	NAP		g2507070	383	105	4.00E-38	36	65	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
		1174..6		1179									

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 1173-	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19686	ENU03480	ANI61C11:71	67-87	1173-	1193	NAP		g1730840	935	196	2.00E-49	36	45	putative cysteinyl-TRNA synthetase C29E6.06C (cysteine--TRNA ligase) (CVSR5) ; probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19687	ENU03481	ANI61C7427:	32-54	1139-	1158	NAP		g4038613	681	184	8.00E-46	50	91	(Z98602) conserved uncharacterized protein domain-containing protein [Schizosaccharomyces pombe]
19688	ENU03482	ANI61C4324:	71-94	1180-	1199	NAP		g3821271	1076	351	4.00E-96	64	66	(AJ009956) alpha-galactosidase 1 [Penicillium simplicissimum]
19689	ENU03483	ANI61C9384:	37-63	1148-	1169	NAP		g2981103	375	140	1.00E-32	33	64	(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]
19690	ENU03484	ANI61C1005	59-78	1173-	1192	NAP		g131768	568	159	4.00E-38	32	69	quinate permease (quinate transporter) ; quinate transport protein - Emeritella nidulans ; (X13525) quinate permease [Emeritella nidulans] (Z98974) putative small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
19691	ENU03485	ANI61C1024:	26-45	1143-	1161	NAP		g2388912	499	80	1.00E-36	49	99	(Z98974) putative small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
19692	ENU03486	ANI61C6064:	52-71	1159-	1187	NAP		g3581921	198	53	0.000004	45	58	(AL031546) ubiquinol-cytochrome c reductase complex subunit [Schizosaccharomyces pombe]
19693	ENU03487	ANI61C7603:	67-87	1173-	1202	NAP		g3859693	68	68	1.00E-10			(AL033497) transport protein [Candida albicans]
19694	ENU03488	ANI61C7603:	67-87	1173-	1202	NAP		g3859693	68	68	1.00E-10			(AL033497) transport protein [Candida albicans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19695	ENU03489	AN161C7187:	65-84	1167-	NAP	g112940	532	134	1.00E-40				Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase precursor (isopenicillin N acyltransferase); acyltransferase AAT - Emericella nidulans; isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans; (X53310) Acyl-CoA [Emericella nidulans]; (M58293) acyl-coenzyme A:isopenicillin N acyltransferase [Emericella nidulans] (AL031603) putative glycosyl transferase [Schizosaccharomyces pombe]
19696	ENU03490	AN161C9634:	52-71	1165-1189	NAP	g3646449	753	206	3.00E-62	48	69		hypothetical 61.8 KD protein C12B10.03 in chromosome 1; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19697	ENU03491	AN161C352:5	22-48	1142-1161	NAP	g1723547	701	170	8.00E-80	46	59		hypothetical 61.8 KD protein C12B10.03 in chromosome 1; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19698	ENU03492	AN161C8306:	60-79	1180-1202	NAP	g1351809	956	397	e-109	53	94		membrane protein YDR331w - yeast (Saccharomyces cerevisiae); (U32517) Ydr331wp [Saccharomyces cerevisiae] (Z80108) lip1 [Mycobacterium tuberculosis]
19699	ENU03493	AN161C1105	37-56	1161-1180	NAP	g1542908		96	6.00E-19				(AL031532) hypothetical protein [Schizosaccharomyces pombe]
19700	ENU03494	AN161C1056	59-89	1180-1202	NAP	g3560245	168	79	5.00E-14	26	51		(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
19701	ENU03495	AN161C2603:	22-48	1138-1165	NAP	g4490992	188	76	3.00E-13	30	79		hypothetical 47.0 KD protein in PET117-CEM1 intergenic region; hypothetical protein YER059w - yeast (Saccharomyces cerevisiae); (U18813) Yer059wp [Saccharomyces cerevisiae]
19702	ENU03496	AN161C6589:	55-74	1174-1199	NAP	g731468	299	114	1.00E-24	38	56		hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region; (D84432) YqkA [Bacillus subtilis]; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19703	ENU03497	AN161C9095:	22-50	1147-1166	NAP	g1731087	67	56	0.000000	21	59		
19704	ENU03498	AN161C1082:	63-82	1181-1208	NAP	g1929089	393	133	3.00E-30	30	65		
19705	ENU03499	AN161C4013:	34-55	1161-1181	NAP	g2804298	792	241	6.00E-63	36	70		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19706	ENU03500	ANI61C410:1	55-74	1179-1204	NAP	g2131476	626	626	210	7.00E-69	44	89	hypothetical protein YDR415c - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr415cp; CAl: 0.14 [Saccharomyces cerevisiae]
19707	ENU03501	ANI61C8114: 64-83		1181-1215	NAP	g1706694	609	609	178	1.00E-46	35	49	"Lanosterol synthase (oxidosqualene—lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC) ; lanosterol synthase (EC 5.4.99.7) - fission yeast (Schizosaccharomyces pombe) ; (U41368) lanosterol synthase [Schizosaccharomyces pombe]"
19708	ENU03502	ANI61C9917: 22-41		1153-1173	NAP	g3581896	443	443	138	8.00E-32	24	70	[Schizosaccharomyces pombe]" (AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19709	ENU03503	ANI61C6104: 28-47		1158-1179	NAP	g4106687	432	432	86	6.00E-20	34	97	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]"
19710	ENU03504	ANI61C6105: 57-75		1190-1209	NAP	g3560215	956	956	252	2.00E-80	49	81	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]"
19711	ENU03505	ANI61C650:3	22-49	1155-1176	NAP	g1711370	326	326	107	5.00E-34	32	96	nuclear pore protein SEH1 ; SEC13 protein homolog YGL100w - yeast (Saccharomyces cerevisiae) ; (X90994) Sec13p-like protein [Saccharomyces cerevisiae] ; (Z72622) ORF YGL100w [Saccharomyces cerevisiae]
19712	ENU03506	ANI61C1054	24-43	1148-1179	NAP	g2648302	290	290	108	1.00E-32	42	97	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
19713	ENU03507	ANI61C8859: 22-41		1153-1178	NAP	g4587097	104	65	0.000000	001	32	67	(AB019045) OMPdecarboxylase [Rhizomucor pusillus]
19714	ENU03508	ANI61C9217: 22-41		1150-1180	NAP	g1169696		36	0.7				Flagellin 1 ; flagellin flhC-1 - Proteus mirabilis ; (L07270) flagellin [Proteus mirabilis]
19715	ENU03509	ANI61C6534: 23-47		1166-1183	NAP	g549699	427	41	0.021	27	89		hypothetical 50.5 KD protein in MDH1-VMA5 intergenic region ; hypothetical protein YKL082c - yeast (Saccharomyces cerevisiae) ; (Z28082) ORF YKL082c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19716	ENU03510	AN161C6741:	48-67	1186-1209	NAP		g1174552	564	99	1.00E-54	43	95	tryptophan YL-TRNA synthetase (tryptophan--TRNA ligase) (TRPRS); tryptophan--TRNA ligase (EC 6.1.1.2) - Haemophilus influenzae (strain Rd KW20); (U32746) tryptophanyl-tRNA synthetase (trpS) [Haemophilus influenzae Rd]
19717	ENU03511	AN161C1046	22-49	1152-1184	NAP		g3123677	610	254	1.00E-66	46	99	(AJ005824) Ufd1 protein [Schizosaccharomyces pombe]; (AJ005825) Ufd1 protein [Schizosaccharomyces pombe]
19718	ENU03512	AN161C8443:	24-55	1154-1186	NAP		g1352074	792	282	3.00E-77			type II proteins geranylgeranyltransferase beta subunit (type II protein geranyl-geranyltransferase beta subunit) (GGTASE-II-beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta subunit); probable protein prenityltransferase (EC 2.5.1.-) BET2 - yeast (Saccharomyces cerevisiae); (U25842) Protein Geranyl-geranyltransferase beta subunit (Swiss Prot. accession number P20133; P32433) [Saccharomyces cerevisiae]
19719	ENU03513	AN161C3364:	56-76	1185-1219	NAP		g603955	1280	349	e-122	71	64	(D43950) KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. [Homo sapiens]
19720	ENU03514	AN161C5704:	24-50	1159-1187	NAP		g1351659	766	311	5.00E-84	46	88	hypothetical 49.3 KD protein C30D11.06C in chromosome I; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein [Schizosaccharomyces pombe]
19721	ENU03515	AN161C7052:	67-87	1213-1233	NAP		g2131781	369	102	8.00E-44	35	42	hypothetical protein YLR114c - yeast (Saccharomyces cerevisiae); (U53878) Ylr114cp [Saccharomyces cerevisiae]; (X89514) putative orf [Saccharomyces cerevisiae]; (Z73286) ORF YLR114c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	5 pos	Primer	3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19722	ENU03516	ANI61C9393:	62-81	1208-	1228-	NAP	g3261633	452	200	2.00E-50	35	95	(Z79700) fadE13 [Mycobacterium tuberculosis]	
19723	ENU03517	2303..3511	23-44	1172-	1172-	NAP	g2499591	1035	296	2.00E-79	69	68	mitogen-activated protein kinase HOG1 (MAP kinase HOG1); (X90586) unnamed protein product [Candida albicans]	
19724	ENU03518	ANI61C9381:	45-67	1194-	1213	NAP	g135025	905	297	7.00E-84	69	83	"succinyl-CoA ligase (GDP-FORMING), alpha-chain precursor (succinyl-CoA synthetase, alpha chain) (SCS-alpha); succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain precursor - rat; (J03621) succinyl-CoA synthetase alpha subunit (EC 6.2.1.4) [Rattus norvegicus]" (AF054512) endoglucanase V [Aspergillus aculeatus]	
19725	ENU03519	ANI61C6226:	44-63	1193-	1212	NAP	g2997731	992	229	3.00E-59	64	92	putative DNA repair protein C12B10.12C; (Z70721) putative dna repair protein [Schizosaccharomyces pombe]	
19726	ENU03520	14274..13064	69-95	1216-	1238	NAP	g1723554	619	237	1.00E-61	39	60	(AL031536) hypothetical zinc finger protein [Schizosaccharomyces pombe]	
19727	ENU03521	ANI50C7567	22-54	1172-	1192	NAP	g3560212		68	5.00E-25	29	20	protein [Schizosaccharomyces pombe]	
19728	ENU03522	2_1:1300..88	22-40	1159-	1193	NAP	g3875242	181	66	3.00E-22	30	90	(Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]	
19729	ENU03523	ANI61C1056	71-90	1223-	1243	NAP	g747710	231	117	1.00E-25	30	20	(X16609) alt. ankyrin (variant 2.2) [Homo sapiens]	
19730	ENU03524	8:3268..2054	41-60	1194-	1213	NAP	g1175958	571	233	1.00E-60	36	55	hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae); (D50617) YFL054C [Saccharomyces cerevisiae]; (D44603) unknown [Saccharomyces cerevisiae]	
19731	ENU03525	ANI61C5132:	22-51	1170-	1195	NAP	g2160161		43	0.003			(AC000132) F21M12.7 gene product [Arabidopsis thaliana]	
19732	ENU03526	376..1591	63-88	1209-	1237	NAP	g4049527	391	71	1.00E-30	45	97	(AL034565) putative transcription initiation factor ttf1f small subunit [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	at Score	Blast Score	Blast Prob	% id	% cvrg	Description
19733	ENU03527	AN161C6659: 61-80	1179..2398	1238	NAP		g2633018	395	205	7.00E-52	32	63	(Z99107) similar to hypothetical proteins from <i>B. subtilis</i> [Bacillus subtilis]
19734	ENU03528	AN161C9013: 22-41	1..1220	1180-1199	NAP		g465483	869	261	7.00E-69	48	61	protein kinase WIS1 ; protein kinase wsi1 (EC 2.7.1.-) - fission yeast [Schizosaccharomyces pombe] ; (X62631) protein kinase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AL032684) putative pre-tRNA nuclear export receptor [Schizosaccharomyces pombe]
19735	ENU03529	AN161C6231: 23-46	2..1222	1182-1201	NAP		g3810833	405	132	6.00E-30	33	36	peroxisomal membrane protein PEX13 [Schizosaccharomyces pombe] (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] peroxin-13 ; (U70067) integral peroxisomal membrane protein [Pichia pastoris] PPex13p [Pichia pastoris] ; putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]
19736	ENU03530	AN161C7020: 65-84	3499..4721	1226-1245	NAP		g1351714	223	73	2.00E-16	35	59	peroxisomal membrane protein PEX13 [Schizosaccharomyces pombe] (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]
19737	ENU03531	AN161C1021: 45-64	9..2366..1144	1201-1225	NAP		g586479	934	294	e-105			peroxisomal membrane protein PEX13 [Schizosaccharomyces pombe] (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]
19738	ENU03532	AN161C1046: 22-52	6:1301..2523	1177-1202	NAP		g3150248	797	304	3.00E-91	53	65	peroxisomal membrane protein PEX13 [Schizosaccharomyces pombe] (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]
19739	ENU03533	AN161C9016: 27-49	1242..19	1189-1208	NAP		g2649648	601	208	3.00E-62	37	95	peroxisomal membrane protein PEX13 [Schizosaccharomyces pombe] (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]
19740	ENU03534	AN161C6369: 63-82	6835..8059	1226-1245	NAP								peroxisomal membrane protein PEX13 [Schizosaccharomyces pombe] (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19741	ENU03535	ANI61C2490:	35-54	1199-1218	NAP	g2507436	922	333	1.00E-90	49	46		glutaminyl-TRNA synthetase (GLNRS); glutamine--tRNA ligase (EC 6.1.1.18) - yeast (Saccharomyces cerevisiae); (U55021) Gln4p [Saccharomyces cerevisiae]; (Z75076) ORF YOR168w [Saccharomyces cerevisiae]
19742	ENU03536	ANI61C5804:	22-47	1183-1205	NAP	g125886	618	169	2.00E-53	41	86		lactate 2-monooxygenase (lactate oxidase); lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
19743	ENU03537	ANI61C1809:	22-47	1174-1207	NAP	g2498337	722	242	2.00E-64	42	78		squalene monooxygenase (squalene epoxidase) (SE); (D88252) squalene epoxidase [Candida albicans]; (U69674) squalene epoxidase [Candida albicans]
19744	ENU03538	ANI61C7512:	64-84	1228-1251	NAP	g2408022	357	125	8.00E-28	47	35		(Z99162) ER protein-translocation complex subunit [Schizosaccharomyces pombe]
19745	ENU03539	ANI61C7486:	57-75	1225-1246	NAP	g117803	1224	452	e-126	62	67		cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala); (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
19746	ENU03540	ANI61C676:	32-51	1203-1221	NAP	g544261	46	0.0006					RNA-binding protein EWS; RNA-binding protein EWS - human; (X66899) RNA binding protein [Homo sapiens]; (X72990) EWS [Homo sapiens]; (Y07848) RNA binding protein [Homo sapiens]; EWS gene [Homo sapiens]
19747	ENU03541	ANI61C5627:	55-74	1227-1246	NAP	g3914984	208	113	3.00E-24	25	10		ferrichrome siderophore peptide synthetase; (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19748	ENU03542	ANI61C164:1	36-55	1195-1227	NAP	g1750122	1071	163	3.00E-64	42	75		"(U66480) xylan beta-1,4-xylosidase [Bacillus subtilis] ; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis]"
19749	ENU03543	ANI61C9610: 72-96	1578..347	1244-1264	NAP	g118298	463	200	2.00E-50				S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC) ; adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - yeast (Saccharomyces cerevisiae) ; (M38434) S-adenosylmethionine decarboxylase [Saccharomyces cerevisiae] ; (X91067) adenosylmethionine decarboxylase [Saccharomyces cerevisiae] ; (Z74794) ORF YOL052c [Saccharomyces cerevisiae]
19750	ENU03544	ANI61C5499: 57-77	269..1504	1215-1250	NAP	g2132395	346	150	3.00E-48	36	71		polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces cerevisiae) ; (Z71292) ORF YNL016w [Saccharomyces cerevisiae]
19751	ENU03545	ANI61C3215: 72-91	1248..12	1247-1266	NAP	g730251	626	208	5.00E-64	49	89		protein phosphatase 2C homolog 1 (PP2C-1) ; phosphoprotein phosphatase (EC 3.1.3.16) 2C - fission yeast (Schizosaccharomyces pombe) ; (L26970) protein phosphatase 2C [Schizosaccharomyces pombe]
19752	ENU03546	ANI61C9596: 22-56	2267..3504	1196-1216	NAP	g1078613	1662	534	e-151	69	80		stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata ; (X85963) delta-9 fatty acid desaturase [Ajellomyces capsulatus]
19753	ENU03547	ANI61C6355: 38-57	17..1253	1207-1232	NAP	g730615	978	393	e-108	47	28		DNA-directed RNA polymerase mitochondrial precursor ; (L25087) mitochondrial RNA polymerase [Neurospora crassa] ; cyf-5 gene [Neurospora crassa]
19754	ENU03548	ANI61C1028	33-55	1207-1228	NAP	g1723906	542	206	3.00E-52	39	48		hypothetical 80.0 KD protein in SNF4-TAF60 intergenic region ; probable membrane protein YGL114w - yeast (Saccharomyces cerevisiae) ; (Z72636) ORF YGL114w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19755	ENU03549	ANI61C1118:	69-88	1246-	NAP		g2132958	354	110	2.00E-23	26	73	probable membrane protein YOR380w - yeast (Saccharomyces cerevisiae) ; (Z75288) ORF YOR380w
		4267..3029		1264									[Saccharomyces cerevisiae] (AF009672) unknown [Acinetobacter sp. ADP1]
19756	ENU03550	ANI61C5525:	26-45	1201-	NAP		g2271503	247	83	1.00E-20	30	91	ATP10 protein ; (J05463) ATP10 protein [Saccharomyces cerevisiae] (U78597) kinesin light chain [Plectonema boryanum]
		420..1657		1221									hypothetical 102.3 KD protein in DAL82-RFA2 intergenic region ; hypothetical protein YNL313c - yeast (Saccharomyces cerevisiae) ; (Z46259) NO364 [Saccharomyces cerevisiae] ; (Z71589) ORF YNL313c
19757	ENU03551	ANI61C8624:	47-68	1223-	NAP		g114699	158	85	9.00E-16	29	67	[Saccharomyces cerevisiae]
		150..1387		1242									
19758	ENU03552	ANI61C1080	72-92	1242-	NAP		g2645229	358	95	1.00E-18	34	29	
		9:396..1635		1269									
19759	ENU03553	ANI61C431:3	22-44	1200-	NAP		g1176586	579	157	1.00E-37	36	36	
		219..1979		1220									
19760	ENU03554	ANI61C1007	44-63	1223-	NAP		g731740	990	363	1.00E-99	50	91	[Saccharomyces cerevisiae] probable ATP-dependent RNA helicase DBP8 ; helicase homolog - yeast (Saccharomyces cerevisiae) ; (U00027) Yhr169wp [Saccharomyces cerevisiae] (AL023780) DNA binding protein [Schizosaccharomyces pombe]
		4:898..2138		1242									[Schizosaccharomyces pombe] alcohol dehydrogenase II ; alcohol dehydrogenase (EC 1.1.1.1) II - Emericella nidulans ; (Z48000) alcohol dehydrogenase II [Emericella nidulans] ; alcohol dehydrogenase II [Emericella nidulans]
19761	ENU03555	ANI61C1111:	66-88	1232-	NAP		g3184115	634	250	1.00E-65	35	80	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]
		1711..2952		1265									zinc finger protein 207 ; (AF046001) zinc finger transcription factor [Homo sapiens]
19762	ENU03556	ANI61C3965:	66-86	1242-	NAP		g1703172	1802	433	e-163	98	93	
		1636..394		1265									
19763	ENU03557	ANI61C290:9	26-47	1207-	NAP		g3646450	1005	148	9.00E-35	41	53	
		99..2241		1226									
19764	ENU03558	ANI61C7312:	66-85	1250-	NAP		g4508017	242	58	4.00E-18	27	76	
		1222..2467		1269									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19765	ENU03559	AN161C1036	25-55	1209-1228	NAP		g549077	974	375	e-103	51	98	"3-ketoacyl-CoA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) ; (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica] "
		6:1735..490											(Z79750) acid phosphatase [Emmericella nidulans]
19766	ENU03560	AN161C170:3	55-74	1232-1260	NAP		g1523784	2260	840	0	97	67	Uroporphyrinogen decarboxylase (UPD) ; uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (Saccharomyces cerevisiae) ; (X63721) uroporphyrinogen decarboxylase [Saccharomyces cerevisiae] ; (Z19089) uroporphyrinogen decarboxylase [Saccharomyces cerevisiae] ; (Z49209) Hem12p [Saccharomyces cerevisiae] (AL035076) putative glutamate-1-semialdehyde aminotransferase [Schizosaccharomyces pombe]
19767	ENU03561	AN161C9890: 23-44		1195-1228	NAP		g416894	1069	392	e-112			(Y16748) malate dehydrogenase [Piromyces sp. E2] (AL034393) predicted using GeneFinder; cDNA EST yk343c12.5 comes from this gene; cDNA EST yk402e12.5 comes from this gene; cDNA EST yk457e8.5 comes from this gene; cDNA EST yk470f2.5 comes from this gene; cDNA EST yk281c3.5 com...
19768	ENU03562	AN161C8571: 71-94		1257-1276	NAP		g4107288	922	216	5.00E-84	52	88	(A1007712) replication factor C subunit [Arxula adenivorans] (AL031788) uv excision repair protein rad23 homolog [Schizosaccharomyces pombe]
19769	ENU03563	AN161C3737: 51-70		1236-1257	NAP		g4029338	627	112	5.00E-41	49	95	probable serine/threonine-protein kinase CID4.11C ; (Z69239) unknown [Schizosaccharomyces pombe]
19770	ENU03564	AN161C8574: 24-48		1204-1230	NAP		g3979938	105	36	0.73	34	31	
		85..1333											
19771	ENU03565	AN161C1023	33-56	1220-1239	NAP		g3367626	867	163	7.00E-87	59	94	
		5:1602..354											
19772	ENU03566	AN161C6252: 31-52		1219-1239	NAP		g3687502	605	65	3.00E-20	48	90	
		5320..4069											
19773	ENU03567	AN161C1155: 22-48		1211-1231	NAP		g1708616	896	175	3.00E-82	57	48	
		4035..2784											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19774	ENU03568	AN161C4414:	22-40	1207-1233	NAP	g1077358	523	196	6.00E-55	37	66		probable membrane protein YLR361c-yeast (Saccharomyces cerevisiae); (U19103) YH361cp [Saccharomyces cerevisiae]
19775	ENU03569	AN161C7023:	59-78	1254-1273	NAP	g1351643	674	161	2.00E-70	41	93		hypothetical 43.0 KD protein C8A4.09C in chromosome I; hypothetical protein SPAC8A4.09c-fission yeast (Schizosaccharomyces pombe); (Z66569) unknown [Schizosaccharomyces pombe]; (AL032824) hypothetical protein [Schizosaccharomyces pombe] (AL033385) conserved hypothetical protein [Schizosaccharomyces pombe] (X58121) SMP3 protein [Saccharomyces cerevisiae] (AL031743) putative protein transport protein [Schizosaccharomyces pombe] (AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe] "hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus] (AE001684) Oxononate Synthase [Chlamydia pneumoniae] probable serine/threonine-protein kinase C24B11.11C; hypothetical protein SPAC24B11.11c - fission yeast (Schizosaccharomyces pombe); (Z67757) unknown [Schizosaccharomyces pombe]
19776	ENU03570	AN161C8693:	37-56	1232-1252	NAP	g3850069	254	85	1.00E-15	32	95		
19777	ENU03571	AN161C6252:	60-83	1257-1276	NAP	g4498	445	163	3.00E-45	35	69		
19778	ENU03572	AN161C3740:	55-75	1242-1272	NAP	g3650391	831	201	1.00E-50	50	78		
19779	ENU03573	AN161C672:4	36-59	1235-1254	NAP	g3850111	561	94	2.00E-45	41	98		
19780	ENU03574	AN161C2194:	46-65	1246-1266	NAP	g731293	286	138	1.00E-31	33	90		
19781	ENU03575	AN161C5263:	32-51	1231-1252	NAP	g4585221	330	101	3.00E-24	39	88		
19782	ENU03576	AN161C1054	42-61	1243-1262	NAP	g4377376	462	165	1.00E-52	39	94		
19783	ENU03577	AN161C7707:	59-78	1256-1280	NAP	g1346360	542	231	6.00E-60	47	31		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19784	ENU03578	AN161C4008:	58-77	1259-1280	NAP	g2276351	329	93	4.00E-18	55	42	(Z97992) putative transcriptional regulator [Schizosaccharomyces pombe]	
19785	ENU03579	AN161C1160:	32-51	1225-1255	NAP	g585007	63	57	0.000000	2		cell division protein kinase 2 homolog CRK1 ; protein kinase (EC 2.7.1.37) cdc2-related CRK1 - Leishmania mexicana ; (X60385) cdc2-like protein [Leishmania mexicana]	
19786	ENU03580	AN161C4268:	22-42	1228-1247	NAP	g400766	447	201	1.00E-50	36	62	phenol 2-monooxygenase (phenol hydroxylase) ; phenol 2-monooxygenase (EC 1.14.13.7) - Pseudomonas sp. plasmid EST1412 (AL031534) protein kinase kin1 [Schizosaccharomyces pombe]	
19787	ENU03581	AN161C8771:	22-48	1213-1247	NAP	g3560139	157	50	0.00003	27	39	maackiain detoxification protein 1 - fungus (Nectria haematococca) ; (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]	
19788	ENU03582	AN161C4868:	71-90	1279-1299	NAP	g2133295	1263	182	4.00E-96	54	77	Meiotic recombination protein DLH1 (DMC1 homolog) ; DMC1/LIM15 homolog 1 - yeast (Candida albicans) ; (U39808) Dlh1p [Candida albicans]	
19789	ENU03583	AN161C1074:	22-46	1230-1250	NAP	g1706446	876	208	5.00E-90	63	99	hypothetical 40.0 KD protein C4G8.14C in chromosome I ; hypothetical protein SPAC4G8.14c - fission yeast (Schizosaccharomyces pombe)	
19790	ENU03584	AN161C1113	22-46	1225-1250	NAP	g1351604	337	123	2.00E-35	35	96	(U52963) mitogen-activated protein kinase [Nectria haematococca var. brevicornis]	
19791	ENU03585	AN161C9449:	29-48	1235-1259	NAP	g1279911	1596	555	e-167	91	99	hypothetical protein YPR023c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]	
19792	ENU03586	AN161C6804:	50-77	1262-1281	NAP	g1084946	276	96	4.00E-25	29	83	(D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]	
19793	ENU03587	AN161C1101:	26-51	1235-1257	NAP	g434759	1403	232	e-147	64	41	(AL023777) hypothetical protein [Schizosaccharomyces pombe]	
19794	ENU03588	AN161C1171:	25-52	1240-1259	NAP	g3184099	637	193	5.00E-51	36	69		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19795	ENU03589	AN161C7713:	22-43	1234-1258	NAP		g3183342	519	135	5.00E-31	38	96	hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein
19796	ENU03590	AN161C8371:	22-46	1235-1259	NAP		g1805251	366	166	4.00E-40	29	74	[Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]
19797	ENU03591	AN161C1137	25-47	1241-1262	NAP		g2388971	1133	260	e-119	57	99	(Z98979) hypothetical protein [Schizosaccharomyces pombe]
19798	ENU03592	AN161C822:1	22-45	1228-1260	NAP		g2739168	229	148	7.00E-35	31	98	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]
19799	ENU03593	AN161C1918:	22-55	1241-1261	NAP		g2764614	510	128	7.00E-58	40	98	(AJ001330) orfT [Lactobacillus sakei]
19800	ENU03594	AN161C9032:	22-41	1242-1262	NAP		g2144467	1212	135	2.00E-84	59	52	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae)
19801	ENU03595	AN161CS905:	70-89	1292-1311	NAP		g2499312	2312	591	e-168	92	77	NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (CI-51KD) ; (X64402) NADH dehydrogenase [Aspergillus niger] (AL034353) probable metabolite transport protein
19802	ENU03596	AN161C6334:	63-83	1272-1304	NAP		g3925778	835	78	1.00E-17	44	26	[Schizosaccharomyces pombe] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] (Y14749) MDM10 [Podospira anserinal]
19803	ENU03597	AN161C3320:	35-55	1246-1276	NAP		g2808725	159	78	1.00E-13	34	53	(AF016448) Similar to glycolate oxidase; coded for by C. elegans cDNA yk151h10.5; coded for by C. elegans cDNA yk151h10.3 [Caenorhabditis elegans]
19804	ENU03598	AN161C2332:	64-87	1283-1307	NAP		g2407968	415	164	9.00E-40	35	87	"3-ketoacyl-CoA thiolase peroxisomal A precursor (beta-ketothiolase A) (acetyl-CoA acyltransferase A) (peroxisomal 3-oxoacyl-CoA thiolase A) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16) A precursor, peroxisomal - rat ; (D90058) 3-ketoacyl-CoA thiolase A [Rattus norvegicus]"
19805	ENU03599	AN161C5370:	23-42	1237-1266	NAP		g2315453	463	123	5.00E-43	40	98	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
19806	ENU03600	AN161C6496:	22-56	1247-1266	NAP		g135746	730	182	2.00E-83	46	93	
19807	ENU03601	AN161C1837:	71-90	1296-1315	NAP		g2625138	2012	190	5.00E-94	48	23	

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19808	ENU03602	ANI61C9767: 23-56		1248-1267	NAP	g1723533	220	109	4.00E-23	38	39		hypothetical 33.6 KD protein C25G10.01 in chromosome I ; (Z70691) ma binding protein [Schizosaccharomyces pombe] (Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]
19809	ENU03603	ANI61C263:1 22-41		1242-1267	NAP	g3875242	181	66	3.00E-22	30	96		
19810	ENU03604	ANI61C526:3 72-93		1290-1317	NAP	g125935	165	65	0.000000	26	64		lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] "(D83732) endo-1,4-beta-glucanase [Aspergillus oryzae] "
19811	ENU03605	ANI61C1086 24-56		1243-1269	NAP	g2467375	1275	527	e-149	63	98		probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) ; (U55021) O3568p [Saccharomyces cerevisiae] ; (Z75069) ORF YOR161c [Saccharomyces cerevisiae]
19812	ENU03606	ANI61C3295: 31-52		1255-1277	NAP	g2132901	833	178	4.00E-75	40	78		
19813	ENU03607	ANI61C435:4 49-68		1269-1295	NAP	g1723809	380	152	7.00E-36	27	78		hypothetical 56.4 KD protein in RPL32-CWH41 intergenic region precursor ; probable membrane protein YGL028c - yeast (Saccharomyces cerevisiae) ; (Z72550) ORF YGL028c [Saccharomyces cerevisiae]
19814	ENU03608	ANI61C2205: 64-84		1290-1310	NAP	g3850125	458	131	9.00E-31	33	76		hypothetical membrane protein [Candida albicans]
19815	ENU03609	ANI61C80:12 55-74		1283-1302	NAP	g114134	236	93	4.00E-18	33	86		Arginine metabolism regulation protein III ; regulatory protein ARGRIII - yeast (Saccharomyces cerevisiae) ; (X05328) ARGRIII protein (AA 1-355) [Saccharomyces cerevisiae] ; (Z46727) Arg3p [Saccharomyces cerevisiae] (AE001015) acyl-CoA dehydrogenase (acd-9) [Archaeoglobus fulgidus]
19816	ENU03610	ANI61C9725: 53-72		1282-1301	NAP	g2649289	300	118	8.00E-26	33	88		hypothetical 34.2 KD protein in CUS1-RPL18A1 intergenic region ; hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae) ; (Z48756) unknown [Saccharomyces cerevisiae]
19817	ENU03611	ANI61C6152: 45-64		1273-1293	NAP	g2497200	1006	332	1.00E-92	70	97		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19818	ENU03612	ANI61C1077	67-86	1295-1316	NAP	g13303051	468	113	2.00E-24	28	76		P58 protein - bovine ; (U04631) PKR inhibitor P58 [Bos taurus]
19819	ENU03613	ANI61C8876	43-63	1271-1295	NAP	g1170767	1490	383	e-154	77	96		26S protease regulatory subunit 8 homolog (LET1 protein) ; transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) ; (U02280) Let1 [Schizosaccharomyces pombe] ; (A1035065) 26S protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]
19820	ENU03614	ANI61C59:19	26-45	1259-1278	NAP	g2492825	374	141	5.00E-41	32	96		"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] " "N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] " (D83970) CPRD8 protein [Vigna unguiculata]
19821	ENU03615	ANI61C59:19	26-45	1259-1278	NAP	g2492825	374	141	5.00E-41	32	96		"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] " (D83970) CPRD8 protein [Vigna unguiculata]
19822	ENU03616	ANI61C1100	29-49	1256-1283	NAP	g1854443	474	180	2.00E-44	39	92		Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19823	ENU03617	ANI61C9270	26-51	1249-1280	NAP	g2500938	115	71	2.00E-11	32	42		Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19824	ENU03618	ANI61C9270	26-51	1249-1280	NAP	g2500938	115	71	2.00E-11	32	42		Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19825	ENU03619	ANI61C3627	22-42	1257-1277	NAP	g4240421	99	1.00E-22					[Schizosaccharomyces pombe] (AF080225) reductase homolog [Streptomyces cyanogenus]

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19826	ENU03620	AN161C9039:	28-51	1264-	NAP		g2330781	972	328	e-103	51	84	"(Z98559) SPAC23C11.17; len:485aa, similar eg. to YPR125W, Q06493, chromosome xvi orf, (454aa), fasta scores, opt:1063, E0:0, (43.5% identity in 418 aa overlap)
		3292..4589		1283									[Schizosaccharomyces pombe] "
19827	ENU03621	AN161C3441:	72-93	1292-	NAP		g731716	646	270	4.00E-73	42	88	hypothetical 49.8 KD protein in ACT3-YCK1 intergenic region precursor ;
		705..2002		1327									hypothetical protein YHR132c - yeast (Saccharomyces cerevisiae) ; (U10398)
19828	ENU03622	AN161C1057	23-42	1262-	NAP		g731846	159	53	0.000003	27	70	Ecml4p [Saccharomyces cerevisiae] "
		2:2746..1446		1281									hypothetical 39.4 KD protein in SGAl-KTR7 intergenic region ;
													hypothetical protein YIL096c - yeast (Saccharomyces cerevisiae) ; (Z38125)
													orf, len: 336, CAL: 0.14
19829	ENU03623	AN150C1282	50-69	1277-	NAP		g137471		134	1.00E-30	38	94	[Saccharomyces cerevisiae] "
		7_1:1701..400		1309									"vacuolar ATP synthase subunit C (V-ATPase C subunit) ; H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - bovine ; (J05681) H+ - ATPase C subunit [Bos taurus] "
19830	ENU03624	AN161C5190:	68-90	1310-	NAP		g1172616	1087	326	2.00E-88	49	54	probable ATP-dependent RNA helicase PRH1 ; PRH1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z54354) probable atp-dependent mna helicase prh1 [Schizosaccharomyces pombe]
		2421..1118		1329									(Y16748) malate dehydrogenase [Piromyces sp. E2]
19831	ENU03625	AN161C8056:	65-84	1306-	NAP		g4029338	632	145	6.00E-65	57	96	(AB016720) carboxylesterase precursor [Aphis gossypii]
		641..1944		1326									putative polyketide biosynthesis protein PKSJ ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksJ [Bacillus subtilis] ; (Z99113) pksJ [Bacillus subtilis]
19832	ENU03626	AN161C6841:	22-42	1267-	NAP		g3426006	302	140	2.00E-32	39	32	(AB011157) KIAA0585 protein [Homo sapiens]
		5143..3838		1285									(Y14749) MDM10 [Podospira anserina]
19833	ENU03627	AN161C5500:	50-71	1299-	NAP		g730334	379	173	2.00E-42	28	76	
		2517..1207		1318									
19834	ENU03628	AN161C1029	22-42	1271-	NAP		g3043694	243	137	2.00E-31	29	64	
		4:4056..2745		1290									
19835	ENU03629	AN161C2332:	64-87	1315-	NAP		g2407968	415	164	9.00E-40	34	88	
		3982..2670		1334									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
19836	ENU03630	ANI61C8090:	22-41	1277-	NAP	g2984184	398	157	2.00E-37	29	82	82	(AE000763) N-methylhydantoinase B [Aquifex aeolicus]
19837	ENU03631	1445..129 ANI61C4285:	46-68	1302-	NAP	g2664292	1594	447	e-171	81	95	95	(Y15744) cellular aspartic protease [Aspergillus fumigatus] ; (AJ132504) aspartic protease [Aspergillus fumigatus]
19838	ENU03632	ANI61C7950:	57-77	1304-	NAP	g2493391	96	4.00E-19					probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
19839	ENU03633	ANI61C4230:	47-75	1289-	NAP	g1351673	367	113	6.00E-32	38	96	96	hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe]
19840	ENU03634	ANI61C3599:	29-52	1288-	NAP	g522302	4000	589	e-167	63	36	36	[Schizosaccharomyces pombe] (L35053) endonuclease [Magnaporthe grisea]
19841	ENU03635	5916..4596 ANI61C4299:	57-80	1316-	NAP	g1351606	196	67	3.00E-10	29	25	25	hypothetical 54.3 KD protein C23D3.03C in chromosome I ; hypothetical protein SPAC23D3.03c - fission yeast (Schizosaccharomyces pombe) ; (Z64354) unknown [Schizosaccharomyces pombe]
19842	ENU03636	ANI61C406:2	30-57	1290-	NAP	g135184	2357	266	e-118	54	38	38	"Valyl-TRNA synthetase, mitochondrial precursor (valine--TRNA ligase) (VALRS) ; valine--tRNA ligase (EC 6.1.1.9) - Neurospora crassa "
19843	ENU03637	ANI61C4412:	45-65	1307-	NAP	g1469396	692	226	8.00E-75	43	94	94	(U43775) secreted aspartic proteinase precursor [Glomerella cingulata]
19844	ENU03638	7822..6499 ANI61C1527:	25-56	1290-	NAP	g730338	1840	565	e-160	58	72	72	Lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348) lysophospholipase [Penicillium chrysogenum]
19845	ENU03639	ANI61C188:1	56-77	1321-	NAP	g1346290	802	166	2.00E-81	45	69	69	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
		375..49		1340									

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19846	ENU03640	AN161C1118	71-94	1334-	NAP	g2621739	762	227	2.00E-87	51	68		(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]
19847	ENU03641	AN161C3898:	65-90	1331-	NAP	g2498971	627	130	3.00E-29	34	75		putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740)
19848	ENU03642	AN161C1085	22-51	1282-	NAP	g3738167	452	173	2.00E-42	41	100		putative FAD-containing monooxygenase [Emmericella nidulans] (AL031856) putative golgi uridine diphosphate-N-acetylglucosamine transporter [Schizosaccharomyces pombe]
19849	ENU03643	AN161C1018	44-63	1314-	NAP	g1723948	1150	469	e-131	55	95		probable histone DEacetylase HOS2 ; probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) ; (Z72716) ORF YGL194c [Saccharomyces cerevisiae] (AB010714) salicylate hydroxylase [Pseudomonas putida]
19850	ENU03644	AN161C8914:	51-70	1315-	NAP	g2826168		62	7.00E-13				hypothetical protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae] (AL023596) hypothetical protein MLCB2407.16c [Mycobacterium leprae]
19851	ENU03645	AN161C1926:	22-42	1295-	NAP	g2131429	236	119	4.00E-26	25	96		probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UNE378 [Saccharomyces cerevisiae] ; (Z74745) ORF YOL003c [Saccharomyces cerevisiae]
19852	ENU03646	AN161C8043:	65-84	1340-	NAP	g3150104	251	129	4.00E-29	36	33		putative glycyl-TRNA synthetase (glycine--TRNA ligase) (GLYRS) ; (Z69369) glycyl tRNA synthetase [Schizosaccharomyces pombe]
19853	ENU03647	AN161C7152:	40-61	1314-	NAP	g2132817	222	75	2.00E-21	33	41		
19854	ENU03648	AN161C3804:	22-41	1299-	NAP	g1711632	2083	396	e-149	62	65		

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19855	ENU03649	AN161C4864:	57-76	1333-	NAP		g1176339	517	136	4.00E-57	36	87	"hypotheical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae) ; (Z49578) ORF YJR078w [Saccharomyces cerevisiae] ; (L47993) ORF YJR078w [Saccharomyces cerevisiae]"
		635..1973		1353									(AL033534) carbamoyl-phosphate synthase [Schizosaccharomyces pombe]
19856	ENU03650	AN161C7945:	72-91	1349-	NAP		g3873545	3360	293	e-150	66	36	(Y13975) phospholipase C [Candida albicans]
		1416..2755		1369									(U62917) glucose transporter TGP2 [Taenia solium]
19857	ENU03651	AN161C1092	47-66	1323-	NAP		g2462982	244	103	8.00E-35	34	23	hypothetical protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae]"
		8:3792..2452		1345									(U62928) multidrug resistance protein, ABC transporter protein [Aureobasidium pullulans] ; (U85909) multidrug resistance-like protein [Aureobasidium pullulans]"
19858	ENU03652	AN161C9031:	63-82	1335-	NAP		g1480799		37	0.000000			(U31348) Gap1 [Saccharomyces cerevisiae]
		342..579		1362									(X81067) probable mitochondrial protein; nearly identical to YME1 [Saccharomyces cerevisiae]
19859	ENU03653	AN161C1926:	22-42	1302-	NAP		g2131429	236	119	4.00E-26	25	96	Galactose-1-phosphate uridylyltransferase ; UDPglucose--hexose-1-phosphate uridylyltransferase (EC 2.7.7.12) - yeast (Kluveromyces marxianus var. lactis) ; (X07039) epimerase (GAL 7) (AA 1 - 370) [Kluveromyces lactis]
		59..1401		1322									(AB025252) reverse transcriptase [Magnaporthe grisea]
19860	ENU03654	AN161C6211:	49-71	1324-	NAP		g4097503	1671	313	2.00E-84	42	34	
		1869..3212		1350									
19861	ENU03655	AN161C3588:	64-84	1347-	NAP		g1002712	351	64	0.000000	54	12	
		2903..2660		1366									
19862	ENU03656	AN161C4066:	58-77	1342-	NAP		g531752	1288	418	e-116	56	57	
		1651..306		1361									
19863	ENU03657	AN161C7448:	22-48	1305-	NAP		g120909	856	314	2.00E-92	51	96	
		1277..2623		1325									
19864	ENU03658	AN161C5998:	50-69	1334-	NAP		g4586458	151	108	1.00E-22	32	62	
		5415..4069		1354									

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19865	ENU03659	AN161C8751:	22-45	1307-	NAP		g2498440	926	297	4.00E-99	48	88	"Homogentisate 1,2-dioxygenase (homogentisicase) (homogentisate oxygenase) (homogentisic acid oxidase) ; 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) - Emericella nidulans ; (U30797) 2,5 dihydroxyphenylacetate oxidase [Emericella nidulans] ; (AJ001836) homogentisate dioxygenase [Emericella nidulans]"
19866	ENU03660	AN161C2872:	28-50	1315-	NAP		g1717973	1184	499	e-140	61	56	"Glycogen (starch) synthase, isoform 2 ; UDP-glucose--starch glucosyltransferase (EC 2.4.1.11) 2-yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae]"
19867	ENU03661	AN161C5204:	42-61	1325-	NAP		g4558826	2307	553	e-156	99	98	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]
19868	ENU03662	AN161C4343:	39-69	1328-	NAP		g1176967	88	71	1.00E-11	28	32	hypothetical 37.6 KD protein in GNT-HTTPG intergenic region ; (AB005554) see SWISS_PROT ACC#: P42106 [Bacillus subtilis] ; (Z99124) yxaG [Bacillus subtilis]
19869	ENU03663	AN161C236:	1 45-65	1328-	NAP		g2266941	1681	559	e-168	87	93	(AF009036) NAD(+) -isocitrate dehydrogenase subunit I [Ajellomyces capsulatus]
19870	ENU03664	AN161C4864:	57-76	1333-	NAP		g1176339	517	136	4.00E-57	35	88	"hypothetical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae) ; (Z49578) ORF YJR078w [Saccharomyces cerevisiae] ; (L47993) ORF YJR078w [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19871	ENU03665	AN161C8878: 23-42		1307-	NAP		g1351651	784	220	1.00E-56	45	99	hypothetical 43.7 KD protein hypothetical C24B11.08C in chromosome 1; hypothetical protein SPAC24B11.08c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emerticella nidulans]
		2850..1496		1335									
19872	ENU03666	AN161C3420: 37-56		1326-	NAP		g1870209	419	158	7.00E-38	95	13	(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe] DNA-3-methyladenine glycosylase (3-methyladenine DNA glycosylase) (3MEA DNA glycosylase) ; DNA-3-methyladenine glycosylase 1 (EC 3.2.2.20) - fission yeast (Schizosaccharomyces pombe) ; (U76637) 3-methyladenine DNA glycosylase [Schizosaccharomyces pombe]
		1372..18		1349									
19873	ENU03667	AN161C6436: 57-76		1350-	NAP		g2842516	589	83	1.00E-34	30	66	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
		2965..1611		1369									
19874	ENU03668	AN161C6064: 22-41		1315-	NAP		g2494171		80	3.00E-14			(AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]
		92..1449		1337									
19875	ENU03669	AN161C313:2 22-41		1319-	NAP		g1711561		105	3.00E-27			
		655..1296		1338									
19876	ENU03670	AN161C8049: 69-90		1367-	NAP		g2832659	249	100	2.00E-20	27	71	
		2384..1025		1386									
19877	ENU03671	AN161C8377: 50-69		1344-	NAP		g117803	591	262	3.00E-69	39	71	
		88..1447		1367									
19878	ENU03672	AN161C722:3 42-61		1342-	NAP		g2499576	2827	357	e-177	85	35	
		078..1715		1362									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19879	ENU03673	AN161C9491:	27-46	1328-	NAP	g4154089	286	98	2.00E-32	35	100	100	(Z98981) putative pyridoxal kinase [Schizosaccharomyces pombe]
19880	ENU03674	1576..1664 AN161C9160:	68-95	1347- 1370-	NAP	g4512109	470	176	2.00E-43	36	40	40	(AF125185) origin recognition complex subunit 4-related protein Orp4p [Schizosaccharomyces pombe]
19881	ENU03675	AN161C2242:	56-75	1356-	NAP	g729014	1043	146	1.00E-95	46	74	74	Arginine permease ; arginine transport protein - yeast (Saccharomyces cerevisiae) ; (M11724) amino acid permease [Saccharomyces cerevisiae] ; (U18795) Can1p: arginine permease [Saccharomyces cerevisiae]
19882	ENU03676	AN161C7470:	65-84	1366-	NAP	g3135990	1056	287	1.00E-76	42	78	78	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19883	ENU03677	3085..1718 AN161C1036	35-58	1390- 1343-	NAP	g2465156	701	255	5.00E-67	45	94	94	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
19884	ENU03678	0:5028..3659 AN161C1018	22-50	1362- 1334-	NAP	g2058345	1215	168	e-110	70	96	96	(Y12693) oxysterol-binding protein [Neurospora crassa]
19885	ENU03679	7:380..1753 AN161C310:1	64-83	1353- 1380-	NAP	g3261633	321	83	5.00E-17	33	94	94	(Z79700) fadE13 [Mycobacterium tuberculosis]
19886	ENU03680	516..2894 AN161C1090	36-56	1399- 1352-	NAP	g3122213	667	236	3.00E-61	39	96	96	histidinol dehydrogenase (HDH) ; (AE000809) histidinol dehydrogenase [Methanobacterium thermoautotrophicum]
19887	ENU03681	AN161C4094:	22-55	1339-	NAP	g1465805	274	87	7.00E-21	32	85	85	(U64852) coded for by C. elegans cDNA cm17d4; Similar to epoxide hydrolase. [Caenorhabditis elegans]
19888	ENU03682	AN161C3456:	70-99	1358- 1407	NAP	g2492816	582	156	5.00E-62	32	73	73	uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
19889	ENU03683	AN161C7433:	35-54	1354-	NAP	g121855	1110	182	7.00E-76				"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellobiohydrolase) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride) ; (M16190) cellobiohydrolase II [Trichoderma reesei] ; cellobiohydrolase II [Trichoderma reesei] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19890	ENU03684	ANI61C1092	57-76	1376-1395	NAP		g461915	829	108	2.00E-43			Dipeptidyl aminopeptidase A (DPAP A) (YSCIV) ; dipeptidyl aminopeptidase (EC 3.4.14.-) - yeast (Saccharomyces cerevisiae) ; (L21944) dipeptidyl aminopeptidase [Saccharomyces cerevisiae] ; (U08230) dipeptidyl aminopeptidase A [Saccharomyces cerevisiae] ; (X92441) YOR50-9 [Saccharomyces cerevisiae] ; (Z75127) ORF YOR219c [Saccharomyces cerevisiae]
19891	ENU03685	ANI61C2498	47-67	1367-1388	NAP		g2315524	682	129	1.00E-67	37	81	[Saccharomyces cerevisiae] (AF016452) Similar to aldehyde dehydrogenase; coded for by C. elegans cDNA yk144e3.3; coded for by C. elegans cDNA CESAC55R; coded for by C. elegans cDNA yk144e3.5 [Caenorhabditis elegans] hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae) ; (Z75105) ORF YOR197w [Saccharomyces cerevisiae]
19892	ENU03686	ANI61C8615	23-42	1329-1364	NAP		g2132083	929	353	2.00E-96	49	95	(AF140505) DEAD box RNA helicase [Candida albicans] "Endo-1,4-beta-xylanase (xylanase) (1,4-beta-D-xylan xylohydrolase)" "ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate smilaldehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-... ; acetylglutamate kinase (EC 2.7.2.8) / N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) precursor, mitochondrial - Neurospora crassa ; (L27746) arg-6 gene product [Neurospora crassa] "
19893	ENU03687	ANI61C8941	64-83	1388-1407	NAP		g4589366	542	226	3.00E-58	39	65	(Z29102) putative transposase [Drosophila hydei] ; transposase [Drosophila hydei]
19894	ENU03688	ANI61C7867	69-88	1391-1413	NAP		g3123294	781	79	2.00E-70	61	97	
19895	ENU03689	ANI61C1061	35-56	1360-1380	NAP		g1703361	1592	467	e-169			
19896	ENU03690	ANI61C7037	22-56	1337-1368	NAP		g436466	162	68	1.00E-10	25	89	

Sequence Summary

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19897	ENU03691	AN161C3244:	25-46	1344-1371	NAP		g1708319	820	349	4.00E-95	45	82	cell cycle protein kinase HSK1 ; protein kinase hsk1 (EC 2.7.1.1) - fission yeast [Schizosaccharomyces pombe] ; (D50493) hsk1+ protein kinase [Schizosaccharomyces pombe] ; (AL035263) cell cycle protein kinase hsk1 [Schizosaccharomyces pombe] (Z29102) putative transposase [Drosophila hydei] ; transposase [Drosophila hydei]
19898	ENU03692	AN161C9575:	22-56	1337-1368	NAP		g436466	143	64	0.000000	24	89	NADPH dehydrogenase 2 (old yellow enzyme 2) ; NADPH dehydrogenase (EC 1.6.99.1) chain OYE2 - yeast (Saccharomyces cerevisiae) ; (L06124) NAD(P)H:oxidoreductase [Saccharomyces cerevisiae] ; (U00027) Oye2p: NAD(P)H oxidoreductase (Old Yellow Enzyme) [Saccharomyces cerevisiae]
19899	ENU03693	AN161C9932:	32-59	1359-1379	NAP		g417432	613	280	1.00E-74	40	91	Conidium-specific protein ; SpoC1-C1D protein - Emericella nidulans ; (X54668) SpoC1-C1D product [Emericella nidulans] (AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]
19900	ENU03694	AN161C7763:	26-45	1353-1376	NAP		g134270	146	54	0.000003	33	31	Zn/Cd resistance gene [Saccharomyces cerevisiae]
19901	ENU03695	AN161C1560:	44-64	1376-1395	NAP		g2648355	167	60	0.000000	38	96	hypothetical protein YDR330w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr330wp [Saccharomyces cerevisiae]
19902	ENU03696	AN161C410:5	41-62	1371-1394	NAP		g227157	333	107	2.00E-22	32	85	ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
19903	ENU03697	AN161C1048	59-79	1387-1412	NAP		g2131432	441	155	5.00E-37	32	83	
19904	ENU03698	AN161C1128	67-87	1401-1420	NAP		g3915963	742	159	3.00E-73	38	26	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19905	ENU03699	AN161C2134:	26-45	1347-4169..5564	NAP		g730893	283	54	7.00E-13			tryptophan permease (tryptophan amino acid transporter) ; tryptophan transport protein - yeast
													(Saccharomyces cerevisiae) ; (L33461) tryptophan permease [Saccharomyces cerevisiae] ; (X79150) tryptophan amino acid permease [Saccharomyces cerevisiae] ; (Z74762) ORF YOL020w [Saccharomyces cerevisiae] ; (U66834) suppressor of ABF1 [Saccharomyces cerevisiae]
19906	ENU03700	AN161C2438:	72-93	1407-160..1556	NAP		g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region ; hypothetical protein YIL144w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 691, CAI: 0.15, possible coiled-coil [Saccharomyces cerevisiae] "
19907	ENU03701	AN161C2438:	72-93	1407-160..1556	NAP		g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region ; hypothetical protein YIL144w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 691, CAI: 0.15, possible coiled-coil [Saccharomyces cerevisiae] "
19908	ENU03702	AN161C1724:	30-51	1356-2191..3589	NAP		g461508	925	393	e-108			"vacuolar aminopeptidase I precursor (polypeptidase) (leucine aminopeptidase IV) (LAPIV) (aminopeptidase III) (aminopeptidase YSCI) ; aminopeptidase yscI (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae) ; (M25548) aminopeptidase I [Saccharomyces cerevisiae] ; (X71133) vacuolar aminopeptidase YSCI [Saccharomyces cerevisiae] ; (Z28103) ORF YKL103c [Saccharomyces cerevisiae] "
19909	ENU03703	AN161C7948:	41-60	1375-5069..4253	NAP		g3925779	71	47	0.0003	28	35	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19910	ENU03704	ANI61C3294:	58-77	1401-	NAP	g3201958	368	159	4.00E-40	39	62		(AF068116) eIF4E-like protein 4E-LP [Mus musculus]
19911	ENU03705	ANI61C3573:	68-90	1398-	NAP	g1078218	961	195	3.00E-80	45	93		probable membrane protein YDR105c - yeast (Saccharomyces cerevisiae) ; (Z47746) unknown [Saccharomyces cerevisiae] ; (Z48758) unknown [Saccharomyces cerevisiae]
19912	ENU03706	ANI61C7316:	30-57	1375-	NAP	g4388565	1265	424	e-125	52	91		[Saccharomyces cerevisiae] (Z35875) ORF YBR006w [Saccharomyces cerevisiae]
19913	ENU03707	ANI61C2435:	51-71	1386-	NAP	g1749554	618	213	7.00E-64	47	95		"(D89173) similar to Saccharomyces cerevisiae hypothetical 36.4KD protein in SOD1-CPA2 intergenic region, SWISS-PROT Accession Number P47143 [Schizosaccharomyces pombe] ; (AL023781) adenosine kinase [Schizosaccharomyces pombe] "
19914	ENU03708	ANI61C9254:	23-52	1370-	NAP	g3738169	1087	314	7.00E-99	58	97		(AL031856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe]
19915	ENU03709	ANI61C1115	22-48	1370-	NAP	g3183342	353	130	2.00E-29	38	96		hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
19916	ENU03710	ANI61C3949:	66-85	1415-	NAP	g1345704	233	62	0.000000	27	33		[Schizosaccharomyces pombe] cell division control protein 15 ; cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe) ; (Z95334) Cdc15p [Schizosaccharomyces pombe]
19917	ENU03711	ANI61C9367:	22-42	1362-	NAP	g131828	998	282	5.00E-98	44	79		[Schizosaccharomyces pombe] LOW-affinity glucose transporter ; glucose transport protein RAG1 - yeast (Kluyveromyces marxianus var. lactis) ; (X53752) putative sugar transporter [Kluyveromyces lactis]
19918	ENU03712	ANI61C212.3	23-42	1367-	NAP	g2996008	1881	666	0	85	99		(AF053983) translation release factor subunit 1 [Podospira anserina]
19919	ENU03713	ANI61C7848:	37-55	1384-	NAP	g3023951	470	205	5.00E-52	30	43		Histone transcription regulator 1 homolog ; (Z97204) putative hiira protein; histone transcription regulator [Schizosaccharomyces pombe]
19920	ENU03714	ANI61C9794:	23-50	1367-	NAP	g2271477	1012	194	e-106	49	97		(AF009631) AP47/50p [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19921	ENU03715	ANI61C7561:	45-64	1391-1421	NAP		g117619	135	50	0.00004	34	18	choleline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		258..87											choleline transport protein [Saccharomyces cerevisiae] ; (Z72599)
													ORF YGL077c [Saccharomyces cerevisiae]
19922	ENU03716	ANI61C9917:	22-41	1380-1399	NAP		g3581896	443	138	9.00E-32	24	75	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19923	ENU03717	ANI61C7944:	36-55	1392-1414	NAP		g1077336	466	127	2.00E-52	35	96	hypothetical protein YLR380w - yeast (Saccharomyces cerevisiae) ; (U19104)
		3165..4585											Ylr380wp [Saccharomyces cerevisiae]
19924	ENU03718	ANI61C2369:	22-44	1380-1402	NAP		g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor ; probable membrane protein YBR004c - yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19925	ENU03719	ANI61C1133	22-44	1383-1403	NAP		g2746775	414	139	9.00E-37	36	82	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]
19926	ENU03720	ANI61C7948:	42-61	1391-1424	NAP		g125407	523	179	1.00E-47	36	95	mevalonate kinase (MVK) ; mevalonate kinase (EC 2.7.1.36) - yeast (Saccharomyces cerevisiae) ; (X55875) mevalonate kinase [Saccharomyces cerevisiae] ; (X06114) ORF1 (put. RAR1 protein) (AA 1-443) [Saccharomyces cerevisiae] ; (Z49809)
		2803..4226											Rar1p [Saccharomyces cerevisiae]
19927	ENU03721	ANI61C316:3	58-84	1423-1442	NAP		g2492782	551	219	5.00E-56	38	97	alpha-galactosidase precursor (melibiase) (alpha-D-galactoside galactohydrolase) ; (L27992) alpha-galactosidase [Coffea arabica]
		290..1864											"DLTE protein ; hypothetical protein - Bacillus subtilis ; dlte productiputative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa] ; (X73124)
19928	ENU03722	ANI61C1271:	22-44	1379-1408	NAP		g729344	45	0.000000	01			ipa-1r [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-1r [Bacillus subtilis]
		2312..2792											"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19929	ENU03723	ANI61C8203:	68-88	1429-	NAP		g4249560	1229	291	e-133	52	96	(AB003109) beta-glucosidase [Humicola grisea var. thermoides]
19930	ENU03724	ANI61C1036	49-68	1421-	NAP		g1730771	1269	330	1.00E-89	41	43	hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL123w - yeast (Saccharomyces cerevisiae) ; (Z69382) N1897 [Saccharomyces cerevisiae] ; (Z71399) ORF YNL123w [Saccharomyces cerevisiae]
19931	ENU03725	ANI61C8805:	24-49	1396-	NAP		g4105567	184	105	9.00E-22	31	93	(AF047707) UDP-glucose:ceramide glycosyltransferase [Rattus norvegicus]
19932	ENU03726	ANI61C1038	23-42	1397-	NAP		g2894272	351	141	1.00E-32	38	76	(AL021839) hypothetical protein [Schizosaccharomyces pombe]
19933	ENU03727	ANI61C9835:	51-69	1425-	NAP		g2132357	148	84	2.00E-15	40	35	NBP2 protein - yeast (Saccharomyces cerevisiae) ; (Z50046) Nbp2p [Saccharomyces cerevisiae] ; (D43693) Nap1-binding protein [Saccharomyces cerevisiae]
19934	ENU03728	ANI61C8985:	57-75	1432-	NAP		g3915140	562	127	2.00E-54	34	94	isotrichoderm C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichoderm C-15 hydroxylase [Fusarium sporotrichioides]
19935	ENU03729	ANI61C7943:	40-59	1419-	NAP		g632081		103	3.00E-21			hypothetical protein 4 - Xanthobacter sp. ; (X79863) orf4 [Xanthobacter sp. Py2]
19936	ENU03730	ANI61C9526:	22-44	1401-	NAP		g2501674	185	61	2.00E-18	39	20	DRAP deaminase ; RIB2 protein - yeast (Saccharomyces cerevisiae) ; (Z21618) DRAP deaminase [Saccharomyces cerevisiae] ; (Z74808) ORF YOL066c [Saccharomyces cerevisiae]
19937	ENU03731	ANI61C8286:	55-74	1426-	NAP		g1172703	484	191	8.00E-48	44	32	"peptide transporter PTR2-A ; (U01171) similar to S. cerevisiae PTR2 gene, GenBank Accession Number L11994 [Arabidopsis thaliana]" (X63029) Uhu [Drosophila heteroneural]
19938	ENU03732	ANI61C408:	72-79	1425-	NAP		g7464		75	1.00E-12			(Z98529) putative RNA-binding protein [Schizosaccharomyces pombe]
19939	ENU03733	ANI61C9882:	22-49	1405-	NAP		g2462671	413	129	4.00E-29	33	97	
		3530..4974		1424									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
19940	ENU03734	AN161C2898:	72-91	1458-1477	NAP		g1709679	753	238	6.00E-85	40	59	probable mitochondrial intermediate peptidase precursor (MIP) ; (Z70690) unknown [Schizosaccharomyces pombe]
19941	ENU03735	AN161C6436:	57-76	1436-1463	NAP		g2842516	589	92	3.00E-37	30	72	(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe]
19942	ENU03736	AN161C8998:	39-58	1427-1446	NAP		g2398820	524	221	8.00E-57	34	43	(Z99126) hypothetical protein. [Schizosaccharomyces pombe]
19943	ENU03737	AN161C8998:	39-58	1427-1446	NAP		g2398820	524	221	8.00E-57	34	43	(Z99126) hypothetical protein. [Schizosaccharomyces pombe]
19944	ENU03738	AN161C7853:	22-48	1411-1430	NAP		g1345707	387	108	6.00E-42	38	73	CCC1 protein ; CCC1 protein - yeast (Saccharomyces cerevisiae) ; (U19027) CCC1p: putative transmembrane Ca2+ transporter [Saccharomyces cerevisiae] ; (L24112) Ccc1p [Saccharomyces cerevisiae]
19945	ENU03739	AN161C5260:	62-81	1441-1474	NAP		g1709784	955	347	8.00E-95			gamma-glutamyl phosphate reductase (GPR) (glutamate-5-semialdehyde dehydrogenase) (glutamyl-gamma-semialdehyde dehydrogenase) ; glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41) - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06155 [Saccharomyces cerevisiae] ; (U43565) gamma-glutamyl phosphate reductase [Saccharomyces cerevisiae] ; (Z75231) ORF YOR323c [Saccharomyces cerevisiae] (AF127176) trichothecene 3-O-acetyltransferase [Fusarium sporotrichoides]
19946	ENU03740	AN161C7017:	22-55	1409-1434	NAP		g4378882		150	3.00E-35			hypothetical 42.3 KD protein in YTA2-DIT1 intergenic region ; hypothetical protein YDR400w - yeast (Saccharomyces cerevisiae) ; (U32274) Ydr400wp; CAI: 0.14 [Saccharomyces cerevisiae]
19947	ENU03741	AN161C6489:	24-50	1417-1437	NAP		g2497466	344	73	3.00E-34	35	98	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19948	ENU03742	ANI61C1056	22-41	1406-1439	NAP		g3881508	259	75	1.00E-12	33	91	(Z47357) cDNA EST EMBL: T00822 comes from this gene, cDNA EST EMBL: T00823 comes from this gene [Caenorhabditis elegans]
19949	ENU03743	ANI61C7184:	32-53	1428-1450	NAP		g1710597	292	121	2.00E-30	33	73	"mitochondrial 60S ribosomal protein L7 precursor (YML7) ; ribosomal protein Yml7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49701) unknown [Saccharomyces cerevisiae]" (AF095898) siderophore biosynthesis repressor SREA [Emericella nidulans] "3-ketoacyl-CoA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) ; (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19950	ENU03744	ANI61C9446:	67-86	1452-1486	NAP		g4585213	2852	484	0	99	81	
19951	ENU03745	ANI61C6203:	68-87	1465-1491	NAP		g549077	840	275	1.00E-75	53	95	
19952	ENU03746	ANI61C3969:	29-48	1420-1452	NAP		g117619	632	213	2.00E-54	33	82	
19953	ENU03747	ANI61C1041	69-90	1467-1493	NAP		g2507070	369	88	1.00E-18	35	61	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19954	ENU03748	ANI61C9290:	55-86	1460-1481	NAP		g1237183	434	146	2.00E-53	33	83	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
19955	ENU03749	ANI61C6471:	24-50	1432-1451	NAP		g3947853	663	232	9.00E-65	53	73	(AL034381) transcriptional regulator [Schizosaccharomyces pombe]
19956	ENU03750	ANI61C222:	1 23-43	1430-1450	NAP		g403179	263	129	5.00E-29	37	25	(L24441) kinesin light chain [Loligo pealii]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19957	ENU03751	AN161C7471: 65-84	6428..4957	1474-1494	NAP		g2507070	442	113	1.00E-50	35	83	N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19958	ENU03752	AN161C1144 35-64	6:2721..1249	1442-1465	NAP		g127024	1418	417	e-163	60	93	homoserine O-acetyltransferase (homoserine O-trans-acetylase); homoserine O-acetyltransferase (EC 2.3.1.31) - fungus (Ascobolus immersus) ; (M26662) met2 [Ascobolus immersus]
19959	ENU03753	AN161C2369: 58-77	810..2283	1467-1489	NAP		g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor; probable membrane protein YBR004c - yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19960	ENU03754	AN161C1056 62-81	5:1164..2638	1474-1494	NAP		g3881508	259	76	7.00E-13	32	96	(Z47357) cDNA EST EMBL.T00822 comes from this gene; cDNA EST EMBL.T00823 comes from this gene [Caenorhabditis elegans]
19961	ENU03755	AN161C5215: 27-54	4956..3482	1440-1459	NAP		g1172824	337	57	0.000000	56	11	DNA repair and recombination protein RAD52 ; (X75086) K.lactis Rad52 [Kluyveromyces lactis]
19962	ENU03756	AN161C9290: 55-86	3960..2484	1470-1489	NAP		g1237183	434	146	2.00E-53	33	84	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
19963	ENU03757	AN161C1118 22-53	5:6237..4760	1438-1457	NAP		g3025028	482	217	2.00E-55	33	83	"hypothetical 47.3 KD protein in OMPX-MOEB intergenic region ; (AE000184) orf, hypothetical protein [Escherichia coli] ; (D90719) ORF_ID:o207#4 [Escherichia coli] ; (D90720) ORF_ID:o207#4 [Escherichia coli]"
19964	ENU03758	AN161C9356: 23-42	1498..19	1440-1460	NAP		g3150152	1177	372	e-121	70	78	(A1006219) clathrin-associated protein [Drosophila melanogaster]
19965	ENU03759	AN161C3300: 22-41	478..1957	1440-1459	NAP		g2388977	152	56	0.000000	39	16	(Z98980) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19966	ENU03760	AN161C7237:	42-63	1451-1481	NAP		g1708578	63	0.000000	006			myo-inositol transporter I ; myo-inositol transport protein ITR1 - yeast (Saccharomyces cerevisiae) ; (U33057)
		3570..5051											It r1p: myo-inositol transporter; YDR497C; CAI: 0.19 [Saccharomyces cerevisiae]
19967	ENU03761	AN161C8669:	46-68	1453-1485	NAP		g1176670	262	90	4.00E-17	33	96	hypothetical 37.7 KD protein C08B11.7 in chromosome II ; (Z46676) similar to thiolesterase; cDNA EST yk221d9.5 comes from this gene [Caenorhabditis elegans] (U59421) Band 17 [Gallus gallus]
19968	ENU03762	AN161C9412:	54-74	1471-1494	NAP		g2795769	36	0.0004				dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae] ; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
19969	ENU03763	AN161C3441:	37-59	1450-1480	NAP		g1706439	1343	469	e-131	56	77	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19970	ENU03764	AN161C5996:	30-55	1454-1475	NAP		g2507070	323	101	1.00E-35	28	93	(AC003027) lclprt seq No definition line found [Arabidopsis thaliana] probable eukaryotic initiation factor C17C9.03 ; (Z73099) probable initiation factor [Schizosaccharomyces pombe]
19971	ENU03765	AN161C3862:	68-95	1495-1515	NAP		g4204312	652	271	1.00E-71	38	42	(U59234) biotin carboxylase [Synechococcus PCC7942] (AJ006487) propionyl-CoA carboxylase [Homo sapiens] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19972	ENU03766	AN161C2424:	72-96	1503-1522	NAP		g1723562	778	291	2.00E-81	46	30	
19973	ENU03767	AN161C2430:	39-58	1470-1489	NAP		g1399818	863	337	1.00E-96	45	98	
19974	ENU03768	AN161C276:	172-94	1505-1524	NAP		g4127990	375	142	5.00E-33	34	83	
19975	ENU03769	AN161C7856:	26-49	1449-1478	NAP		g3702646	458	81	5.00E-26			

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19976	ENU03770	AN161C1113	38-57	1476-1495	NAP		g416582	1318	276	e-127			actin-like protein ARP2 ; actin-like protein ACT2 - yeast (Saccharomyces cerevisiae) (strain X2180) ; (X61502)
		3:1690..192											actin-like protein [Saccharomyces cerevisiae] ; (Z71781) actin-like protein ACT2 [Saccharomyces cerevisiae] ; (Z74077) ORF YDL029w [Saccharomyces cerevisiae] ; actin-like protein ACT2 [Saccharomyces cerevisiae]
19977	ENU03771	AN161C1093	53-79	1480-1510	NAP		g3006137	942	324	9.00E-88	44	53	(AL022229) Cu++-transporting ATPase [Schizosaccharomyces pombe]
		5:1563..64											(U51327) versicolorn B synthase [Aspergillus parasiticus] ; (U51328) versicolorn B synthase [Aspergillus parasiticus]
19978	ENU03772	AN161C3308	58-77	1495-1517	NAP		g1293655	880	347	1.00E-94	41	73	Vitellogenin II precursor (major vitellogenin) [contains: lipovitellin I (LV1); phosvitin (PV); lipovitellin II (LVII); YGP40] ; vitellogenin II precursor - chicken ; (X13607)
		2458..957											vitellogenin [Gallus gallus] "hypothetical 43.7 KD protein in OST6-RSP2 intergenic region ; probable membrane protein YML018c - yeast (Saccharomyces cerevisiae) ; (Z46659) unknown orf, len: 393, CAI: 0.13 [Saccharomyces cerevisiae] "
19979	ENU03773	AN161C6810	32-60	1473-1492	NAP		g138595	57	41	0.02	26	8	maackia detoxification protein 1 - fungus (Nectria haematococca) ; (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]
		6538..8040											nuclear polyadenylated RNA-binding protein NAB2 ; RNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae) ; (L10288) RNA-binding protein [Saccharomyces cerevisiae] ; (Z72644) ORF YGL122c [Saccharomyces cerevisiae]
19980	ENU03774	AN161C5895	43-63	1474-1504	NAP		g2497105	546	166	4.00E-40	38	97	
		2179..672											
19981	ENU03775	AN161C9701	65-84	1501-1526	NAP		g2133295	664	187	2.00E-73	38	96	
		1300..2803											
19982	ENU03776	AN161C3368	22-41	1467-1486	NAP		g417337	77	3.00E-13				
		5624..4118											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19983	ENU03777	ANI61C7316:	28-47	1463-1493	NAP		g2132651	161	2.00E-45				probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
19984	ENU03778	ANI61C4256:	52-71	1497-1517	NAP		g2143220	1826	681	0	79	93	(Y13338) cellular serine proteinase [Aspergillus fumigatus]
19985	ENU03779	ANI61C905:2	22-53	1458-1489	NAP		g3328946	155	80	4.00E-14	34	30	(AE001323) S13 Ribosomal Protein [Chlamydia trachomatis]
19986	ENU03780	ANI61C6340:	22-48	1472-1492	NAP		g2132374	501	205	5.00E-52	34	57	p-aminobenzoate synthase (EC 4.1.3.-) - yeast (Saccharomyces cerevisiae) ; (Z71648) ORF YNR033w [Saccharomyces cerevisiae]
19987	ENU03781	ANI61C1036	47-65	1499-1520	NAP		g4502041	818	147	1.00E-75	44	83	"aldehyde dehydrogenase 6 ; aldehyde dehydrogenase 6 ; aldehyde precursor, salivary - human ; (U07919) aldehyde dehydrogenase 6 [Homo sapiens]" (M95300) csGA [Stigmatella aurantiaca]
19988	ENU03782	ANI61C1098	26-51	1483-1503	NAP		g152650		54	0.000000			(U62028) negative acting factor [Fusarium solani f. sp. pisi]
19989	ENU03783	ANI61C6204:	71-90	1525-1549	NAP		g1470090	243	64	0.000000	30	72	serine/threonine-protein kinase COT-1 ; probable protein kinase cot-1 (EC 2.7.1.-) - Neurospora crassa
19990	ENU03784	ANI61C5953:	68-88	1520-1547	NAP		g729186	474	194	2.00E-51	38	52	"met-10+ protein - Neurospora crassa ; (L40806) Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126 [Neurospora crassa] ; met-10 gene [Neurospora crassa] ; "glutathione reductase (GR) (GRASE) ; glutathione reductase (NADPH) (EC 1.6.4.2) - yeast (Saccharomyces cerevisiae) ; (U43281) G1r1p, Lpg17p [Saccharomyces cerevisiae]"
19991	ENU03785	ANI61C9152:	61-80	1522-1541	NAP		g2133315	914	330	2.00E-89	45	94	fumarate hydratase (EC 4.2.1.2) - Rhizopus oryzae
19992	ENU03786	ANI61C800:1	22-56	1476-1502	NAP		g1708060	1088	179	e-107	53	94	
19993	ENU03787	ANI61C6075:	72-91	1535-1554	NAP		g2118296	1531	550	e-159	69	87	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20002	ENU03796	AN161C3788:	72-96	1544-1577	NAP		g1351102	1128	342	4.00E-93	65	57	putative agmatinase precursor (agmatine ureohydrolase) (AUH); (Z68166) unknown
20003	ENU03797	AN161C7597:	45-64	1527-1550	NAP		g549620	349	122	7.00E-27	33	85	[Schizosaccharomyces pombe] hypothetical 46.5 KD protein in MRS4-DYN1 intergenic region; hypothetical protein YKR053c - yeast (Saccharomyces cerevisiae); (Z28278) ORF YKR053c [Saccharomyces cerevisiae]
20004	ENU03798	AN161C9849:	24-54	1513-1531	NAP		g3122249	687	296	3.00E-79	41	97	"D-hydantoinase (dihydropyrimidinase) (DHPASE); dihydropyrimidinase (EC 3.5.2.2) - Bacillus stearothermophilus; (S73773) hydantoinase [Bacillus stearothermophilus, NS1122A, Peptide, 471 aa] [Bacillus stearothermophilus]; hydantoinase [Bacillus stearothermophilus]" (Z97211) probable inosine-5'-monophosphate dehydrogenase [Schizosaccharomyces pombe]
20005	ENU03799	AN161C1077:	24-43	1512-1531	NAP		g2239243	1343	374	e-103	64	82	26S protease regulatory subunit 6A homolog 1 (TBP-1); (D88663) Tat binding protein 1 [Brassica rapa] hypothetical 61.1 KD protein C11D3.05 in chromosome 1; (Z68166) unknown [Schizosaccharomyces pombe]
20006	ENU03800	AN161C1086:	42-62	1521-1551	NAP		g3024434	1475	344	e-151	69	99	"aldehyde dehydrogenase (ALDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]"
20007	ENU03801	AN161C821:	4	25-48	NAP		g1351702	608	149	2.00E-62	35	84	tubulin alpha-2 chain; tubulin alpha-2 chain - Emericella nidulans (AL031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]
20008	ENU03802	AN161C5992:	47-66	1547-1568	NAP		g118498	1272	437	e-142	54	96	
20009	ENU03803	AN161C5357:	57-76	1560-1579	NAP		g135407	1608	455	e-156	73	94	
20010	ENU03804	AN161C1612:	22-57	1522-1545	NAP		g3581893	1005	336	e-112	51	70	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20011	ENU03805	ANI61C2135:	32-52	1543-1562	NAP		g2493387	804	261	1.00E-93	43	96	probable sterigmatoctylin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emericella nidulans] (AF130355) Pad-1 [Neurospora crassa]
20012	ENU03806	ANI61C486:1	35-58	1537-1566	NAP		g4530579	1474	483	e-151	71	79	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda]"
20013	ENU03807	ANI61C1046	26-46	1532-1558	NAP		g2245570	437	89	1.00E-36	32	63	PRL1/PRL2-like protein ; (AB004535)
20014	ENU03808	ANI61C385:3	45-64	1558-1578	NAP		g3122623	1340	511	e-144	56	98	PRL1 [Schizosaccharomyces pombe] (Z98951) hypothetical protein [Schizosaccharomyces pombe] ; (AL031546) putative dna-binding protein [Schizosaccharomyces pombe] (D49827) alpha-mannosidase [Aspergillus phoenicis]
20015	ENU03809	ANI61C4744:	22-47	1534-1556	NAP		g2370467	1132	441	e-123	49	75	putative dioxxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae] (Z95436) hypothetical protein Ry3633 [Mycobacterium tuberculosis]
20016	ENU03810	ANI61C1035	70-89	1583-1606	NAP		g1171477	1118	724	0	72	95	hypothetical 54.2 KD TRP-ASP repeats containing protein C29A4.08C in chromosome I ; (Z97210) beta-transducin [Schizosaccharomyces pombe]
20017	ENU03811	ANI61C5378:	22-52	1540-1559	NAP		g2497056	557	202	5.00E-51	44	35	serine/threonine-protein kinase PRP4 ; (L10739) serine/threonine kinase [Schizosaccharomyces pombe] ; (AL031532) mRNA splicing-associated serine-threonine protein kinase [Schizosaccharomyces pombe]
20018	ENU03812	ANI61C9607:	25-46	1544-1563	NAP		g2105061	180	85	2.00E-15	30	40	hypothetical 51.9 KD protein C27F1.04C in chromosome I ; (Z69368) unknown [Schizosaccharomyces pombe]
20019	ENU03813	ANI61C1014	36-55	1552-1574	NAP		g3219948	474	123	4.00E-43	33	96	
20020	ENU03814	ANI61C1559:	64-82	1585-1604	NAP		g2851498	1058	386	e-109	49	90	
20021	ENU03815	ANI61C7:410	25-46	1548-1570	NAP		g1723245	419	131	1.00E-29	28	89	

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20022	ENU03816	ANI61C318:8	22-41	1548-1572	NAP	g1063421	412	95	5.00E-28	27	89		(L48797) toxin pump [Cochiobolus carbonum]
20023	ENU03817	ANI61C7785: 53-72	1583-1604		NAP	g4507707	330	144	1.00E-33	37	60		thiosulfate sulfoxidation (rhodanese) ; 3-mercaptothiolate sulfoxidation (EC 2.8.1.1) - human ; (X59434) rhodanese [Homo sapiens]
20024	ENU03818	ANI61C1069 33-52	1557-1585		NAP	g2833225	1329	275	e-113	60	85		Nucleolar protein NOP5 ; hypothetical protein YOR310c - yeast
20025	ENU03819	ANI61C7618: 34-54	1570-1589		NAP	g1723769	363	82	3.00E-15	29	81		(Saccharomyces cerevisiae) ; (X90565) orf 06108 [Saccharomyces cerevisiae] ; (Z75217) ORF YOR310c [Saccharomyces cerevisiae] ; (AF056070) nucleolar protein Nop5p [Saccharomyces cerevisiae]
20026	ENU03820	ANI61C6527: 22-48	1557-1579		NAP	g2414603	443	89	3.00E-31	38	99		putative transporter YGR260W ; probable membrane protein YGR260W - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260W [Saccharomyces cerevisiae] ; (Y07777) YGR260W ORF [Saccharomyces cerevisiae]
20027	ENU03821	ANI61C30:82 23-47	1561-1580		NAP	g3668171	2167	531	e-150	69	41		(Z99295) (Z99295) aminolipid phosphotransferase [Schizosaccharomyces pombe] (AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]
20028	ENU03822	ANI61C1185: 69-88	1599-1629		NAP	g3219963	1564	235	e-135	53	78		"putative GTP-binding protein C1B3.04C ; (Z98598) putative gtp binding protein, gtpase; Elongation factor Tu family [Schizosaccharomyces pombe]"
20029	ENU03823	ANI61C1894: 36-64	1566-1598		NAP	g3650387	510	170	3.00E-41	35	20		(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe] (AC000133) ORF [Emmericella nidulans]
20030	ENU03824	ANI61C1794: 22-49	1570-1594		NAP	g1870209	1025	324	e-102	42	94		tubulin-specific chaperone e ; (U61232) cofactor E [Homo sapiens]
20031	ENU03825	ANI61C7709: 43-64	1594-1618		NAP	g4507375	255	65	8.00E-19	30	84		(AL031907) trp-asp repeat containing protein [Schizosaccharomyces pombe]
20032	ENU03826	ANI61C4819: 62-82	1609-1637		NAP	g3766367	1267	338	e-125	52	97		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20033	ENU03827	ANI61C6841:	26-47	1581-1602	NAP		g3702646	681	280	2.00E-74	33	98	(AL031825) putative membrane transport protein
		4850..6468											[Schizosaccharomyces pombe]
20034	ENU03828	ANI61C9043:	22-45	1584-1603	NAP		g1346290	750	282	2.00E-80	40	82	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
		645..2268											(AL022103) hypothetical protein [Schizosaccharomyces pombe]
20035	ENU03829	ANI61C3809:	48-76	1603-1631	NAP		g2956784	549	228	1.00E-58	44	79	"ATP synthase beta chain, mitochondrial precursor ; H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Neurospora crassa ; (X53720) F(1)-ATPase beta-subunit precursor (519 AA)
		3146..4771											[Neurospora crassa] ; (M84192) mitochondrial A TPase beta-subunit [Neurospora crassa] "
20036	ENU03830	ANI61C896:	34-54	1592-1617	NAP		g114555	2077	439	0	86	83	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
		3..1638											Maltose permease MAL6T (maltose transport protein MAL6T) ; maltose transport protein MAL61 - yeast (Saccharomyces cerevisiae) ; (X17391) maltose permease [Saccharomyces cerevisiae] ; (M27823) maltose permease [Saccharomyces carlsbergensis]
20037	ENU03831	ANI61C1139	22-53	1588-1608	NAP		g1346290	456	125	3.00E-50	31	88	glutathione synthetase (glutathione synthase) (GSH synthetase) (GSH-S) ; hypothetical protein YOL049w - yeast (Saccharomyces cerevisiae) ; (Z74791) ORF YOL049w [Saccharomyces cerevisiae] ; (Y13804) Glutathione synthetase [Saccharomyces cerevisiae] (AL034564) hypothetical protein [Schizosaccharomyces pombe] (AF009417) cytochrome P450 [Myrothecium roridum]
		6:500..2128											
20038	ENU03832	ANI61C6331:	59-78	1630-1651	NAP		g126694	225	103	4.00E-21	27	62	
		7851..6217											
20039	ENU03833	ANI61C4568:	37-56	1598-1629	NAP		g2495096	629	250	2.00E-65	39	98	
		2950..1316											
20040	ENU03834	ANI61C1188:	72-91	1645-1667	NAP		g4049539	85	57	0.000000	34	18	
		4935..6572											
20041	ENU03835	ANI61C3095:	61-80	1636-1656	NAP		g2267601	723	233	1.00E-74	34	93	
		1688..3330											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20042	ENU03836	ANI61C9933:	28-47	1607-1626	NAP	g127289	1692	458	0	73	99		mitochondrial processing peptidase beta subunit precursor (beta-MPP) (ubiquinol-cytochrome C reductase complex CORE protein I) ; mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - Neurospora crassa ; (M20928) processing enhancing protein precursor [Neurospora crassa]
20043	ENU03837	ANI61C2470:	52-71	1632-1651	NAP	g3395585	735	129	5.00E-65	49	86		(AL031179) hypothetical protein [Schizosaccharomyces pombe]
20044	ENU03838	ANI61C1647:	72-94	1651-1672	NAP	g1169291	1259	277	e-116	54	96		aldehyde dehydrogenase (ALDH) ; (M32351) aldehyde dehydrogenase [Aspergillus niger]
20045	ENU03839	ANI61C349:3	22-48	1594-1622	NAP	g2132652	1240	222	7.00E-57	34	41		probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) ; (Z73136) ORF YLL031c [Saccharomyces cerevisiae]
20046	ENU03840	ANI61C6338:	23-47	1606-1625	NAP	g2330697	400	52	0.000000	24	43		(Z98529) mating and morphogenesis protein Scd1p. [Schizosaccharomyces pombe]
20047	ENU03841	ANI61C9837:	69-89	1649-1675	NAP	g1351714	588	146	2.00E-60	33	94		putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
20048	ENU03842	ANI61C54:20	23-46	1603-1631	NAP	g3915154	602	156	4.00E-68	33	96		Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20049	ENU03843	ANI61C7279:	30-60	1621-1641	NAP	g399006	844	232	3.00E-64	48	98		potential transcriptional adaptor ; probable transcriptional adaptor ADA2 - yeast (Saccharomyces cerevisiae) ; (M95396) ADA2 [Saccharomyces cerevisiae] ; (U33007) Ada2p: probable transcriptional adaptor; YDR448W; CAI: 0.12 [Saccharomyces cerevisiae]
20050	ENU03844	ANI61C1109	44-64	1639-1657	NAP	g2879861	59	1.00E-10					(AL021815) hypothetical protein [Schizosaccharomyces pombe] ; (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20051	ENU03845	ANI61C1085	46-66	1640-1659	NAP	g2132080	918	230	1.00E-71	37	29		hypothetical protein YOR191w - yeast (Saccharomyces cerevisiae) ; (Z75099) ORF YOR191w [Saccharomyces cerevisiae]
20052	ENU03846	ANI61C1145	22-50	1616-1637	NAP	g3560233	582	182	5.00E-45	32	54		(AL031530) putative b-zip transcription factor [Schizosaccharomyces pombe]
20053	ENU03847	ANI61C8860	40-61	1638-1657	NAP	g3184114	344	61	0.000000	34	17		(AL023780) hypothetical protein [Schizosaccharomyces pombe]
20054	ENU03848	ANI61C3943	50-69	1647-1668	NAP	g3874345	84	48	0.0001				(Z81035) predicted using GeneFinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from....
20055	ENU03849	ANI61C6208	51-70	1650-1669	NAP	g4502169	673	189	4.00E-69	34	95		unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] ; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens] (AC000133) ORF [Emericella nidulans] (AC000133) ORF [Emericella nidulans] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
20056	ENU03850	ANI61C9150	23-44	1606-1641	NAP	g1870209	2694	1027	0	94	99		"(AL034358) predicted using hexExon; L4830.1, Hypothetical protein, len: 1107 [Leishmania major]" (AF041049) 4-coumarate:CoA ligase [Populus tremuloides]
20057	ENU03851	ANI61C1229	23-44	1606-1641	NAP	g1870209	2917	1107	0	99	99		(U33265) complement fixation antigen [Coccidioides immitis] ; (U51271) complement-fixation antigen [Coccidioides immitis]
20058	ENU03852	ANI61C6693	24-47	1621-1642	NAP	g3702646	66	2.00E-29					[Coccidioides immitis]
20059	ENU03853	ANI61C5910	67-95	1665-1686	NAP	g4493738	35	1.3					[Schizosaccharomyces pombe]
20060	ENU03854	ANI61C5282	42-69	1641-1661	NAP	g3258635	526	218	3.00E-60	32	97		(AF041049) 4-coumarate:CoA ligase [Populus tremuloides]
20061	ENU03855	ANI61C1045	22-47	1621-1643	NAP	g1255728	1081	195	1.00E-94	56	96		(U33265) complement fixation antigen [Coccidioides immitis] ; (U51271) complement-fixation antigen [Coccidioides immitis]

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20062	ENU03856	AN161C1000: 4222..2557	23-48	1619-1645	NAP	g2498883	821	821	363	2.00E-99	43	50	Spliceosome associated protein 145 (SAP 145) (SF3B150) ; (U41371) spliceosome associated protein [Homo sapiens]
20063	ENU03857	AN161C4380: 1178..2844	38-59	1643-1662	NAP	g2791647	700	168	3.00E-78	41	90	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]	
20064	ENU03858	AN161C6812: 2103..437	25-44	1623-1650	NAP	g2635698	234	74	3.00E-25	37	49	(Z99120) yu1 [Bacillus subtilis]	
20065	ENU03859	AN161C6552: 1967..299	60-79	1666-1686	NAP	g137461	2306	363	0	80	80	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit); H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa ; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]"	
20066	ENU03860	AN161C5299: 1205..2876	61-81	1671-1690	NAP	g2804298	813	261	2.00E-88	38	94	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]	
20067	ENU03861	AN161C4054: 1151..2824	31-50	1644-1662	NAP	g1176239	470	207	2.00E-52	36	62	hypothetical ABC transporter ATP-binding protein YHES ; (U18997) ORF_o637 [Escherichia coli]; (AE000411) putative ATP-binding component of a transport system [Escherichia coli]	
20068	ENU03862	AN161C7785: 3418..5091	27-47	1639-1658	NAP	g3850071	823	260	3.00E-74	48	56	(AL033385) cadmium resistance protein [Schizosaccharomyces pombe]	
20069	ENU03863	AN161C9135: 2422..4097	40-59	1654-1673	NAP	g171085	1225	276	e-121	66	96	(M35237) argininosuccinate synthetase (ARG1; E.C. 6.8.4.5) [Saccharomyces cerevisiae]	
20070	ENU03864	AN161C1100: 2732..1056	22-48	1623-1656	NAP	g1703220	57	38	0.2	30	38	AI02 protein ; (U40857) AI02 [Arabidopsis thaliana]	
20071	ENU03865	AN161C6528: 30..1710	23-43	1641-1660	NAP	g2131358	588	166	3.00E-40	52	28	hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae) ; (X99000) ORF D1075 [Saccharomyces cerevisiae] ; (Z74249) ORF YDL201w [Saccharomyces cerevisiae]	
20072	ENU03866	AN161C1117: 5555..7234	22-54	1638-1659	NAP	g3560142	651	167	2.00E-40	31	83	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]	

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20073	ENU03867	AN161C8874: 2557..877	49-76	1667-1687	NAP	g1170324	1662	422	e-170	56	64		Heavy metal tolerance protein precursor ; vacuolar membrane protein HMT1 - fission yeast (Schizosaccharomyces pombe) ; (Z14055) HMT1 [Schizosaccharomyces pombe]
20074	ENU03868	AN161C9789: 3347..5030	22-55	1630-1663	NAP	g543187	46	0.000003					"ankyrin, erythrocyte - mouse ; (X69063) erythroid ankyrin [Mus musculus]" (AJ223630) homocitrate synthase [Penicillium chrysogenum]
20075	ENU03869	AN161C5161: 880..2565	22-52	1645-1664	NAP	g4165570	1971	551	0	86	99		"hypothetical 23.6 KD protein C23C11.13C in chromosome I ; (Z98559) SPAC23C11.13c; len:206aa; similar eg. to YJR133W, YJ9B_yeast, P47165, hypothetical 23.7 kd protein, (209aa), fasta scores, opt:737, E(0):0, (59.0% identity in 200 aa overlap) [Schizosaccharomyces pombe]" (AL035076) putative carboxylesterase-lipase family member [Schizosaccharomyces pombe]
20076	ENU03870	AN161C6798: 3320..5007	25-45	1650-1670	NAP	g3183352	490	104	2.00E-32	64	26		(AF010145) hexose transporter [Aspergillus parasiticus]
20077	ENU03871	AN161C2287: 340..2028	26-54	1652-1672	NAP	g4107289	569	237	1.00E-61	35	96		unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] ; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens] (AB003102) 26S proteasome subunit p44.5 [Homo sapiens]
20078	ENU03872	AN161C903:1 894..206	23-43	1650-1669	NAP	g2306977	1793	432	e-176	72	98		(Z50044) similar to phenylalanyl-tRNA synthetase; cDNA EST EMBL:701401 comes from this gene; cDNA EST yk303c5.3 comes from this gene; cDNA EST yk303c5.5 comes from this gene; cDNA EST yk452d5.3 comes from this gene; cDNA EST yk...
20079	ENU03873	AN161C6208: 1181..2876	25-54	1659-1678	NAP	g4502169	673	189	5.00E-72	35	97		
20080	ENU03874	AN161C7715: 3303..1604	60-84	1698-1717	NAP	g1945609	951	328	5.00E-89	55	65		
20081	ENU03875	AN161C5156: 3261..1560	22-55	1648-1681	NAP	g3876233	1161	223	e-112	48	83		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20082	ENU03876	ANI61C5447:	30-49	1682-2892..1180	NAP		g2493011	1294	434	e-145	48	33	probable calcium-transporting ATPase 8; probable membrane protein YMR162c - yeast (Saccharomyces cerevisiae) ; (Z49705) unknown [Saccharomyces cerevisiae]
20083	ENU03877	ANI61C7051:	34-63	1686-2926..1213	NAP		g1778093	334	134	4.00E-40	27	89	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]
20084	ENU03878	ANI61C1717:	55-76	1708-86..183	NAP		g124159	1022	205	e-107			"isocitrate dehydrogenase [NAD], mitochondrial subunit 2 precursor (isocitric dehydrogenase) (NAD+-specific ICDH) ; isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) chain IDH2 precursor - yeast (Saccharomyces cerevisiae) ; (M74131) isocitrate dehydrogenase kinase/phosphatase [Saccharomyces cerevisiae] ; (X94335) YOR3326w [Saccharomyces cerevisiae] ; (Z75043) ORF YOR136w [Saccharomyces cerevisiae] "
20085	ENU03879	ANI61C5779:	22-54	1677-1281..2998	NAP		g4127832	513	163	2.00E-51	29	97	(Y17243) cytochrome P450 [Gibberella fujikuroi]
20086	ENU03880	ANI61C2392:	28-48	1683-100..1817	NAP		g417726	667	179	7.00E-71			Recessive suppressor of secretory defect ; RSD1 protein - yeast (Saccharomyces cerevisiae) ; (X75951) RSD1 (SAC1) [Saccharomyces cerevisiae] ; (Z28212) ORF YKL212w [Saccharomyces cerevisiae] ; (X51672) recessive suppressor of secretory defect [Saccharomyces cerevisiae] ; RSD1 gene [Saccharomyces cerevisiae]
20087	ENU03881	ANI61C9372:	22-56	1666-155..1872	NAP		g1723769	297	92	8.00E-18	27	88	putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]

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20088	ENU03882	ANI61C54:20	22-51	1663-1698	NAP		g3915154	602	156	1.00E-67	33	99	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20089	ENU03883	ANI50C2738	24-46	1682-1701	NAP		g114303		300	e-125	47	53	Calcium-transporting ATPase 3 ; Ca2+-transporting ATPase (EC 3.6.1.38) - fission yeast (Schizosaccharomyces pombe) ; (J05634) Ca-2+-ATPase (caa3) [Schizosaccharomyces pombe] ; (AL021816) calcium-transporting atpase 3 [Schizosaccharomyces pombe]
20090	ENU03884	ANI61C6494:	48-67	1706-1726	NAP		g125349	591	277	2.00E-73	40	46	Carboxypeptidase KEX1 precursor (carboxypeptidase D) ; KEX1 protein precursor - yeast (Saccharomyces cerevisiae) ; (M17231) carboxypeptidase B-like peptide [Saccharomyces cerevisiae] ; (Z72725) ORF YGL203c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20091	ENU03885	ANI61C1084	33-52	1689-1711	NAP	g2914624		152	9.00E-39		61	94	"Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl[cyclo-7(2r)-((N-Valyl) Amino)-2-(Hydroxyl-(1s)-1-Methoxycarbonyl)-2-Phenylethoxy] Phosphinyloxy-Ethyl]-1-Naphthaleneacetamide] Sodium Sa... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-Formyl)-L-Valyl)amino-2-(2-Naphthyl)ethyl) Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin,... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-(1-Naphthaleneacetyl))-L-Valyl)aminomethyl) Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Macrocyclic Inhibitor: Methyl[cyclo-7(2r)-((N-Valyl)amino)-2-(Hydroxyl-(1s)-1-Methoxycarbonyl)-2-Phenylethoxy] Phosphinyloxy-Ethyl]-1-Naphthaleneacetamid..."
20092	ENU03886	ANI61C7117	61-80	1722-1741	NAP	g548494		1662	539	0	61	94	Phosphoglucumutase 2 (glucose phosphomutase 2) (PGM 2) ; phosphoglucumutase (EC 5.4.2.2) PGM2 - yeast (Saccharomyces cerevisiae) ; (X74823) phosphoglucumutase [Saccharomyces cerevisiae] ; (U09499) phosphoglucumutase [Saccharomyces cerevisiae] ; (Z49702) Pgm2p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20093	ENU03887	AN161C6918:	22-49	1683-1703	NAP	g4154078	253	122	7.00E-27	29	55	55	(AL035161) putative efflux protein [Streptomyces coelicolor]
20094	ENU03888	AN161C593:6	71-90	1723-1753	NAP	g731613	558	196	3.00E-49	32	88	88	hypothetical 60.6 KD protein in CBP2-SSBRI intergenic region ; hypothetical protein YHL036w - yeast (Saccharomyces cerevisiae) ; (U11583) Small region of weak similarity to ectopic retrovirus receptor [Saccharomyces cerevisiae]
20095	ENU03889	AN161C1065:	55-79	1718-1737	NAP	g4218005	95	59	0.000000	1			(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20096	ENU03890	AN161C3446:	72-92	1730-1756	NAP	g585356	268	61	1.00E-15	32	40	40	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) ; kdud protein - Erwinia chrysanthemi ; (X62073) 2-keto-3-deoxygluconate oxidoreductase [Erwinia chrysanthemi]
20097	ENU03891	AN161C8444:	22-54	1691-1710	NAP	g4160583	626	273	2.00E-72	47	58	58	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
20098	ENU03892	AN161C1118	69-89	1738-1758	NAP	g3876093	650	148	5.00E-43	40	77	77	(Z69635) cDNA EST yk472e10.5 comes from this gene; cDNA EST yk473c9.5 comes from this gene; cDNA EST yk472e10.3 comes from this gene [Caenorhabditis elegans]
20099	ENU03893	AN161C6296:	65-84	1741-1760	NAP	g1711561	535	59	1.00E-12	34	37	37	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20100	ENU03894	AN161C1948:	23-52	1695-1719	NAP	g2250699	289	128	1.00E-28	36	16	16	(AB001517) PWP2 protein [Homo sapiens]
20101	ENU03895	AN161C7713:	23-43	1703-1722	NAP	g2293058	324	94	4.00E-21	33	93	93	(AJ000318) putative RNA-binding protein [Schizosaccharomyces pombe] ; (AL022304) putative mna-binding protein. [Schizosaccharomyces pombe] (Z98979) hypothetical protein [Schizosaccharomyces pombe]
20102	ENU03896	AN161C884:1	50-70	1727-1750	NAP	g2388969	162	76	5.00E-13	30	50	50	[Schizosaccharomyces pombe]

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20103	ENU03897	ANI61C6290:	66-85	1748-	NAP		g4103070	597	277	2.00E-73	45	37	(AF020705) protein kinase homolog [Schizosaccharomyces pombe]
20104	ENU03898	ANI61C8572:	24-44	1710-	NAP		g2388980	1225	233	5.00E-84	40	62	(Z98980) hypothetical protein [Schizosaccharomyces pombe]
20105	ENU03899	ANI61C1026	71-106	1757-	NAP		g2132053	568	237	1.00E-61	46	49	hypothetical protein YOR091w - yeast (Saccharomyces cerevisiae) ; (X94335) YOR3160w [Saccharomyces cerevisiae] ; (Z74999) ORF YOR091w [Saccharomyces cerevisiae]
20106	ENU03900	ANI61C9080:	43-62	1726-	NAP		g2258125	399	87	2.00E-33	27	97	(Z83828) ApmMst-1 [Amanita muscaria]
20107	ENU03901	ANI61C9442:	39-58	1734-	NAP		g3881018	389	210	3.00E-53	34	79	(AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL: D75425 comes from this gene; cDNA EST EMBL: M89392 comes from this gene; cDNA EST EMBL: M89303 comes from this gene; cDNA EST EMBL: D27766 comes from this gene; cDNA EST ... Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] EMP70 protein precursor - yeast (Saccharomyces cerevisiae) ; (U53880) Emp7Op: P24A protein [Saccharomyces cerevisiae] ; (Z73255) ORF YLR083c [Saccharomyces cerevisiae] (AC002328) F22O2.16 [Arabidopsis thaliana]
20108	ENU03902	ANI61C498:	65-84	1751-	NAP		g3915154	868	304	1.00E-81	39	96	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae) ; (Z74192) ORF YDL144c [Saccharomyces cerevisiae]
20109	ENU03903	ANI61C382:	65-74	1744-	NAP		g2131246	1035	247	e-119	49	70	
20110	ENU03904	ANI61C2254:	29-48	1736-	NAP		g3953471	288	146	3.00E-34	32	35	
20111	ENU03905	ANI61C9764:	41-60	1745-	NAP		g2132443	124	75	2.00E-12	30	21	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20112	ENU03906	ANI61C9185	45-65	1753-1776	NAP		g121855	1258	176	2.00E-87			"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellobiohydrolase) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride) ; (M16190) cellobiohydrolase II [Trichoderma reesei] ; cellobiohydrolase II [Trichoderma reesei]"
20113	ENU03907	ANI61C1113	50-71	1763-1782	NAP		g543928	697	162	6.00E-59	38	87	Adenylyl cyclase-associated protein (CAP) ; adenylyl cyclase-associated protein cap - fission yeast (Schizosaccharomyces pombe) ; (L16577) adenylyl cyclase-associated protein [Schizosaccharomyces pombe] formyltetrahydrofolate D-formylase (formyl-FH(4) hydrolase) ; formyltetrahydrofolate deoformylase (EC 3.5.1.10) - Corynebacterium sp. ; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.] (AF067947) contains similarity to NADH oxidase [Caenorhabditis elegans]
20114	ENU03908	ANI61C9049	33-52	1743-1767	NAP		g2500006	708	289	4.00E-77	52	56	(Z50108) esterase [Streptomyces lividans] hypothetical 75.2 KD protein in ACS1-GCV3 intergenic region ; probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae) ; (U12980) Ya1048cp [Saccharomyces cerevisiae] (AL034433) hypothetical protein [Schizosaccharomyces pombe] (AF103949) cytochrome P450 alkane hydroxylase [Debaryomyces hanseii] probable membrane protein YLR004c - yeast (Saccharomyces cerevisiae) ; (Z73176) ORF YLR004c [Saccharomyces cerevisiae]
20115	ENU03909	ANI61C1144	71-91	1781-1805	NAP		g3193204	256	65	0.000000	36	19	
20116	ENU03910	ANI61C203	2 46-74	1756-1780	NAP		g908888	95	55	0.000002	31	27	
20117	ENU03911	ANI61C352	2 45-64	1759-1780	NAP		g731284	1337	475	e-133	47	80	
20118	ENU03912	ANI61C2376	44-71	1755-1781	NAP		g4007753	513	166	2.00E-53	33	81	
20119	ENU03913	ANI61C6098	72-95	1790-1811	NAP		g4557164	805	233	5.00E-83	45	74	
20120	ENU03914	ANI61C1044	44-64	1749-1784	NAP		g2132659	404	94	4.00E-29	32	77	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20121	ENU03915	ANI61C1119:	69-88	1793-1812	NAP	g2342601	2120	161	1.00E-38	36	5		(X89442) peptidase synthetase [Metarhizium anisopliae]
20122	ENU03916	ANI61C9379:	27-47	1751-1770	NAP	g2851586	1085	300	2.00E-84	48	94		repressible alkaline phosphatase precursor ; alkaline phosphatase (EC 3.1.3.1) - yeast (Saccharomyces cerevisiae) ; (U33050) Pho8p: repressible alkaline phosphatase; CAI: 0.16 [Saccharomyces cerevisiae]
20123	ENU03917	ANI61C8749:	70-89	1788-1819	NAP	g131768		118	1.00E-53				quinic permease (quinic transporter) ; nidulans ; (X13525) quinate permease [Emmericella nidulans] (AC000133) ORF [Emmericella nidulans]
20124	ENU03918	ANI61C1159:	35-68	1751-1786	NAP	g1870209	2185	195	2.00E-77	84	61		hypothetical 45.2 KD GTP-binding protein in TRX1-RTA1 intergenic region ; probable membrane protein YGR210c - yeast (Saccharomyces cerevisiae) ; (Z49133) unknown [Saccharomyces cerevisiae] ; (U40843) ORF57: Method: conceptual translation supplied by author. [Saccharomyces cerevisiae] ; (Z72995) ORF YGR210c [Saccharomyces cerevisiae]
20125	ENU03919	ANI61C1488:	24-43	1744-1779	NAP	g1176059	1059	157	e-105				fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens] ; (AF098019) fatty acid amide hydrolase [Homo sapiens] (AL035216) component of chaperonin-containing T-complex (zeta subunit) [Schizosaccharomyces pombe]
20126	ENU03920	ANI61C8242:	27-52	1763-1782	NAP	g4557575	453	105	2.00E-33	36	87		SEL-10 protein ; (Z79757) Similarity to Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:DJ27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:DJ33271 comes from this gene;
20127	ENU03921	ANI61C6145:	58-81	1797-1816	NAP	g4160347	1694	549	e-180	69	95		...
20128	ENU03922	ANI61C8452:	56-75	1790-1820	NAP	g3915881	467	210	2.00E-53	38	30		...

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20129	ENU03923	ANI61C1699:	22-47	1771-1790	NAP	g2983324	578	201	9.00E-51	43	52	(AE000705) hypothetical protein [Aquifex aeolicus]
20130	ENU03924	ANI61C1046	23-49	1777-1796	NAP	g1084975	522	130	6.00E-68	38	76	"endo-beta-1,6-glucanase - fungus (Trichoderma harzianum) ; (X79197) glucan endo-1,6-beta-glucosidase [Trichoderma harzianum]"
20131	ENU03925	ANI61C7744:	60-79	1807-1834	NAP	g2995342	890	206	3.00E-94	52	69	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
20132	ENU03926	ANI61C9735:	61-90	1804-1835	NAP	g2495263	2565	473	e-177	75	43	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA-reductase [Gibberella fujikuroi]
20133	ENU03927	ANI61C8580:	22-41	1790-1809	NAP	g2956763	936	300	4.00E-87	46	71	(AL022104) kinase-binding protein 1. [Schizosaccharomyces pombe]
20134	ENU03928	ANI61C3143:	28-47	1798-1817	NAP	g127562	437	152	7.00E-36	43	56	hydroxymethylglutaryl-CoA lyase (HMG-CoA lyase) (HL) (3-hydroxy-3-methylglutarate-CoA lyase) ; hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) - Pseudomonas sp ; (M31807) HMG-CoA-lyase (mvaB) [Pseudomonas mevalonii] ; (M24016) HMG-CoA lyase (EC 4.1.3.4) [Pseudomonas mevalonii] (AF052688) putative transmembrane transporter Lzl1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Lzl1p [Schizosaccharomyces pombe]
20135	ENU03929	ANI61C7424:	52-71	1822-1842	NAP	g2981103	75	8.00E-25				[Schizosaccharomyces pombe] (Z98974) hypothetical protein [Schizosaccharomyces pombe] (Z98597) hypothetical protein [Schizosaccharomyces pombe] (Z83828) AmMst-1 [Amanita muscaria]
20136	ENU03930	ANI61C7315:	22-47	1793-1812	NAP	g2388904	144	65	2.00E-12	36	14	Oligosaccharyl transferase STT3 subunit ; STT3 protein - yeast (Saccharomyces cerevisiae) ; (Z72544) ORF YGL022w [Saccharomyces cerevisiae]
20137	ENU03931	ANI61C4353:	68-90	1838-1861	NAP	g2330711	737	282	7.00E-75	43	65	
20138	ENU03932	ANI61C9080:	37-56	1804-1833	NAP	g2258125	399	87	2.00E-33	26	99	
20139	ENU03933	ANI61C8981:	37-56	1812-1833	NAP	g1711565	2232	493	0	64	78	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20140	ENU03934	ANI61C1122:	32-67	1802-1828	NAP	g730721	751	182	9.00E-45	40	99		SCD2 protein ; (U12539) scd2 [Schizosaccharomyces pombe] ; (Z69730) mating and morphogenesis protein [Schizosaccharomyces pombe] (AJ223327) rAsp f9 [Aspergillus fumigatus]
20141	ENU03935	ANI61C3398:	22-49	1794-1818	NAP	g2879890	665	276	3.00E-73	49	97		hypothetical 34.4 KD protein in IDS2-MP12 intergenic region ; hypothetical protein YJL145w - yeast (Saccharomyces cerevisiae) ; (X87371) ORF10 [Saccharomyces cerevisiae] ; (Z49420) ORF YJL145w [Saccharomyces cerevisiae]
20142	ENU03936	ANI61C4813:	25-46	1804-1823	NAP	g1353018	177	103	3.00E-21	33	29		Acetamidase ; amdS protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans] (U84350) hypothetical hydroxylase a [Amycolatopsis orientalis] (AL035259) conserved hypothetical protein [Schizosaccharomyces pombe] "(D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.]" (AL031786) putative atp dependent ma helicase [Schizosaccharomyces pombe] hypothetical 64.5 KD protein in COX4-GT1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae) ; (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae] ; (Z72708) ORF YGL186c [Saccharomyces cerevisiae] hypothetical protein 1 - Pseudomonas cepacia ; (U19883) unknown [Burkholderia cepacia]
20143	ENU03937	ANI61C1056	62-85	1839-1861	NAP	g113701	469	98	8.00E-26	40	68		
20144	ENU03938	ANI61C1054	41-60	1807-1842	NAP	g1872509	256	98	3.00E-19	31	67		
20145	ENU03939	ANI61C7623:	33-52	1809-1836	NAP	g4176557	522	132	2.00E-44	30	73		
20146	ENU03940	ANI61C6128	69-91	1854-1876	NAP	g286165	397	191	1.00E-47	41	41		
20147	ENU03941	ANI61C7855:	40-59	1833-1858	NAP	g3687476	907	161	6.00E-65	42	91		
20148	ENU03942	ANI61C7388:	46-64	1845-1865	NAP	g1723945	480	144	4.00E-37	32	87		
20149	ENU03943	ANI61C6750:	22-50	1824-1843	NAP	g2120652		126	5.00E-28	45	42		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
20150	ENU03944	ANI61CS845:	53-72	1853-1879	NAP	g731893	815	286	3.00E-76	38	97		putative transporter YIL166C; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
20151	ENU03945	ANI61C1049	22-55	1833-1852	NAP	g1709915	2011	695	0	72	95		phosphoribosylaminoimidazolecarboxamide formyltransferase 2 (AICAR transformylase) / IMP cyclohydrolase (inosinase) (IMP synthetase) (ATIC); hypothetical protein YMR120c - yeast (Saccharomyces cerevisiae); (Z49273) unknown [Saccharomyces cerevisiae]
20152	ENU03946	ANI61C9731:	32-52	1843-1864	NAP	g2145376	505	218	1.00E-55	47	33		"(Y09476) Yisk [Bacillus subtilis]; (Z99109) similar to 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase [Bacillus subtilis]" (AL031534) Major facilitator superfamily protein
20153	ENU03947	ANI61C916:2	64-82	1866-1899	NAP	g3560142	669	131	9.00E-60	32	95		[Schizosaccharomyces pombe] (AL034490) putative PHD-type zinc finger [Schizosaccharomyces pombe] (Z98602) hypothetical WW domain-containing protein
20154	ENU03948	ANI61C1096	41-63	1858-1878	NAP	g4008555	305	104	4.00E-32	28	95		[Schizosaccharomyces pombe] (AL023860) short chain dehydrogenase [Schizosaccharomyces pombe]
20155	ENU03949	ANI61C8717:	49-70	1865-1887	NAP	g2330816	792	205	3.00E-75	35	64		hypothetical 65.3 KD protein in MAD1-SCY1 intergenic region; probable membrane protein YGL084c - yeast (Saccharomyces cerevisiae); (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
20156	ENU03950	ANI61CS32:4	32-62	1852-1872	NAP	g3218393	261	125	1.00E-27	35	32		quinone permease (quinate transporter); quinate transport protein - Emericella nidulans; (X13525) quinate permease [Emericella nidulans]
20157	ENU03951	ANI61C9167:	22-51	1838-1867	NAP	g1723878	1097	374	e-111	47	92		
20158	ENU03952	ANI61C8749:	22-49	1848-1869	NAP	g131768		118	1.00E-53				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20159	ENU03953	ANI61C7362:	44-63	1877-1897	NAP		g140371	516	206	2.00E-56	32	95	"hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region ; hypothetical protein YCL038c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL038c, len.:528 [Saccharomyces cerevisiae]"
20160	ENU03954	ANI61C1642:	22-48	1848-1877	NAP		g2822399	320	84	1.00E-33	43	37	(AF016485) ORF H1434 [Halobacterium sp. NRC-1]
20161	ENU03955	ANI61C1137	40-61	1878-1897	NAP		g464876	363	82	4.00E-31			transcription factor TAU 131 KD subunit (TFIIC 131 KD subunit) ; transcription factor IIIC chain TFC4 - yeast (Saccharomyces cerevisiae) ; (L12722) transcription factor IIIB 131kDa subunit [Saccharomyces cerevisiae] ; (Z72832) ORF YGR047c [Saccharomyces cerevisiae]
20162	ENU03956	ANI61C888.2	24-52	1866-1885	NAP		g731640	1216	392	e-134	58	49	putative prolyl-TRNA synthetase YHR020W (proline--TRNA ligase) (PRORS) ; multifunctional amino acid--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10399) Yhr020wp [Saccharomyces cerevisiae] (X05204) arom polypeptide [Emericella nidulans]
20163	ENU03957	ANI61C4369:	24-45	1866-1888	NAP		g3834343	3235	888	0	99	38	homolog Oxi [Corynebacterium glutamicum]
20164	ENU03958	ANI61C4856:	45-66	1885-1909	NAP		g4583402	259	55	1.00E-19	32	55	DNA replication licensing factor MCM6 (P105MCM) ; (D84557) HsMcm6 [Homo sapiens]
20165	ENU03959	ANI61C8873:	23-51	1869-1888	NAP		g2497824	1471	324	e-127	47	72	NEMPA protein precursor ; (U62332) NEMPA [Emericella nidulans]
20166	ENU03960	ANI61C3272:	31-50	1873-1898	NAP		g2499479	2644	481	e-135	97	96	(Z99163) very hypothetical protein [Schizosaccharomyces pombe]
20167	ENU03961	ANI61C1676:	48-67	1898-1917	NAP		g4584706	300	53	4.00E-10	36	25	(AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]
20168	ENU03962	ANI61C2883:	22-45	1874-1893	NAP		g3738200	918	207	4.00E-96	35	65	(AL023518) hypothetical protein [Schizosaccharomyces pombe]
20169	ENU03963	ANI61C5338:	69-88	1922-1941	NAP		g3130053	967	277	7.00E-97	45	80	[Schizosaccharomyces pombe]

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20170	ENU03964	ANI61C1051	54-79	1908-1927	NAP		g3879809	172	85	1.00E-15			(Z47356) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ...; (Z47358) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ... comes from this gene; cDNA EST ... "(AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe] (D45893) acr-2 [Neurospora crassa]
20171	ENU03965	ANI61C8625	63-82	1919-1938	NAP		g4107478	1900	541	0	73	98	tubulin alpha-2 chain; tubulin alpha-2 chain - Emericella nidulans (AL035259) putative utp--glucose-1-phosphate uridylyltransferase [Schizosaccharomyces pombe] (AL009146) alternatively spliced form [Drosophila melanogaster] (AL031786) hypothetical protein [Schizosaccharomyces pombe] L-aminic acid oxidase precursor (LAO) ; L-aminic acid oxidase (EC 1.4.3.2) precursor - Neurospora crassa hypothetical protein YDR425w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr425wp; CAI: 0.15 [Saccharomyces cerevisiae]
20172	ENU03966	ANI61C1025	58-78	1910-1940	NAP		g1754596	129	92	1.00E-17	25	72	Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease ; reverse transcriptase ; endonuclease] ; hypothetical protein - common tobacco ; (X13777) ORF [Nicotiana tabacum]
20173	ENU03967	ANI61C3731	62-81	1927-1946	NAP		g133407	1617	592	e-168	97	67	
20174	ENU03968	ANI61C7229	50-69	1912-1934	NAP		g4176544	1741	691	0	68	81	
20175	ENU03969	ANI61C1097	22-45	1878-1908	NAP		g2827482		41	0.027			
20176	ENU03970	ANI61C9827	22-44	1890-1909	NAP		g3687484	193	79	9.00E-14	38	22	
20177	ENU03971	ANI61C1125	29-48	1902-1921	NAP		g129307	885	126	5.00E-55	52	22	
20178	ENU03972	ANI61C8860	68-87	1947-1966	NAP		g2131481	271	116	5.00E-25	34	43	
20179	ENU03973	ANI61C3512	55-90	1926-1955	NAP		g130582		77	4.00E-13			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20180	ENU03974	ANI61C9440:	37-58	1908-1938	NAP	g2257503	484	195	1.00E-53	42	52		(AB004535) BEM46 protein [Schizosaccharomyces pombe]
20181	ENU03975	ANI61C4271:	38-57	1919-1939	NAP	g2896767	656	157	8.00E-78	42	51		(AL021899) hypothetical protein Rv2030c [Mycobacterium tuberculosis]
20182	ENU03976	ANI61C8421:	68-90	1942-1969	NAP	g2492615	280	68	2.00E-10	35	26		acetate kinase (acetokinase) ; (X89084) acetate kinase [Corynebacterium glutamicum]
20183	ENU03977	ANI61C3682:	22-45	1900-1926	NAP	g1408257	222	88	2.00E-16	32	16		(U60989) putative transposase [Magnaporthe grisea]
20184	ENU03978	ANI61C4018:	22-51	1896-1926	NAP	g231361	332	167	2.00E-40	38	62		l-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) ; (M73488) l-aminocyclopropane-1-carboxylate deaminase [Pseudomonas sp.]
20185	ENU03979	ANI61C7081:	22-48	1903-1928	NAP	g2622063	272	99	2.00E-28	32	48		(AE000870) conserved protein [Methanobacterium thermoautotrophicum]
20186	ENU03980	ANI61C1105	22-44	1906-1935	NAP	g1542908		96	1.00E-18				(Z80108) lipI [Mycobacterium tuberculosis]
20187	ENU03981	ANI61C9507:	54-73	1948-1970	NAP	g586354	353	136	4.00E-31	28	88		putative 60.3 KD transcriptional regulatory protein in PRP5-THI2 intergenic region ; probable regulatory protein - yeast (Saccharomyces cerevisiae) ; (Z36108) ORF YBR239c [Saccharomyces cerevisiae]
20188	ENU03982	ANI61C7071:	56-77	1954-1973	NAP	g3281851	707	94	2.00E-18	43	26		(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]
20189	ENU03983	ANI61C1040	71-95	1979-1999	NAP	g3075511	968	385	e-106	47	82		(AF059534) severin kinase [Dictyostelium discoideum]
20190	ENU03984	ANI61C9829:	35-67	1946-1967	NAP	g4249357	275	92	2.00E-28	31	40		(U22463) T-2 toxin biosynthesis protein; TRI7 [Fusarium sporotrichioides]
20191	ENU03985	ANI61C7972:	40-62	1955-1974	NAP	g2116732	277	68	2.00E-10	34	55		(DB5129) bphC [Pseudomonas stutzeri]

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20192	ENU03986	AN161C6593:	42-61	1956-1980	NAP	g117619	500	230	2.00E-59	28	67		chooline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		5081..3101											chooline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20193	ENU03987	AN161C6331:	53-82	1981-2001	NAP	g3130051	1240	311	e-132	52	86		(AL023518) conserved hypothetical protein [Schizosaccharomyces pombe]
20194	ENU03988	AN161C8122:	45-65	1979-1998	NAP	g2132851	303	122	1.00E-26	29	52		probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
20195	ENU03989	AN161C4157:	70-89	1996-2026	NAP	g1723584	698	234	1.00E-60	48	60		hypothetical 41.3 KD protein C26F1.12C in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe]
20196	ENU03990	AN161C6693:	58-77	2001-2020	NAP	g913016	651	188	1.00E-46	31	19		"(S76267) Sng2 homolog=bf1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa]
20197	ENU03991	AN161C7484:	42-61	1989-2008	NAP	g1709060	437	157	3.00E-37	39	46		[Schizosaccharomyces pombe] "mitochondrial outer membrane protein MMM1 ; mitochondrial outer membrane protein MMM1 - yeast (Saccharomyces cerevisiae) ; (Z73111) ORF YLL006w [Saccharomyces cerevisiae] ; (X91488) L1357/MMM1 protein [Saccharomyces cerevisiae] (AL034567) putative protein [Arabidopsis thaliana] (AL023704) weak similarity to B.subtilis spore outgrowth factor B [Schizosaccharomyces pombe] (AL049609) hypothetical protein [Schizosaccharomyces pombe] (Z97204) hypothetical protein [Schizosaccharomyces pombe]
20198	ENU03992	AN161C1217:	22-45	1981-2003	NAP	g4049341	402	74	2.00E-37	38	53		
20199	ENU03993	AN161C314.2:	22-47	1983-2004	NAP	g3169059	1605	207	e-140	57	75		
20200	ENU03994	AN161C6921:	24-43	1988-2007	NAP	g4584703	569	214	1.00E-54	29	63		
20201	ENU03995	AN161C1070:	30-49	1996-2015	NAP	g2226422	2075	744	0	58	97		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20202	ENU03996	AN161C9941: 22-51	2745..704	2021	NAP		g401441	1673	263	0	50	85	dolichyl-phosphate-mannose--protein mannosyltransferase 2 ; hypothetical protein YAL023 - Yeast (Saccharomyces cerevisiae) ; (L05146)
20203	ENU03997	AN161C1146	48-68	2027-2047	NAP		g4007778	284	166	5.00E-40	30	38	Pmt2p: protein O-D-mannosyltransferase [Saccharomyces cerevisiae] ; (L05027) ORF YAL23 [Saccharomyces cerevisiae] (Z69730) similar to RanBP7-importin-beta-Cse1p superfamily
20204	ENU03998	AN161C6137: 45-68	2940..896	2021-2046	NAP		g3766370	698	129	1.00E-67	39	88	[Schizosaccharomyces pombe] (AL031907) lysyl-tRNA synthetase [Schizosaccharomyces pombe]
20205	ENU03999	AN161C3240: 32-52	2321..270	2009-2041	NAP		g2507312	402	141	7.00E-39	56	35	60S ribosomal protein L23A (L25) ; (U44800) ribosomal protein L23a [Puccinia graminis f. sp. avenae] (U89924) protein phosphatase 1 binding protein PTG [Mus musculus] (AL031534) Major facilitator superfamily protein
20206	ENU04000	AN161C1068	22-54	2016-2036	NAP		g1888566	73	5.00E-12				[Schizosaccharomyces pombe] (AF015771) putative transcriptional regulator [Magnaporthe grisea] (X97657) serine/threonine kinase [Neurospora crassa]
20207	ENU04001	AN161C6812: 70-89	2231..4290	2052-2087	NAP		g3560142	479	90	1.00E-37	31	78	hypothetical 143.6 KD protein C26A3.09C in chromosome I ; (Z69240) hypothetical protein [Schizosaccharomyces pombe]
20208	ENU04002	AN150C8879	60-79	2066-2085	NAP		g2367591	136	5.00E-31	45	71		"hypothetical zinc metalloproteinase YIL108W" ; probable membrane protein YIL108w - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 696, CAl: 0.15 [Saccharomyces cerevisiae]
20209	ENU04003	AN161C7903: 36-55	1959..4027	2041-2062	NAP		g1870019	1576	254	e-176	57	97	(U68040) polyketide synthase [Cochliobolus heterostrophus] (AL034490) putative ATP-dependent DNA helicase [Schizosaccharomyces pombe]
20210	ENU04004	AN161C6374: 39-64	1829..3908	2056-2076	NAP		g1723237	319	103	2.00E-34	38	13	
20211	ENU04005	AN161C6284: 29-55	4146..6226	2047-2067	NAP		g731856	820	348	9.00E-95	37	92	
20212	ENU04006	AN161C195:2	67-87	2080-2106	NAP		g1546072	364	96	2.00E-28	33	14	
20213	ENU04007	AN161C8249: 28-50	1665..3749	2049-2069	NAP		g4008550	656	154	2.00E-36	34	97	

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20214	ENJU04008	ANI61C1046	22-52	2044-	NAP		g2648250		73	7.00E-12			(AE000946) 3-hydroxyacyl-CoA dehydrogenase (hbd-10)
		7:3670..1587		2063									[Archaeoglobus fulgidus]
20215	ENJU04009	ANI61C8491:	40-59	2062-	NAP		g1872502	184	83	5.00E-15	35	29	(U84349) hypothetical hydroxylase a [Amycolatopsis orientalis]
		55..2138		2081									"probable taurine catabolism
20216	ENJU04010	ANI61C7424:	56-75	2078-	NAP		g2506921	322	66	1.00E-29	42	51	dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613)
		1403..3487		2098									dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE000143) taurine
													dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
20217	ENJU04011	ANI61C1159:	23-44	2036-	NAP		g1870209	2185	353	e-124	84	87	(AC000133) ORF [Emerticella nidulans]
		4526..4419		2071									(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20218	ENJU04012	ANI61C378:6	66-85	2098-	NAP		g3885836	769	258	1.00E-67	33	91	hypothetical 49.7 KD protein in GIN2-STE3 intergenic region ; hypothetical protein YKL172w - yeast
		832..8934		2126									(Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28172) ORF YKL172w
20219	ENJU04013	ANI61C5355:	32-52	2077-	NAP		g549736	485	154	2.00E-36	37	52	[Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
		3871..5977		2096									Phosphatidylinositol 4-kinase STT4 (P14-kinase) (PTDINS-4-kinase) ; probable 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) - yeast
20220	ENJU04014	ANI61C257:4	29-50	2073-	NAP		g586048	1636	431	e-148	54	31	(Saccharomyces cerevisiae) ; (D13717) homologous protein to P13-kinase (STT4) [Saccharomyces cerevisiae] ; (U17247) Stt4p: Phosphatidylinositol-4-kinase [Saccharomyces cerevisiae]
		869..2761		2095									alpha-adaptin homolog ; (Y11104) melanogaster]
20221	ENJU04015	ANI61C8788:	22-55	2067-	NAP		g3912968	1229	362	e-128	41	72	(AF094516) E1-1-like protein [Homo sapiens]
		65..2177		2092									
20222	ENJU04016	ANI61C6107:	22-48	2067-	NAP		g3820614	949	231	e-106	43	84	
		2158..45		2093									

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20223	ENU04017	ANI61C9256:	72-94	2119-2143	NAP		g401172		65	0.000000			Tetracycline resistance protein (transposon TN4351 / TN4400); NADP-requiring oxidoreductase - Bacteroides fragilis; (M37699) tetracycline resistance protein [Transposon Tn4351]
20224	ENU04018	ANI61C6644:	45-64	2096-2117	NAP		g481285	3041	1143	0	85	98	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger]; NADPH cytochrome P450 reductase [Aspergillus niger] (AL023777) hypothetical protein [Schizosaccharomyces pombe] (AF094516) E1-like protein [Homo sapiens]
20225	ENU04019	ANI61C1430:	40-62	2086-2114	NAP		g3184096	1012	263	e-115	40	98	phenylalanine ammonia-lyase; (AF094516) E1-like protein [Homo sapiens]
20226	ENU04020	ANI61C6107:	30-59	2079-2105	NAP		g3820614	949	231	e-106	43	84	phenylalanine ammonia-lyase (EC 4.3.1.5) - fungus (Rhodospiridium toruloides) (strain CBS14); (X51513) phenylalanine ammonia-lyase [Rhodospiridium toruloides]; (X12702) L-phenylalanine ammonia-lyase [Rhodospiridium toruloides]
20227	ENU04021	ANI61C467:	4 62-81	2135-2154	NAP		g129593	1039	270	e-115	43	79	phenylalanine ammonia-lyase precursor; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae); (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae]; (Z71659) ORF YNR044w [Saccharomyces cerevisiae]
20228	ENU04022	ANI61C6214:	43-62	2113-2137	NAP		g416592		40	0.052			pisatin demethylase (cytochrome P450 57A2); pisatin demethylase - fungus (Nectria haematococca); (X73145) pisatin demethylase [Nectria haematococca]
20229	ENU04023	ANI61C4312:	24-55	2086-2118	NAP		g585695	208	120	4.00E-26	29	54	pisatin demethylase (cytochrome P450 57A2); pisatin demethylase - fungus (Nectria haematococca); (X73145) pisatin demethylase [Nectria haematococca]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20230	ENU04024	AN161C1100	22-45	2096-	NAP		g731771	453	148	1.00E-47	31	82	"hypothetical 59.7 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL001w - yeast (Saccharomyces cerevisiae) ; (Z38062) orf, len: 513, CAL: 0.12 [Saccharomyces cerevisiae]"
20231	ENU04025	AN161C5348:	29-48	2115-	NAP		g2501339	2759	813	0	80	99	Copper amine oxidase 1 ; (U31869) copper amine oxidase [Aspergillus niger]
20232	ENU04026	AN161C9151:	37-59	2129-	NAP		g2959373	297	137	2.00E-32	34	62	(AL022117) hypothetical protein [Schizosaccharomyces pombe]
20233	ENU04027	AN161C9700:	70-89	2161-	NAP		g2435522	619	164	9.00E-73	38	72	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]
20234	ENU04028	AN161C9533:	54-75	2153-	NAP		g2130244	120	46	0.001	39	31	hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
20235	ENU04029	AN161C1143	58-77	2159-	NAP		g4033481	304	148	1.00E-34	33	33	putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
20236	ENU04030	AN161C1020	29-52	2127-	NAP		g4007795	1053	407	e-115	34	55	(AL034463) putative nuclear envelope pore membrane protein [Schizosaccharomyces pombe]
20237	ENU04031	AN161C8814:	22-57	2130-	NAP		g2226427	1130	318	e-120	44	91	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
20238	ENU04032	AN161C5857:	23-43	2139-	NAP		g3334847	392	180	2.00E-44	41	30	(AJ007840) Clr4 protein [Schizosaccharomyces pombe] ; (AL034382) mating-type locus and centromeric silencing protein Clr4p [Schizosaccharomyces pombe]
20239	ENU04033	AN161C466:4	28-47	2142-	NAP		g2501570	395	137	1.00E-36	35	70	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae]
20240	ENU04034	AN161C5683:	23-45	2141-	NAP		g729091	1165	418	e-130	48	83	cell division control protein 5 ; probable transcription factor cdc5 - fission yeast (Schizosaccharomyces pombe) ; (L19525) Cdc5 [Schizosaccharomyces pombe]

Sequence Definition

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20241	ENJU04035	ANI61C5347:	23-58	2164-2183	NAP		g3646451	391	158	1.00E-37	41	44	(AL031603) mRNA cap methyltransferase
20242	ENJU04036	ANI61C1073	32-51	2174-2200	NAP		g4291	167	87	6.00E-16	41	22	[Schizosaccharomyces pombe] (X00528) URF c-ras (sc-2)
20243	ENJU04037	ANI61C9737:	61-80	2212-2231	NAP		g3184082	1297	494	e-139	39	95	[Saccharomyces cerevisiae] (AL023781) N-terminal acetyltransferase 1
20244	ENJU04038	ANI61C4134:	57-76	2209-2230	NAP		g1709439	951	262	e-102	53	69	[Schizosaccharomyces pombe] 2-oxoisovalerate dehydrogenase alpha subunit precursor (branched-chain alpha-keto acid dehydrogenase component alpha chain (E1)) (BCKDH E1-alpha) ; (L47335) branched chain alpha ketoacid decarboxylase E1a subunit [Mus musculus]
20245	ENJU04039	ANI61C4107:	42-61	2202-2219	NAP		g1703215	400	147	2.00E-34	28	54	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c
20246	ENJU04040	ANI61C1092	29-52	2185-2211	NAP		g131761		59	4.00E-28			[Saccharomyces cerevisiae] quinate permease (quate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
20247	ENJU04041	ANI61C1113	64-83	2256-2275	NAP		g416866	1065	273	1.00E-92	65	53	Cyanide hydratase (formamide hydrolyase) ; cyanide hydratase (EC 4.2.1.66) - imperfect fungus (Gloeocercospora sorghi) ; (M99044) cyanide hydratase [Gloeocercospora sorghi]
20248	ENJU04042	ANI61C1109	22-51	2227-2246	NAP		g2276360	848	330	3.00E-89	36	98	(Z97992) N'-acetylglucosaminyl-phosphatidylinositol biosynthetic protein [Schizosaccharomyces pombe]
20249	ENJU04043	ANI61C1047	41-63	2247-2266	NAP		g3929362	396	113	2.00E-30	32	80	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mp VI]

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20250	ENU04044	AN161C5969:	32-51	2247-	2266	NAP		g731746	119	52	0.000000	30	38	hypothetical 42.4 KD protein in ENO2-STB5 intergenic region ; hypothetical protein YHR176w - yeast
		3987..1712									003			(Saccharomyces cerevisiae) ; (U00027) Yhr176wp [Saccharomyces cerevisiae]
20251	ENU04045	AN161C6532:	46-65	2260-	2281	NAP		g136287	3886	1273	0	99	98	Anthranilate synthase component II (contains: glutamine amidotransferase; indole-3-glycerol phosphate synthase (IGPS); N-(5'-phosphoribosyl)anthranilate isomerase (PRAII) ; anthranilate synthase multifunctional protein - Emericella nidulans
		3329..1053												(U62935) multidrug resistance protein 2 [Aspergillus fumigatus] ; (U62936) multidrug resistance protein 2 [Aspergillus fumigatus]
20252	ENU04046	AN161C2678:	42-62	2261-	2280	NAP		g2673955	755	192	8.00E-48	67	13	hypothetical 104.5 KD protein C26A3.10 in chromosome I ; (Z69240) putative zinc finger protein [Schizosaccharomyces pombe]
		273..2553												D-lactate dehydrogenase (cytochrome) precursor (D-lactate ferricytochrome C oxidoreductase) (D-LCR) ; D-lactate dehydrogenase (cytochrome) (EC 1.1.2.4) - yeast (Saccharomyces cerevisiae) ; (Z67750) D-lactate dehydrogenase [Saccharomyces cerevisiae] ; (Z74222) ORF YDL174c [Saccharomyces cerevisiae]
20253	ENU04047	AN161C2605:	63-89	2282-	2308	NAP		g1723238	578	193	4.00E-48	31	72	(AF059202) A CAT related gene product 1 [Homo sapiens]
		2520..233												(U68040) polyketide synthase [(Cochliobolus heterostrophus)]
20254	ENU04048	AN161C9553:	23-51	2243-	2268	NAP		g2506961	640	139	7.00E-50	41	75	fatty acid amide hydrolase ; (Homo sapiens) ; (AF098019) fatty acid amide hydrolase [Homo sapiens]
		2365..4652												
20255	ENU04049	AN161C1074:	65-84	2297-	2318	NAP		g3746533	379	175	1.00E-42	34	46	
		7:1744..4039												
20256	ENU04050	AN161C6708:	58-88	2298-	2317	NAP		g1546072	1290	169	9.00E-41	35	10	
		2595..4897												
20257	ENU04051	AN161C8242:	24-55	2272-	2291	NAP		g4557575	453	105	3.00E-33	35	71	
		2932..623												

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20258	ENU04052	AN161C153:2	39-61	2285-2308	NAP	g1168266	1199	316	3.00E-85	45	96		alpha-L-arabinofuranosidase A precursor (arabinosidase A) (ABF A) ; (L29005) alpha-L-arabinofuranosidase [Aspergillus niger]
20259	ENU04053	AN161C6248: 8568..6252	35-57	2280-2309	NAP	g3023956	1360	344	1.00E-93	38	42		Vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserinal]
20260	ENU04054	AN150C2773 4_1:2361..39	46-66	2308-2326	NAP	g548630		349	e-128	46	92		peptide transporter PTR2 (peptide permease PTR2) ; peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae) ; (X73541) ORF YKR413 [Saccharomyces cerevisiae] ; (Z28318) ORF YKR093w [Saccharomyces cerevisiae]
20261	ENU04055	AN161C8136: 285..2616	61-83	2331-2350	NAP	g3123199	953	354	e-102	40	94		CUT9 protein ; anaphase control protein cut9 - fission yeast (Schizosaccharomyces pombe) ; (Z98533) cut9 protein; possible anaphase control [Schizosaccharomyces pombe] ; cut9 gene [Schizosaccharomyces pombe] "hypothetical protein WP6 - Chlamydomonas eugametos ; (L29028) amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular pro...
20262	ENU04056	AN161C1097 6:4140..3035	38-61	2314-2337	NAP	g1076205	86	45	0.003	26	26		Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20263	ENU04057	AN161C498:3 824..5910	35-55	2313-2334	NAP	g3915154	868	115	1.00E-24	43	16		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
20264	ENNU04058	ANI61C9423:	64-84	2343-2368	NAP	g4506957	412	152	1.00E-35	57	30		unknown ; clathrin coat assembly protein AP19 (clathrin coat associated protein AP19) (GOLGI adaptor AP-1 19 KD adaptin) (HA1 19 KD subunit) (clathrin assembly protein complex 1 small chain) ; (AB015320) sigma1B subunit of AP-1 clathrin adaptor complex [Homo sapiens]
20265	ENNU04059	ANI61C3730:	34-53	2306-2341	NAP	g2498971	725	173	3.00E-65	39	75		putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans]
20266	ENNU04060	ANI61C753:4	22-51	2313-2332	NAP	g1352945	188	63	2.00E-19	28	49		hypothetical 39.0 KD protein in DAL5 TH11 intergenic region ; hypothetical protein YJRI154w - yeast (Saccharomyces cerevisiae) ; (Z49654) ORF YJRI154w [Saccharomyces cerevisiae]
20267	ENNU04061	ANI61C9176:	27-53	2320-2340	NAP	g1711561	261	62	7.00E-22	29	67		SUGAR transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20268	ENNU04062	ANI61C5315:	70-89	2370-2390	NAP	g1351637	581	168	5.00E-57	39	74		"hypothetical 58.5 KD protein C12G12.14 in chromosome I ; hypothetical protein SPAC12G12.14 - fission yeast (Schizosaccharomyces pombe) ; (Z66568) SPAC12G12.14, unknown, len: 510, some similarity to PIR:A24907 hypothetical protein 1 (chromosome 4 centromere) - yeast [Schizosaccharomyces pombe]" (D73369) pyranose oxidase [Coriolus versicolor]
20269	ENNU04063	ANI61C9185:	24-49	2323-2348	NAP	g1845549	555	192	8.00E-48	38	57		"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda]"
20270	ENNU04064	ANI61C1046	63-81	2365-2391	NAP	g2245570	437	89	2.00E-36	33	43		hypothetical 38.5 KD protein C3H8.04 in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
20271	ENNU04065	ANI61C1113	22-57	2333-2352	NAP	g1723215	162	94	4.00E-18	36	24		hypothetical 38.5 KD protein C3H8.04 in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]

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20272	ENU04066	AN161C9602:	22-50	2345-2364	NAP		g3915154	334	156	5.00E-37	26	75	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (U96968) alcohol oxidase [Pichia pastoris] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] (AF092565) splicing factor Ptp8 [Homo sapiens]
20273	ENU04067	AN161C4610:	47-66	2366-2393	NAP		g2104963	2260	330	e-177	68	98	probable serine/threonine-protein kinase YJL057C ; probable membrane protein YJL057c - yeast (Saccharomyces cerevisiae) ; (Z49332) ORF YJL057c [Saccharomyces cerevisiae]
20274	ENU04068	AN161C1053	49-84	2377-2396	NAP		g3549879	649	256	5.00E-67	46	27	(AF091342) neurofilament-M subunit [Bos taurus]
20275	ENU04069	AN161C1031	42-62	2362-2390	NAP		g3661610	9138	1158	0	73	33	putative ATP-dependent RNA helicase C12C2.06 ; (Z54140) probable ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20276	ENU04070	AN161C7390:	28-49	2356-2377	NAP		g1346384	293	166	6.00E-40	30	32	Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100) ; nuclear pore complex protein NUP100 - yeast (Saccharomyces cerevisiae) ; (Z15035) nuclear pore complex protein NUP100 [Saccharomyces cerevisiae] ; (X75780) B959 [Saccharomyces cerevisiae] ; (Z28068) ORF YKL068w [Saccharomyces cerevisiae] ; nuclear pore complex protein NUP100 [Saccharomyces cerevisiae]
20277	ENU04071	AN161C1117	36-55	2384-2405	NAP		g3641350	132	63	0.000000			
20278	ENU04072	AN161C8270:	22-47	2372-2391	NAP		g1175426	889	150	2.00E-66	56	39	
20279	ENU04073	AN161C6479:	22-56	2413-2432	NAP		g400320	296	85	2.00E-15			

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20280	ENU04074	AN161C6479:	22-56	2413-2432	NAP		g400320	296	85	2.00E-15			Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100); nuclear pore complex protein NUP100 - yeast (Saccharomyces cerevisiae); (Z15035) nuclear pore complex protein NUP100 [Saccharomyces cerevisiae]; (X75780) B959 [Saccharomyces cerevisiae]; (Z28068) ORF YKL068w [Saccharomyces cerevisiae]; nuclear pore complex protein NUP100 [Saccharomyces cerevisiae]
20281	ENU04075	AN161C1047	22-54	2426-2445	NAP		g2132942	206	122	5.00E-27	25	50	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c [Saccharomyces cerevisiae] (U51927) SpIR [Salmonella typhimurium]
20282	ENU04076	AN161C1016	26-45	2434-2453	NAP		g1498305	233	96	8.00E-19	26	43	Sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20283	ENU04077	AN161C9107:	72-95	2486-2509	NAP		g1711561	718	180	8.00E-54	38	46	hypothetical 61.8 K D protein in KOD1-SIM1 intergenic region; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae); (Z46833) unknown [Saccharomyces cerevisiae]
20284	ENU04078	AN161C9639:	27-52	2438-2469	NAP		g731864	383	176	4.00E-43	25	67	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" hypothetical 90.6 K D protein C1D4.10 in chromosome I; (Z69239) unknown [Schizosaccharomyces pombe]
20285	ENU04079	AN161C3499:	22-43	2464-2483	NAP		g1166378	271	132	1.00E-29	36	15	(Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe]
20286	ENU04080	AN161C8896:	44-63	2515-2534	NAP		g1723232	404	89	2.00E-16	27	86	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpv]
20287	ENU04081	AN161C6543:	38-59	2508-2530	NAP		g2414650	346	95	2.00E-31	66	34	
20288	ENU04082	AN161C1047	32-51	2503-2531	NAP		g3929362	396	113	2.00E-30	31	75	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20289	ENU04083	AN161C6741:	22-50	2532-2551	NAP		g115642	412	134	1.00E-36	37	85	acid protease precursor ; acid proteinase (EC 3.4.23.-) PEP1 precursor - yeast (Saccharomycopsis fibuligera) ; (D00313) open reading frame of PEP1 (putative secretible acid protease) [Saccharomycopsis fibuligera] ; acid protease PEP1 [Saccharomycopsis fibuligera]
20290	ENU04084	AN161C7542:	72-93	2580-2610	NAP		g2293233		159	6.00E-38			(AF008220) YtcJ [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
20291	ENU04085	AN150C1102	52-71	2566-2592	NAP		g1175420		386	e-106	43	64	hypothetical 63.9 KD protein C12C2.03C in chromosome II ; (Z54140) putative oxidoreductase [Schizosaccharomyces pombe]
20292	ENU04086	AN161C1043	67-86	2576-2608	NAP		g2388966	188	105	1.00E-21	32	15	(Z98979) putative phosphatidylserine decarboxylase proenzyme [Schizosaccharomyces pombe]
20293	ENU04087	AN161C9480:	23-49	2550-2569	NAP		g3915964	1332	319	e-145	37	84	hypothetical 112.2 KD protein in T1F35-NPL3 intergenic region (ORF1) ; hypothetical protein YDR430c - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr430cp; CAI: 0.15 [Saccharomyces cerevisiae]
20294	ENU04088	AN161C9498:	22-47	2554-2581	NAP		g117619	371	90	5.00E-33	27	81	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20295	ENU04089	AN161C9516:	23-42	2571-3271..656	NAP		g2330659	2225	816	0	53	67	(Z98595) putative snf2 family helicase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20296	ENU04090	ANI61C5840:	26-48	2618-2637	NAP		g115208	2843	555	0			"C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (methy)ENETetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase ; methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) - yeast (Saccharomyces cerevisiae) ; (M12878) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae] ; (Z49133) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae] ; (Z72989) ORF YGR204w [Saccharomyces cerevisiae] "
20297	ENU04091	ANI61C8143:	23-43	2617-2643	NAP		g125935	553	138	1.00E-60	33	54	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactic) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactic] DHP1 protein ; dhp1 protein - fission yeast (Schizosaccharomyces pombe) ; (D17752) Dhp1 protein [Schizosaccharomyces pombe] ; (Z69240) dna exoribonuclease [Schizosaccharomyces pombe] mitotic control protein DIS3 ; mitotic control protein DIS3 ; mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) ; (M74094) mitotic control protein [Schizosaccharomyces pombe] ; (AL031743) mitotic control protein dis3 . [Schizosaccharomyces pombe]
20299	ENU04093	ANI61C1106	70-93	2684-2715	NAP		g585053	2427	562	0	56	86	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (U58946) transposase [Aspergillus awamori]
20300	ENU04094	ANI61C9176:	40-58	2680-2699	NAP		g1711561	261	62	9.00E-22	29	58	
20301	ENU04095	ANI61C9979:	24-45	2671-2695	NAP		g1805251	367	188	1.00E-46	30	60	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
20302	ENU04096	ANI61C6593:	41-62	2708-2732	NAP		g117619	500	230	3.00E-59	26	75	choleline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		3013..2451											choleline transport protein [Saccharomyces cerevisiae] ; (Z72599)
													ORF YGL077c [Saccharomyces cerevisiae]
20303	ENU04097	ANI61C3011:	22-55	2744-2763	NAP		g131761	449	163	5.00E-49	28	71	quinine permease (quinine transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
20304	ENU04098	ANI61C1560:	31-53	2751-2774	NAP		g1168802	578	275	1.00E-72	37	56	Carboxypeptidase S precursor (YSCS) (GLY-X carboxypeptidase) ; Gly-X carboxypeptidase (EC 3.4.17.4) precursor - yeast (Saccharomyces cerevisiae) ; (X63068)
		2550..5335											carboxypeptidase yscS [Saccharomyces cerevisiae] ; (Z49447) ORF YJL172w [Saccharomyces cerevisiae]
20305	ENU04099	ANI61C3679:	29-50	2749-2775	NAP		g4512618	665	252	2.00E-93	28	63	(AC004793) Strong similarity to g13600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gblAF080119 and is a member of the reverse transcriptase family PF100078.
20306	ENU04100	ANI61C1146	71-91	2802-2820	NAP		g1711561	592	282	8.00E-75	37	57	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057)
		4:4675..1884											Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20307	ENU04101	ANI61C9791:	32-58	2776-2795	NAP		g1402634	288	155	1.00E-36	32	29	(D83125) secretory component [Sarcophaga peregrina]
20308	ENU04102	ANI61C8214:	56-77	2824-2843	NAP		g104311	2172	541	0	54	87	"Ca2+-transporting ATPase (EC 3.6.1.38), fast skeletal muscle - edible frog ; (X63009) fast skeletal muscle Ca-ATPase [Rana esculenta] ; Ca ATPase [Rana esculenta]"
20309	ENU04103	ANI61C241:	3	67-85	NAP		g1723448		37	0.0003			hypothetical protein C56F8.17C in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe]
		468..636		2836-2857									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20310	ENU04104	AN161C230:1	39-58	2815-2834	NAP	g1166378	924	442	e-123	33	84	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
20311	ENU04105	34..2683 AN161C7266: 46-65	2830-2855		NAP	g422615	277	125	1.00E-27	21	26	"myosin heavy chain form B, nonmuscle - African clawed frog ; (L09740) nonmuscle myosin heavy chain b [Xenopus laevis]"
20312	ENU04106	AN161C716:3	68-97	2867-2888	NAP	g4580007	3063	1016	0	61	91	(D87259) poly(A)+ RNA transport protein Ptt3p [Schizosaccharomyces pombe]
20313	ENU04107	AN161C8701: 22-52	2834-2862		NAP	g3150139	720	131	6.00E-78	36	57	(AL023594) amino-acid permease [Schizosaccharomyces pombe]
20314	ENU04108	1942..4824 AN161C7618: 22-45	2882-2911		NAP	g1710803	714	145	2.00E-33	42	21	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRF588; EMBL:SCRTG2X:M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
20315	ENU04109	AN161C9:204	45-65	2919-2938	NAP	g125935	459	108	8.00E-43	30	45	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]
20316	ENU04110	AN161C8661: 72-91	2947-2968		NAP	g4263786	850	225	1.00E-99	37	74	"(AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana]"
20317	ENU04111	AN161C1760: 69-89	2948-2966		NAP	g2808634	1017	211	3.00E-60	45	49	(A1001909) transcriptional activator [Aspergillus niger]
20318	ENU04112	2948..9 AN161C8623: 41-60	2949-2968		NAP	g3913798	1430	348	e-115	59	41	"Exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase I) (beta-glucanocellobiohydrolase I) ; (AB002821) cellobiohydrolase I [Aspergillus aculeatus]"
20319	ENU04113	AN161C7699: 22-45	2923-2953		NAP	g1723974	1511	564	e-160	50	74	"hypothetical 75.4 KD protein in HAP2-ADE5,6 intergenic region ; hypothetical protein YGL236c - yeast (Saccharomyces cerevisiae) ; (Z72758) ORF YGL236c [Saccharomyces cerevisiae]"

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20320	ENU04114	ANI61C4655:	38-57	2952-3399..423	NAP		g730723	1444	604	e-171	67	38	CAMP-dependent protein kinase SCH9 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (U00029) Sch9p: CAMP-dependent protein kinase [Saccharomyces cerevisiae]
20321	ENU04115	ANI61C9768:	28-61	2936-3378..6362	NAP		g118901	2303	426	0	45	63	DNA polymerase zeta catalytic subunit ; DNA-directed DNA polymerase (EC 2.7.7.) REV3 - yeast (Saccharomyces cerevisiae) ; (M29683) DNA polymerase (pot.) ; putative [Saccharomyces cerevisiae] ; (Z73523) ORF YPL167c [Saccharomyces cerevisiae] ; (X96770) P2535 protein [Saccharomyces cerevisiae]
20322	ENU04116	ANI61C8537:	45-64	2973-5851..8841	NAP		g549755	360	89	2.00E-26	27	50	"Carboxylic acid transporter protein homolog ; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae) ; (X75951) ORF3, A616 [Saccharomyces cerevisiae] ; (Z28217) ORF YKL217w [Saccharomyces cerevisiae] ; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae]"
20323	ENU04117	ANI61C6226:	33-64	2970-4891..7889	NAP		g728850		43	0.009			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_yeast P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus]"
20324	ENU04118	ANI61C7076:	62-81	944-963	NAP		g2132846	495	156	2.00E-37	29	58	probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20325	ENU04119	AN161C1070	63-86	944-965	NAP		g120777	1144	373	e-103	57	64	"Succinate-semialdehyde dehydrogenase (NADP+) (SSDH) ; (M88334) succinic semialdehyde dehydrogenase [Escherichia coli] ; (AE000351) succinate-semialdehyde dehydrogenase, NADP-dependent activity [Escherichia coli] "
		5:1016..72											
20326	ENU04120	AN161C4798:	41-62	924-944	NAP		g2388907	606	65	6.00E-10	29	22	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
		1015..1960											(Y17243) cytochrome P450 [Gibberella fujikuroi]
20327	ENU04121	AN161C1948:	25-46	908-928	NAP		g4127832	475	171	6.00E-42	37	57	"Elongation factor TU, mitochondrial precursor ; translation elongation factor Tu precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z75095) ORF YOR187w [Saccharomyces cerevisiae] "
20328	ENU04122	AN161C681:2	58-80	946-965	NAP		g119216	1224	322	3.00E-87	65	63	(U78168) cAMP-regulated guanine nucleotide exchange factor I [Homo sapiens]
		529..1579											hypothetical 53.9 KD protein C1F5.08C in chromosome I ; (Z68136) unknown [Schizosaccharomyces pombe]
20329	ENU04123	AN161C6816:	48-70	938-957	NAP		g4079649	162	63	7.00E-18	32	21	D-hydantoinase (dihydropyrimidinase) (DHPASE) ; (X91070) D-hydantoinase [Agrobacterium radiobacter]
		1106..155											(AL031644) hypothetical protein [Schizosaccharomyces pombe]
20330	ENU04124	AN161C1101	66-85	957-979	NAP		g1351683	341	139	2.00E-32	35	55	hypothetical 154.9 KD protein in CPR7-PET191 intergenic region ; hypothetical protein YJR033c - yeast (Saccharomyces cerevisiae) ; (Z49533) ORF YJR033c [Saccharomyces cerevisiae]
		6:2127..1172											(U77983) WD-domain protein [Schizosaccharomyces pombe]
20331	ENU04125	AN161C1047:	38-57	934-954	NAP		g3122248	669	233	1.00E-60	40	67	"chitinase (Trichoderma harzianum) ; (X80006) chitinase [Trichoderma harzianum] "
		1301..343											
20332	ENU04126	AN161C6326:	22-49	917-943	NAP		g3647336	439	102	3.00E-44	52	46	
		1017..54											
20333	ENU04127	AN161C1037	36-66	938-957	NAP		g1352875	801	66	1.00E-22	33	19	
		9:6723..5760											
20334	ENU04128	AN161C9715:	42-61	946-965	NAP		g1794292	1171	353	1.00E-96	55	65	
		101..1066											
20335	ENU04129	AN161C627:4	69-93	981-1001	NAP		g2133298	552	233	1.00E-60	49	82	
		53..1427											

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20336	ENU04130	AN161C9947:	43-62	942-977	NAP		g3915154	647	154	1.00E-36	34	57	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichoides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichoides]
		1228..252											
20337	ENU04131	AN161C942:4	22-40	942-964	NAP		g2228233	336	130	1.00E-29	40	27	(U24215) p-cumic aldehyde dehydrogenase [Pseudomonas putida]
		85..1469											
20338	ENU04132	AN161C7124:	56-74	980-1001	NAP		g2497154	337	133	2.00E-30	35	73	hypothetical 42.9 KD protein in IL V2-ADE17 intergenic region ; hypothetical protein YMR114c - yeast (Saccharomyces cerevisiae) ; (Z49702) unknown [Saccharomyces cerevisiae] (Y16399) multidrug resistance protein [Candida albicans] (Y16399) multidrug resistance protein [Candida albicans]
		179..1169											
20339	ENU04133	AN161C8753:	72-94	997-1020	NAP		g3378550		84	1.00E-15			Proline iminopeptidase (prolyl aminopeptidase) ; prolyl aminopeptidase (EC 3.4.11.5) - Aeromonas sobria ; (D30714) prolyl aminopeptidase [Aeromonas sobria] (AC006570) putative polypeptide [Arabidopsis thaliana]
		2205..3193											
20340	ENU04134	AN161C8753:	72-94	997-1020	NAP		g3378550		84	1.00E-15			"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (L48982) exo-alpha 1,4-polygalacturonase [Cochliobolus carbonum] "
		2205..3193											
20341	ENU04135	AN161C1583:	42-61	974-999	NAP		g1730576	316	90	3.00E-17	35	58	(AL021841) amiB [Mycobacterium tuberculosis]
		1992..993											
20342	ENU04136	AN161C8605:	63-90	997-1023	NAP		g4432807	477	89	5.00E-36	32	20	(AL031739) beta transducin [Schizosaccharomyces pombe]
		3730..4732											
20343	ENU04137	AN161C1048	50-69	989-1012	NAP		g2499717	430	86	3.00E-16	34	25	hypothetical 58.0 KD protein C2C6.08 in chromosome I ; (AL031324) hypothetical protein [Schizosaccharomyces pombe]
		4:1053..2057											
20344	ENU04138	AN161C7225:	28-47	976-996	NAP		g2894215	427	139	4.00E-34	37	71	(AL031154) putative transmembrane transporter [Schizosaccharomyces pombe]
		3375..2365											
20345	ENU04139	AN161C3186:	23-43	961-992	NAP		g3650407	435	115	7.00E-25	43	59	
		2508..1497											
20346	ENU04140	AN161C5164:	41-59	989-1010	NAP		g3183406	846	274	6.00E-73	49	57	
		1993..3004											
20347	ENU04141	AN161C9636:	22-50	971-993	NAP		g3367790	723	100	1.00E-31	49	60	
		1270..2283											

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20348	ENU04142	ANI61C9116:	45-67	997-1017	NAP		g1293655	778	109	4.00E-46	40	47	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
20349	ENU04143	ANI61C6687:	24-46	977-996	NAP		g2226429	826	260	2.00E-78	47	53	(Z97204) putative vacuolar protein sorting-associated protein. [Schizosaccharomyces pombe]
20350	ENU04144	ANI61S2225:	56-75	1010-1029	NAP		g3810866		108	6.00E-30	50	94	(AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
20351	ENU04145	ANI61C9501:	34-53	987-1009	NAP		g2132474	1332	518	e-146	74	55	probable membrane protein YDR091c - yeast (Saccharomyces cerevisiae) ; (Z50111) unknown [Saccharomyces cerevisiae]
20352	ENU04146	ANI61C164:3	42-64	998-1018	NAP		g114971	1677	276	2.00E-73	45	37	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosylhydrolase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast (Kluyveromyces marxianus var. marxianus) ; (X05918) beta-glucosidase (AA 1 - 845)
20353	ENU04147	ANI61C9646:	30-50	990-1011	NAP		g4538856	247	111	6.00E-24	35	49	[Kluyveromyces marxianus] (AJ223758) 54 kDa vacuolar H(+)-ATPase subunit [Sus scrofa]
20354	ENU04148	ANI61C8673:	23-47	980-1011	NAP		g3183238	529	181	7.00E-54	36	46	hypothetical 81.2 KD protein C3D6.13C in chromosome II ; (Z95620) putative thioredoxin [Schizosaccharomyces pombe]
20355	ENU04149	ANI61C8886:	71-90	1037-1060	NAP		g1084944	742	319	3.00E-86	59	32	hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

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20356	ENU04150	ANI61C7428:	62-81	1030-1051	NAP		g125401	163	94	2.00E-18			choine kinase ; choline kinase (EC 2.7.1.32) - yeast [Saccharomyces cerevisiae] ; (J04454) choline kinase [Saccharomyces cerevisiae] ; (X91258) choline kinase [Saccharomyces cerevisiae] ; (U53881) Cki1p: choline kinase [Saccharomyces cerevisiae] ; (Z73305) ORF YLR133w [Saccharomyces cerevisiae]
20357	ENU04151	ANI61C1035	47-67	1016-1041	NAP		g3334221	1166	203	3.00E-90	60	74	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) ; (AF038152) 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]
20358	ENU04152	ANI61C3101:	22-54	999-1018	NAP		g3023999	1801	210	e-108	85	55	"Isocitrate dehydrogenase (NADP), mitochondrial precursor (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) ; (AB000261) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger] ; (AB000262) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger]"
20359	ENU04153	ANI61C7048:	70-89	1055-1076	NAP		g3378447	462	153	6.00E-48	39	73	(AF079317) unknown [Sphingomonas aromaticivorans]
20360	ENU04154	ANI61C299:1	40-59	1020-1046	NAP		g2408044	108	56	0.000000	22	43	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
20361	ENU04155	ANI61C1017	22-50	1014-1035	NAP		g2673947	994	346	1.00E-98	67	23	(U62931) multidrug resistance protein 1 [Aspergillus flavus] ; (U62932) multidrug resistance protein 1 [Aspergillus flavus]
20362	ENU04156	ANI61C9779:	70-97	1062-1086	NAP		g465668	930	235	3.00E-61	42	22	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"

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20363	ENU04157	ANI61C4566: 1873..809	33-58	1034-1054	NAP	g3041656	717	110	1.00E-43	43	62		NADPH:adrenodoxin oxidoreductase precursor (adrenodoxin reductase) (ferredoxin-NADP(+) reductase) ; (J03826) adrenodoxin reductase precursor species 1 [Homo sapiens]
20364	ENU04158	ANI61C269:9 58..2023	22-47	1017-1045	NAP	g113600	99	41	0.000000	29	89		alcohol dehydrogenase (NADP(+)) (aldehyde reductase) ; alcohol dehydrogenase (NADP(+)) (EC 1.1.1.2) - human ; (J04794) aldehyde reductase (EC 1.1.1.2) [Homo sapiens] ; (AF036683) aldehyde reductase [Homo sapiens]
20365	ENU04159	ANI61C7606: 2390..1323	60-79	1065-1084	NAP	g3411013	450	175	6.00E-43	33	35		(AF000232) protein mannosyltransferase 1 [Candida albicans]
20366	ENU04160	ANI61C1879: 1257..2325	29-54	1037-1055	NAP	g3702635	532	184	1.00E-45	35	79		(AL031825) hypothetical protein [Schizosaccharomyces pombe]
20367	ENU04161	ANI61C4366: 1466..396	23-44	1032-1051	NAP	g3434965	1013	316	2.00E-85	54	66		(AB002530) mus-23 [Neurospora crassa]
20368	ENU04162	ANI61C1061 3:3032..1957	71-90	1083-1102	NAP	g3850152	564	184	3.00E-54	36	76		(AL033396) hypothetical protein [Candida albicans]
20369	ENU04163	ANI61C7489: 2110..1036	22-46	1035-1054	NAP	g1363755	931	244	7.00E-64	50	26		hypothetical protein YLR410w - yeast (Saccharomyces cerevisiae) ; (U20162) Ylr410wp [Saccharomyces cerevisiae]
20370	ENU04164	ANI61C2606: 2026..951	31-50	1042-1063	NAP	g2599117	1269	189	e-125	80	93		(AF028783) proteasome regulatory subunit 12 [Hypocrea jecorina]
20371	ENU04165	ANI61C8172: 1317..243	64-83	1077-1096	NAP	g3947854	481	148	2.00E-38	50	76		(AL034381) conserved hypothetical PFAM UPP0031 containing protein [Schizosaccharomyces pombe]
20372	ENU04166	ANI61C4401: 135..1211	67-86	1081-1101	NAP	g3336839	290	81	3.00E-28	30	57		(Y16834) hexose transporter [Candida albicans]
20373	ENU04167	ANI61C2761: 1270..194	54-73	1067-1088	NAP	g3549891	364	102	7.00E-42	32	61		(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
20374	ENU04168	ANI61C1042 5:576..1655	22-51	1040-1059	NAP	g4502369	324	156	3.00E-37	30	89		gamma-Butyrobetaine Hydroxylase ; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]

Sequence Annotation

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20375	ENU04169	ANI61C7010:	42-61	1052-1080	NAP		g1176483	500	129	2.00E-33	45	45	hypothetical 70.2 KD protein in GSH1-CHS6 intergenic region ; hypothetical protein YJL100w - yeast
		21..1103											(Saccharomyces cerevisiae) ; (X85021) orf 12 [Saccharomyces cerevisiae] ; (Z49375) ORF YJL100w
													[Saccharomyces cerevisiae]
20376	ENU04170	ANI61C1082	25-48	1033-1063	NAP		g4539596	179	102	2.00E-22	28	44	(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe]
		7:471..1551											probable membrane protein YDR282c - yeast (Saccharomyces cerevisiae) ; (U51030) Ydr282cp [Saccharomyces cerevisiae]
20377	ENU04171	ANI61C5138:	25-43	1041-1063	NAP		g21332490	228	100	3.00E-24	41	29	(AL033389) aminotransferase [Schizosaccharomyces pombe]
		172..1252											"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (X99795) exopolysaccharuronase [Aspergillus tubingensis] "
20378	ENU04172	ANI61C22:30	69-92	1096-1115	NAP		g3850081	987	294	7.00E-79	50	67	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c
		60..4145											[Saccharomyces cerevisiae]
20379	ENU04173	ANI61C9101:	60-78	1090-1109	NAP		g2499716	564	97	2.00E-52	38	68	(AL023554) dna topoisomerase iii. [Schizosaccharomyces pombe]
		1688..597											(Y12819) putative RNA helicase (DEAD box) [Danio rerio]
20380	ENU04174	ANI61C5379:	22-49	1051-1071	NAP		g21332942	348	145	7.00E-34	29	66	
		58..1149											
20381	ENU04175	ANI61C2460:	25-51	1053-1077	NAP		g4388617	1412	259	7.00E-80	49	52	
		2020..3114											
20382	ENU04176	ANI61C1138	59-83	1103-1122	NAP		g2558533	596	94	2.00E-29	39	42	
		2:1354..2459											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20383	ENU04177	ANT61C9581:	61-80	1106-1125	NAP		g3876562	194	88	1.00E-16	28	37	(Z81074) Similarity to Soybean 3-methylcrotonyl-CoA carboxylase (TR:Q42777); cDNA EST EMBL:M75819 comes from this gene; cDNA EST EMBL:M89099 comes from this gene; cDNA EST EMBL:D32763 ...
20384	ENU04178	ANT61C9305:	47-68	1089-1112	NAP		g1020413	363	59	0.000000	22	68	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
20385	ENU04179	ANT61C5766:	65-88	1108-1130	NAP		g3738180	216	52	0.000000			(AL031854) hypothetical protein [Schizosaccharomyces pombe]
20386	ENU04180	ANT61C5933:	71-90	1111-1137	NAP		g1175958	445	194	1.00E-48	35	46	hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region ; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL054C [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae]
20387	ENU04181	ANT61C2930:	43-62	1080-1110	NAP		g2190550	420	182	3.00E-51	42	95	"(AC001229) ESTs gb T45673.gb N37512 come from this gene. [Arabidopsis thaliana] "
20388	ENU04182	ANT61C1100	53-78	1108-1127	NAP		g127286	1673	316	4.00E-93	62	63	mitochondrial processing peptidase alpha subunit precursor (alpha-MPP) ; mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - Neurospora crassa
20389	ENU04183	ANT61C1104	48-68	1099-1123	NAP		g1050956	1043	273	e-104	52	84	(U26160) 43 kDa secreted glycoprotein precursor [Paracoccidioides brasiliensis] ; glycoprotein gp43 [Paracoccidioides brasiliensis] (AL022070) yeast m1c1 homolog [Schizosaccharomyces pombe]
20390	ENU04184	ANT61C9293:	41-61	1100-1119	NAP		g2950486	249	111	7.00E-24	30	33	"(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe] "
20391	ENU04185	ANT61C1010	35-54	1095-1114	NAP		g1749480	332	96	4.00E-19	35	77	

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20392	ENU04186	ANI61C1135	22-57	1086-	NAP		g4008554		53	0.000003			(AL034490) putative tyrosine kinase [Schizosaccharomyces pombe]
20393	ENU04187	ANI61C5254:	59-78	1127-	NAP		g731688	641	107	2.00E-35	32	37	hypothetical 104.0 KD protein in HXT5-NRK1 intergenic region; hypothetical protein YHR098c - yeast (Saccharomyces cerevisiae); (U00060) Yhr098c [Saccharomyces cerevisiae]; (AJ009784) Sfb3 [Saccharomyces cerevisiae]
20394	ENU04188	ANI61C2574:	23-42	1091-	NAP		g2894293	380	93	3.00E-18	32	62	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
20395	ENU04189	ANI61C7640:	37-56	1109-	NAP		g1711561	495	165	3.00E-47	34	57	sugar transporter STL1 - yeast transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20396	ENU04190	ANI61C1134:	63-82	1131-	NAP		g3256111		38	0.13			(AL024456) 1-evidence=predicted by motif; 1-match_accession=PROSITE:PS00017; 1-match_description=ATP/GTP-binding site motif A (P-loop); 1-method=ppsearch;; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS...
20397	ENU04191	ANI61C8073:	46-74	1122-	NAP		g2842688	558	77	2.00E-13	26	21	hypothetical 70.6 KD protein C1F8.03C in chromosome 1; (Z81312) unknown [Schizosaccharomyces pombe]
20398	ENU04192	ANI61C6332:	29-56	1102-	NAP		g549755	690	156	2.00E-37	39	27	"carboxylic acid transporter protein homolog; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae); (X75951) ORF3, A616 [Saccharomyces cerevisiae]; (Z28217) ORF YKL217w [Saccharomyces cerevisiae]; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae]"

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20399	ENU04193	ANT61C4155:	22-42	1104-1123	NAP		g2497126	96	64	0.000000	26	54	actin-like protein ARP9 ; probable membrane protein YMR033w - yeast (Saccharomyces cerevisiae) ; (Z49213) unknown [Saccharomyces cerevisiae] "GNS1 protein ; probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae) ; (X56909) YCR521 [Saccharomyces cerevisiae] ; (S78624) YCR521 [Saccharomyces cerevisiae=yeast, Peptide, 347 aa] [Saccharomyces cerevisiae] ; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae] ; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae] "
20400	ENU04194	ANT61C2929:	27-47	1110-1129	NAP		g140489	735	142	2.00E-68			(AL023634) protein kinase dsk1 [Schizosaccharomyces pombe] sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
20401	ENU04195	ANT61C7783:	22-52	1105-1126	NAP		g3150261		85	1.00E-15			potassium-activated aldehyde dehydrogenase precursor ; probable aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) YOR374w - yeast (Saccharomyces cerevisiae) ; (Z75282) ORF YOR374w [Saccharomyces cerevisiae]
20402	ENU04196	ANT61C6885:	72-91	1154-1181	NAP		g729862	157	72	4.00E-16	32	32	(AL033391) COO3 homologue [Candida albicans] (AL022071) fructosyl amine [Schizosaccharomyces pombe] hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
20403	ENU04197	ANT61C4087:	25-44	1099-1134	NAP		g2506349	449	109	8.00E-46	33	67	
20404	ENU04198	ANT50C1851	46-65	1128-1155	NAP		g3850128		120	2.00E-26	34	76	
20405	ENU04199	ANT61C1123	25-44	1110-1134	NAP		g2950465	216	85	7.00E-16			
20406	ENU04200	ANT61C1724:	39-60	1136-1155	NAP		g3183342	350	109	2.00E-41	33	83	

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20407	ENU04201	ANI61C5929:	56-75	1153-	NAP		g3929399	2005	438	0	99	67	proline-specific permease (proline transport protein) ; (X79797) proline permease [Emmericella nidulans]
		1346..188		1172									(AB011173) KIAA0601 protein [Homo sapiens]
20408	ENU04202	ANI61C9268:	22-52	1124-	NAP		g3043726	505	176	2.00E-43	45	22	(AL031534) putative vacuolar protein sorting-associated protein
		4133..2971		1142									[Schizosaccharomyces pombe]
20409	ENU04203	ANI61C6430:	22-43	1115-	NAP		g3560143	77	55	0.000000	35	10	(AL031534) putative vacuolar protein sorting-associated protein
		8426..7264		1142						7			[Schizosaccharomyces pombe]
20410	ENU04204	ANI61C9220:	22-49	1123-	NAP		g2500937	1219	221	5.00E-96	48	62	probable glucose transporter RCO-3 ; (U54768) RCO3 [Neurospora crassa]
		2429..1263		1146									(U54768) RCO3 [Neurospora crassa]
20411	ENU04205	ANI61C9825:	44-63	1139-	NAP		g3367585	164	90	3.00E-17	33	44	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
		23..1190		1169									(AL031135) putative polygalacturonase [Arabidopsis thaliana]
20412	ENU04206	ANI61C3276:	28-47	1141-	NAP		g3687231	208	114	1.00E-24	31	51	(AC005169) hypothetical protein [Arabidopsis thaliana]
		3347..2173		1160									(AC005169) hypothetical protein [Arabidopsis thaliana]
20413	ENU04207	ANI61C2648:	54-73	1166-	NAP		g1077378	522	179	2.00E-44	35	39	probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae) ; (U19027) YH222cp [Saccharomyces cerevisiae]
		1339..165		1186									(U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
20414	ENU04208	ANI61C5015:	24-43	1124-	NAP		g517205	261	134	1.00E-30	31	59	(U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
		1300..122		1159									(AL021411) putative oxidoreductase [Streptomyces coelicolor]
20415	ENU04209	ANI61C7035:	59-78	1167-	NAP		g2808776	242	125	6.00E-28	33	62	(AL021411) putative oxidoreductase [Streptomyces coelicolor]
		40..1217		1194									(AL031515) putative secreted cellulase [Streptomyces coelicolor]
20416	ENU04210	ANI61C5367:	22-47	1131-	NAP		g3560020	520	210	1.00E-53	38	40	putative sterigmatocystin biosynthesis peroxidase STCC ; (U34740) putative peroxidase [Emmericella nidulans]
		1331..151		1160									thiamin pyrophosphokinase (TPK) (thiamin kinase) ; thiamin pyrophosphokinase (EC 2.7.6.2) - fission yeast (Schizosaccharomyces pombe) ; (X84417) thiamin pyrophosphokinase
20417	ENU04211	ANI61C3671:	55-74	1177-	NAP		g2498968	112	50	0.000000	30	57	[Schizosaccharomyces pombe] ; (Z98533) thiamin pyrophosphokinase [Schizosaccharomyces pombe]
		1222..34		1200						03			[Schizosaccharomyces pombe]
20418	ENU04212	ANI61C1123	47-67	1173-	NAP		g1174727	199	52	7.00E-14	38	37	[Schizosaccharomyces pombe]
		2:1473..284		1193									[Schizosaccharomyces pombe]

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20419	ENU04213	ANT61C1041	22-48	1141-	NAP	g2384693	91	48	5.00E-10	28	51		(AF013216) unknown [Myxococcus xanthus]
20420	ENU04214	ANT61C3678:	22-43	1165-	NAP	g3819705	726	187	6.00E-62	37	53		(AL032824) syntaxin binding protein 1; sec1 family secretor y protein [Schizosaccharomyces pombe]
20421	ENU04215	ANT61C2667:	54-76	1204-	NAP	g2289244		37	0.000005				(U97107) membrane glycoprotein C1G30 [Mus musculus]
20422	ENU04216	ANT61C1041	56-75	1201-	NAP	g4490992	312	122	4.00E-27	37	76		(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
20423	ENU04217	ANT61C1191:	22-54	1175-	NAP	g417358	260	113	5.00E-37	30	56		ADA3 protein (NGG1 protein) ; NGG1 protein - yeast (Saccharomyces cerevisiae) ; (L12137) NGG1 [Saccharomyces cerevisiae] ; (Z46727) Ngg1p [Saccharomyces cerevisiae] (L35487) mannanase [Aspergillus aculeatus]
20424	ENU04218	ANT61C1120	31-51	1185-	NAP	g558311	1277	332	e-121	66	93		probable calcium-transporting ATPase 6 ; hypothetical protein YEL031w - yeast (Saccharomyces cerevisiae) ; (U18530) P-type ATPase; YEL031W [Saccharomyces cerevisiae]
20425	ENU04219	ANT61C6026:	22-55	1181-	NAP	g731415	1049	317	7.00E-86	56	29		putative transporter YTL166C ; probable membrane protein YTL166C - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae]
20426	ENU04220	ANT61C433:3	22-45	1174-	NAP	g731893	922	217	2.00E-62	39	67		(Z98981) hypothetical protein [Schizosaccharomyces pombe]
20427	ENU04221	ANT61C9916:	59-87	1211-	NAP	g2388995	159	66	7.00E-13	27	30		hypothetical 50.5 KD protein in RNAI-RNT1 intergenic region ; probable membrane protein YMR238w - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
20428	ENU04222	ANT61C5847:	28-52	1207-	NAP	g2497199	514	152	5.00E-48	33	77		(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
20429	ENU04223	ANT61C8210:	22-40	1203-	NAP	g4104775		46	0.0005				(AJ001261) NIPSNAP2 protein [Mus musculus]
20430	ENU04224	ANT61C6527:	59-79	1240-	NAP	g2769258	367	53	3.00E-12	26	55		
		5092..6335		1260									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20431	ENU04225	ANI61C9146:	31-52	1219-	NAP		g4585875	169	48	0.000000	32	89	(AC005850) Unknown protein [Arabidopsis thaliana]
20432	ENU04226	ANI61C8955:	33-52	1225-	NAP		g1175374	1122	433	e-120	57	75	hypothetical 57.8 KD protein C2F7.11 in chromosome I ; hypothetical protein SPAC2F7.11 - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe] ; (AF079876) Nrd1p [Schizosaccharomyces pombe] ; (AF014950) chitinase A [Stenotrophomonas maltophilia] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] proline-specific permease (proline transport protein) ; (X79797) proline permease [Emeticella nidulans] (AL022244) hypothetical protein [Schizosaccharomyces pombe] (M82963) hexose transporter [Saccharomyces cerevisiae] hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) ; (U10400) Ysc84p [Saccharomyces cerevisiae] (AJ235272) SCO2 protein precursor (sco2) [Rickettsia prowazekii] "(AF031228) D-arabinono-1,4-lactone oxidase; L-galactono-gamma-lactone oxidase [Candida albicans]" transcription factor btf3 homolog ; (U29488) similar to human transcription factor BTF3 and to S. cerevisiae GAL4 DNA-binding enhancer protein [Caenorhabditis elegans]
20433	ENU04227	ANI61C5197:	22-50	1222-	NAP		g2429326	89	62	2.00E-15	30	36	
20434	ENU04228	ANI61C1024	32-55	1225-	NAP		g3560142	716	173	2.00E-42	33	64	
20435	ENU04229	ANI61C1120	61-80	1263-	NAP		g3929399	1125	380	e-104	48	76	
20436	ENU04230	ANI61C9721:	42-61	1245-	NAP		g2995339	1134	337	e-109	56	46	
20437	ENU04231	ANI61C7513:	41-61	1248-	NAP		g171741	395	164	1.00E-39	25	74	
20438	ENU04232	ANI61C352:1	72-92	1290-	NAP		g626598	707	247	7.00E-72	43	83	
20439	ENU04233	ANI61C1051	26-49	1248-	NAP		g3861132	225	97	3.00E-19	29	60	
20440	ENU04234	ANI61C6078:	23-47	1247-	NAP		g4090945	619	307	1.00E-82	38	76	
20441	ENU04235	ANI61C3595:	60-79	1284-	NAP		g2493356	309	125	5.00E-28	47	39	

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20442	ENU04236	ANT61C1023	23-48	1252-1273	NAP		g1352621	1338	303	e-115	64	83	dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex precursor (E2) (PDC-E2) (MRP3) ; dihydrolipoamide acetyltransferase homolog - Neuropora crassa ; (J04432) ribosomal protein [Neuropora crassa]
20443	ENU04237	ANT61C5788: 4310..3016	22-46	1247-1274	NAP		g3581917	200	86	6.00E-16	40	65	(AL031545) hypothetical protein [Schizosaccharomyces pombe]
20444	ENU04238	ANT61C8008: 882..2188	22-48	1268-1286	NAP		g3885836	584	113	5.00E-62	37	62	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20445	ENU04239	ANT61C132:1 038..1569	38-61	1284-1303	NAP		g2645229	430	163	3.00E-39	37	40	(U78597) kinesin light chain [Plectonema boryanum]
20446	ENU04240	ANT61C7007: 94..1402	23-52	1257-1289	NAP		g2213548	432	181	8.00E-45	33	70	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20447	ENU04241	ANT61C7007: 94..1402	23-52	1257-1289	NAP		g2213548	432	181	8.00E-45	33	70	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20448	ENU04242	ANT61C194:2 083..757	53-76	1317-1337	NAP		g1911486	269	81	1.00E-14	41	47	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
20449	ENU04243	ANT61C756:1 778..449	71-91	1336-1358	NAP		g544049	263	78	1.00E-13			"3',5'-cyclic-nucleotide phosphodiesterase (PDEASE) ; probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) pdel-fission yeast (Schizosaccharomyces pombe) ; (S64907) Dictyostelium discoideum phosphodiesterase homolog [Schizosaccharomyces pombe=fission yeast, Peptide, 346 aa] [Schizosaccharomyces pombe] ; (AL031545) 3',5'-cyclic-nucleotide phosphodiesterase [Schizosaccharomyces pombe] ; pde1 gene [Schizosaccharomyces pombe]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20450	ENJU04244	ANI61C2416:	22-45	1293-3066..1734	NAP		g400276	531	142	2.00E-53			"mitochondrial peptide chain release factor 1 precursor (MRF-1) ; translation releasing factor RF-1, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X60381) mitochondrial release factor 1 [Saccharomyces cerevisiae] ; (Z72665) ORF YGL143c [Saccharomyces cerevisiae] ; (X99960) YGL143c [Saccharomyces cerevisiae] " high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces fragilis] hypothetical protein YER060w - yeast (Saccharomyces cerevisiae) (Z95397) unknown [Schizosaccharomyces pombe]
20451	ENJU04245	ANI61C1065	22-43	1290-1312	NAP		g1346290	339	87	2.00E-35	29	63	cycloheximide resistance protein ; (M64932) cyclohexamide resistance protein [Candida maltosa] hypothetical 44.9 KD protein in ERG7-NMD2 intergenic region ; hypothetical protein YHR075c - yeast (Saccharomyces cerevisiae) ; (U10556) Yhr075cp [Saccharomyces cerevisiae] Peroxisomal targeting signal receptor (peroxisomal protein PAY32) (peroxin-5) (PTS1 receptor) ; (U28155) Pay32p [Yarrowia lipolytica] ; Pay32 gene [Yarrowia lipolytica]
20452	ENJU04246	ANI61C5171:	68-90	1345-1364	NAP		g1072485	442	166	4.00E-40	31	79	Hypothetical 55.6 KD protein C13F4.15C in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]
20453	ENJU04247	ANI61C3347:	42-64	1326-1345	NAP		g2104457	666	244	1.00E-68	46	92	
20454	ENJU04248	ANI61C1024	72-96	1351-1375	NAP		g416864		103	3.00E-21			
20455	ENJU04249	ANI61C2921:	38-57	1321-1345	NAP		g731676	349	85	8.00E-16	38	84	
20456	ENJU04250	ANI61C6844:	68-89	1345-1378	NAP		g2501342	1085	409	e-113	54	68	
20457	ENJU04251	ANI61C2078:	44-63	1333-1356	NAP		g1723275	544	189	4.00E-47	35	80	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20458	ENU04252	AN161C2445:	48-71	1348-	NAP		g3915154	523	198	6.00E-50	34	76	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
		1772..411		1367									(AL031532) putative acetylornithine aminotransferase precursor [Schizosaccharomyces pombe]
20459	ENU04253	AN161C6612:	56-73	1361-	NAP		g3560246	806	327	9.00E-89	45	90	urea active transporter ; urea transport protein - yeast (Saccharomyces cerevisiae) ; (U11582) No definition line found [Saccharomyces cerevisiae]
		1528..162		1380									hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae) ; (Z74799) ORF YOL057w [Saccharomyces cerevisiae]
20460	ENU04254	AN161C6742:	22-47	1325-	NAP		g729376	787	201	1.00E-50	31	61	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
		685..2056		1351									hypothetical 123.7 KD protein C14C4.02 in chromosome I (AL031530) hypothetical protein [Schizosaccharomyces pombe]
20461	ENU04255	AN161C211:3	25-46	1336-	NAP		g2132005	271	59	4.00E-11	29	49	(AF014950) chitinase A [Stenotrophomonas maltophilia]
		451..2076		1357									(ACO05724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana] (Z29098) transposase (putative) [Drosophila hydei]
20462	ENU04256	AN161C1019	36-56	1347-	NAP		g2132942	525	189	4.00E-47	33	79	
		6:1027..2404		1371									
20463	ENU04257	AN161C3867:	24-44	1341-	NAP		g3287945	447	140	1.00E-34	36	22	
		3780..2398		1363									
20464	ENU04258	AN161C6734:	26-48	1348-	NAP		g3560227	558	158	2.00E-65	39	83	
		2085..3468		1367									
20465	ENU04259	AN161C5197:	22-50	1347-	NAP		g2429326	89	69	1.00E-17	31	38	
		4347..2961		1366									
20466	ENU04260	AN161C9460:	22-54	1347-	NAP		g4185142	795	314	9.00E-85	41	37	
		60..1448		1368									
20467	ENU04261	AN161C9182:	22-56	1337-	NAP		g436464	179	71	2.00E-11	24	89	
		704..2092		1368									

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20468	ENJU04262	ANI61C1082	22-51	1356-1374	NAP		g1351640	1327	354	6.00E-97	55	78	hypothetical 62.7 KD protein C8A4.06 in chromosome I; hypothetical protein SPAC8A4.06 - fission yeast (Schizosaccharomyces pombe); (Z66569) unknown [Schizosaccharomyces pombe]; (AL032824) putative chromatin binding snw family nuclear protein. [Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]
20469	ENJU04263	ANI61C5930	22-51	1356-1375	NAP		g1805251	1103	150	2.00E-35	40	29	"hypothetical 107.9 KD protein in POL4-SRD1 intergenic region; probable membrane protein YCCR017c - yeast (Saccharomyces cerevisiae); (X59720) YCCR017c, len:953 [Saccharomyces cerevisiae]" (U78597) kinesin light chain [Plectonema boryanum]
20470	ENJU04264	ANI50C2449	48-68	1383-1411	NAP		g140464		195	2.00E-88	48	48	dynamitin-related protein DNM1; dynamitin-related protein DNM1 - yeast (Saccharomyces cerevisiae); (Z73106) ORF YLL001w [Saccharomyces cerevisiae]; (X91488) L1381/DNM1 protein [Saccharomyces cerevisiae] (AF052515) eburicol 14alpha demethylase; CYP51; cytochrome P450 sterol 14-demethylase [Erysiphe graminis f. sp. hordei]
20471	ENJU04265	ANI61C3644	54-73	1396-1418	NAP		g2645229	494	153	2.00E-36	37	57	"putative leucyl-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS); (Z73100) unknown [Schizosaccharomyces pombe]"
20472	ENJU04266	ANI61C1085	68-91	1415-1437	NAP		g1706485	1827	277	1.00E-73	55	52	
20473	ENJU04267	ANI61C1059	22-43	1371-1396	NAP		g4049645	1538	484	e-136	64	82	
20474	ENJU04268	ANI61C7107	53-83	1408-1434	NAP		g1711638	1372	128	e-105	51	39	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20475	ENU04269	ANI61C8415:	72-91	1445-1464	NAP		g121146	602	209	2.00E-67	48	59	geranylgeranyl pyrophosphate synthetase (GGP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
20476	ENU04270	ANI61C2838:	44-64	1411-1439	NAP		g3182996	539	78	1.00E-30	42	92	translation initiation factor EIF-2B beta subunit (EIF-2B GDP-GTP exchange factor) (S20115) ; (U40756) S20115 [Fugu rubripes]
20477	ENU04271	ANI61C7391:	38-59	1416-1436	NAP		g448379	681	155	5.00E-52	41	82	lignostilbene dioxygenase [Sphingomonas paucimobilis]
20478	ENU04272	ANI61C1048	44-63	1423-1446	NAP		g422215	825	290	8.00E-94	43	89	alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
20479	ENU04273	ANI61C1029	52-71	1441-1460	NAP		g1351676	992	330	e-101	52	87	probable peptidyl-prolyl cis-trans isomerase C21E11.05C ; hypothetical protein SPAC21E11.05c - fission yeast (Schizosaccharomyces pombe) ; (Z67999) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
20480	ENU04274	ANI61C8002:	69-88	1463-1485	NAP		g3758890	2466	656	0	65	65	(Y14317) catalase/peroxidase [Streptomyces reticuli]
20481	ENU04275	ANI61C6047:	52-71	1447-1469	NAP		g1709501	414	181	1.00E-44	30	97	putative dolichyl-diphosphooligosaccharide--protein glycosyltransferase alpha subunit precursor (oligosaccharyl transferase alpha subunit) ; (Z69368) unknown [Schizosaccharomyces pombe]
20482	ENU04276	ANI61C1060:	23-42	1417-1441	NAP		g2879870		59	0.000000	06		(AL021816) hypothetical protein [Schizosaccharomyces pombe]
20483	ENU04277	ANI61C5186:	23-51	1420-1443	NAP		g3746666	281	101	3.00E-23	36	98	(AF076848) trihydroxytoluene oxygenase [Burkholderia cepacia]

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20484	ENU04278	ANT61C9834:	72-93	1480-1499	NAP		g2621739	892	308	6.00E-83	46	74	(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]
20485	ENU04279	ANT61C5211:	65-85	1474-1493	NAP		g4007751	485	125	6.00E-28	36	62	(Z99126) putative chromatin assembly factor subunit [Schizosaccharomyces pombe]
20486	ENU04280	ANT61C8457:	48-68	1458-1485	NAP		g731422	724	110	4.00E-30	43	33	hypothetical 70.6 KD protein in HXT8-CAN1 intergenic region ; hypothetical protein YEL065w - yeast (Saccharomyces cerevisiae) ; (U18795) Yel065wp [Saccharomyces cerevisiae]
20487	ENU04281	ANT61C1136	22-41	1440-1459	NAP		g731864	438	154	1.00E-36	29	79	hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YTL120w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
20488	ENU04282	ANT61C1015	36-55	1455-1474	NAP		g118507	771	236	2.00E-79	41	96	"aldehyde dehydrogenase, dimeric nadp-prefering (class 3) (tumor-associated aldehyde dehydrogenase) (HTC-ALDH) ; aldehyde dehydrogenase (NADP+) (EC 1.2.1.4) 3, tumor-associated - rat ; (J03637) aldehyde dehydrogenase [Rattus norvegicus] "
20489	ENU04283	ANT61C6871:	22-47	1442-1462	NAP		g112800	524	130	3.00E-55	39	73	4-coumarate--CoA ligase 1 (4CL) ; 4-coumarate--CoA ligase (EC 6.2.1.12) (clone pc4CL-1) - parsley ; (X13324) 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544) [Petroselinum crispum]
20490	ENU04284	ANT61C3461:	30-49	1442-1476	NAP		g2605934	2542	914	0	98	94	(AF029885) putative homoserine O-acetyltransferase [Emicella nidulans]
20491	ENU04285	ANT61C7333:	71-90	1500-1519	NAP		g493580	1781	287	e-111	58	57	(U09580) beta-D-glucoside glucosyltransferase [Trichoderma reesei]
20492	ENU04286	ANT50C7209	23-47	1453-1472	NAP		g2257513		147	4.00E-52	31	66	(AB004533) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]
20493	ENU04287	ANT50C7209	23-47	1453-1472	NAP		g2257513		147	4.00E-52	31	66	(AB004533) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]

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20494	ENJU04288	ANI61C1125	23-50	1456-1476	NAP		g730942	744	134	1.00E-47			probable thiamin biosynthetic bifunctional enzyme [contains: thiamin-phosphate pyrophosphorylase (TMP pyrophosphorylase) (TMP-PPASE); hydroxyethylthiazole kinase (4-methyl-5-beta-hydroxyethylthiazole kinase) (THZ kinase) ... ; thid4 protein - fission yeast (Schizosaccharomyces pombe) ; (X78824) thid4 [Schizosaccharomyces pombe] ; (Z98977) thiamin biosynthetic bifunctional enzyme [Schizosaccharomyces pombe]
20495	ENJU04289	ANI61C1139:	22-44	1450-1480	NAP		g1723423	602	92	2.00E-33	27	70	hypothetical 70.4 KD protein C4G9.04C in chromosome I ; (Z69727) hypothetical protein [Schizosaccharomyces pombe]
20496	ENJU04290	ANI61C1055	27-46	1466-1487	NAP		g2924503	979	306	3.00E-82	44	84	[Schizosaccharomyces pombe] (AL022019) glucosyltransferase [Schizosaccharomyces pombe]
20497	ENJU04291	ANI61C5108:	36-56	1481-1500	NAP		g3417417	357	116	1.00E-34	36	59	(AL031261) hypothetical protein [Schizosaccharomyces pombe]
20498	ENJU04292	ANI61C901:4	22-41	1477-1496	NAP		g3915154	728	173	2.00E-73	39	84	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombax mori]
20499	ENJU04293	ANI61C9197:	25-46	1481-1501	NAP		g1549144		70	3.00E-11			amino acid permease 2 ; (AF053231) amino acid permease [Neurospora crassa]
20500	ENJU04294	ANI61C1903:	60-79	1504-1538	NAP		g3929337	271	114	1.00E-24	25	44	dihydroxy-acid dehydratase (EC 4.2.1.9) - Methanococcus jannaschii ; (U67568) dihydroxy-acid dehydratase (ilvD) [Methanococcus jannaschii] (M16076) low temperature essential protein [Saccharomyces cerevisiae]
20501	ENJU04295	ANI61C8936:	43-63	1502-1522	NAP		g2127851	616	136	6.00E-44	34	82	
20502	ENJU04296	ANI61C1103	44-68	1508-1527	NAP		g171850	350	152	5.00E-36	31	65	

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20503	ENU04297	ANI61C3982:	37-57	1500-1171..2702	NAP		g544017	624	268	7.00E-71	35	90	protein kinase CHK1 (checkpoint kinase CHK1) ; protein kinase chk1 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe) ; (L13742) protein kinase [Schizosaccharomyces pombe] ; (U37421) protein kinase [Schizosaccharomyces pombe] ; (AL034564) protein kinase chk1 [Schizosaccharomyces pombe] (AF027687) GTPase activating protein homolog [Cochliobolus heterotrophus] (AL033389) aminotransferase [Schizosaccharomyces pombe] peroxisome biosynthesis protein PAS1 (peroxin-1) ; PAS1 protein - yeast (Pichia pastoris) ; (Z36987) PAS1 [Pichia pastoris]
20504	ENU04298	ANI61C8369:	48-67	1518-1620..81	NAP		g2598189	899	123	1.00E-39	47	60	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20505	ENU04299	ANI61C2578:	22-57	1507-4121..5669	NAP		g3850081	962	293	6.00E-84	45	97	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20506	ENU04300	ANI61C1144	63-86	1551-4:1677..128	NAP		g1172019	1098	345	4.00E-94	50	37	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20507	ENU04301	ANI61C1100	59-77	1561-4:8033..9596	NAP		g1346422	1720	624	e-178	62	84	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20508	ENU04302	ANI61C1042	64-87	1558-7:4705..3139	NAP		g3169065	1046	181	e-108	52	44	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20509	ENU04303	ANI61C8276:	40-59	1554-48..1626	NAP		g1749480	431	154	1.00E-36	61	16	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20510	ENU04304	ANI61C4319:	63-82	1582-4290..5870	NAP		g3882297	2494	460	e-128	48	37	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20511	ENU04305	ANI61C8432:	67-95	1577-2298..709	NAP		g2801701	575	134	2.00E-48	32	49	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]

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20512	ENU04306	ANT61C3797:	31-54	1549-237..1828	NAP		g2132851	204	82	1.00E-14	24	87	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
20513	ENU04307	ANT61C9558:	22-47	1555-4822..3228	NAP		g1711561	506	199	5.00E-50	30	85	sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) STL1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20514	ENU04308	ANT61C8986:	23-44	1556-99..1693	NAP		g4007794	111	69	1.00E-10	28	41	(AL034463) hypothetical protein [Schizosaccharomyces pombe]
20515	ENU04309	ANT61C5894:	26-46	1565-1725..125	NAP		g1351684	1064	314	e-109	43	13	hypothetical 420.8 KD protein C1F5.11C in chromosome I ; (Z68136) unknown [Schizosaccharomyces pombe]
20516	ENU04310	ANT61C1677:	40-59	1589-1762..1704	NAP		g2506776	993	410	e-113	42	79	"translation initiation factor IF-2, mitochondrial precursor (IF-2MT) ; translation initiation factor IF-2, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z74765) ORF YOL023w [Saccharomyces cerevisiae]"
20517	ENU04311	ANT61C8887:	70-90	1642-227..1875	NAP		g1723769	177	61	0.000000	27	41	putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
20518	ENU04312	ANT61C1038:	26-45	1608-7:2377..735	NAP		g3560201	423	153	2.00E-36	34	45	(AL031528) pseudouridine synthase [Schizosaccharomyces pombe]
20519	ENU04313	ANT61C9601:	48-70	1642-4936..3281	NAP		g2408051	1465	271	e-119	45	57	(Z99164) hypothetical protein [Schizosaccharomyces pombe]

Genetic Variation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20520	ENU04314	ANI61C6953:	22-44	1625-1645	NAP		g1175369	331	126	4.00E-28	32	83	hypothetical DNA polymerase beta-like protein C2F7.06c ; hypothetical protein SPAC2F7.06c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown
		1015..2681											[Schizosaccharomyces pombe] (L25310) beta-mannase [Trichoderma reesei]
20521	ENU04315	ANI61C2457:	68-86	1669-1692	NAP		g506848	771	327	2.00E-88	47	66	"5-aminolevulinic acid synthase, mitochondrial precursor (delta-aminolevulinic synthase) (delta-Ala synthetase) ; 5-aminolevulinic synthase (EC 2.3.1.37) precursor - Emerticella nidulans ; (X64170) 5-aminolevulinic acid synthase [Emerticella nidulans]"
		611..2271											hypothetical 76.8 KD protein in chromosome II ; (AF064207) putative histone deacetylase
20522	ENU04316	ANI50C4730	33-52	1641-1660	NAP		g585244		1033	0	99	82	[Schizosaccharomyces pombe] (AL035065) putative urea active transporter [Schizosaccharomyces pombe]
		_1:12..1681											(AL021816) hypothetical protein [Schizosaccharomyces pombe] (AE000703) N-methylhydantoinase A [Aquifex aeolicus]
20523	ENU04317	ANI61C1190:	33-54	1645-1667	NAP		g3023933	1040	73	8.00E-31	42	55	(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi]
		15284..13607											pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVII] (AF027979) carnitine acetyl transferase [Magnaporthe grisea]
20524	ENU04318	ANI61C8043:	70-93	1678-1708	NAP		g4106690	758	220	3.00E-56	41	48	
		4994..3314											
20525	ENU04319	ANI61C7218:	69-93	1699-1722	NAP		g2879870	1686	182	5.00E-45	35	48	
		6352..8047											
20526	ENU04320	ANI61C8090:	40-61	1670-1695	NAP		g2983296	794	309	4.00E-83	36	82	
		3206..1509											
20527	ENU04321	ANI61C1567:	39-70	1682-1701	NAP		g3549879	742	292	4.00E-78	39	91	
		99..1803											
20528	ENU04322	ANI61C3019:	22-55	1663-1688	NAP		g3929362	432	197	3.00E-49	32	72	
		4317..2609											
20529	ENU04323	ANI61C8724:	22-47	1677-1698	NAP		g2688966	537	139	2.00E-55	26	90	
		3953..5671											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20530	ENU04324	ANI61C379:2	38-57	1700-1721	NAP		g2497193	785	170	2.00E-60	36	69	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
20531	ENU04325	ANI61C1536: 15..1749	35-55	1708-1727	NAP		g3650401	278	137	2.00E-31	27	52	(AL031739) zinc finger protein [Schizosaccharomyces pombe]
20532	ENU04326	ANI61C8724: 22-51	22-51	1707-1728	NAP		g2688966	537	139	2.00E-55	26	90	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]
20533	ENU04327	ANI61C1070: 63-83	63-83	1776-1795	NAP		g4033486	274	82	5.00E-23	31	40	putative tartrate transporter ; (U25634) putative tartrate transporter; inducible by tartrate; Method: conceptual translation supplied by author. [Agrobacterium vitis] ; ttuB gene [Agrobacterium vitis]
20534	ENU04328	ANI61C8868: 22-52	22-52	1725-1756	NAP		g2144167	1713	362	e-143	55	71	beta-glucosidase (EC 3.2.1.21) - yeast (Candida molischiana) ; (U16259) beta-glucosidase [Pichia capsulata]
20535	ENU04329	ANI61C9692: 58-77	58-77	1836-1855	NAP		g3924850	252	109	8.00E-23	32	27	"(Z81586) predicted using GeneFinder; similar to Alcohol/other dehydrogenases, short chain type [Caenorhabditis elegans] "
20536	ENU04330	ANI61C7957: 67-87	67-87	1853-1872	NAP		g4502497	149	69	2.00E-19	32	59	chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens]
20537	ENU04331	ANI61C791: 23-46	23-46	1819-1841	NAP		g1169823		61	0.000000			regulatory protein GAL4 ; regulatory protein GAL4 - yeast (Saccharomyces cerevisiae) ; (K01486) GAL4 protein [Saccharomyces cerevisiae] ; (Z67751) GAL4 [Saccharomyces cerevisiae] ; (Z73604) ORF YPL248c [Saccharomyces cerevisiae]
20538	ENU04332	ANI61C1004	70-92	1867-1889	NAP		g1872514	513	120	3.00E-26	37	33	(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens] ; (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens]

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20539	ENJU04333	ANI61C7032:	22-54	1823-	NAP		g466152	446	173	9.00E-48	35	44	hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
		1524..3386		1842									
20540	ENJU04334	ANI61C7032:	22-54	1823-	NAP		g466152	446	173	9.00E-48	35	44	hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
		1524..3386		1842									
20541	ENJU04335	ANI61C6610:	28-47	1847-	NAP		g3929362	555	147	2.00E-70	36	98	pisatin demethylase [cytochrome P450 57A1] ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mp VI]
		3603..3426		1880									
20542	ENJU04336	ANI61C9614:	68-86	1915-	NAP		g3184088	392	160	8.00E-44	29	76	(AL023781) hypothetical protein [Schizosaccharomyces pombe]
		47..1956		1934									
20543	ENJU04337	ANI61C7030:	22-48	1873-	NAP		g2626826		98	3.00E-19			"(D83967) Yfkn [Bacillus subtilis] ; (Z99108) similar to 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis] "
		3655..1743		1892									
20544	ENJU04338	ANI61C7115:	71-90	1931-	NAP		g2133268	97	85	2.00E-15	25	52	DNA-binding protein amda - Emericella nidulans ; (L28810) regulatory protein [Emericella nidulans]
		130..2055		1954									
20545	ENJU04339	ANI61C3433:	22-41	1890-	NAP		g3925758	182	84	3.00E-15	26	76	(AL034332) hypothetical C2H2-type zinc-finger protein [Schizosaccharomyces pombe]
		1237..3168		1909									
20546	ENJU04340	ANI61C7725:	22-51	1900-	NAP		g2688313		59	0.000000			"(AE001146) sensory transduction histidine kinase, putative [Borrelia burgdorferi] "
		2046..107		1919									
20547	ENJU04341	ANI61C6803:	43-70	1932-	NAP		g4519181	3365	1236	0	99	63	(AB023911) chitin synthase [Emericella nidulans]
		6..1995		1960									
20548	ENJU04342	ANI61C6259:	51-72	1955-	NAP		g1546072	1439	149	7.00E-35	30	22	(U68040) polyketide synthase [Cochliobolus heterostrophus]
		5140..7105		1974									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20549	ENU04343	ANI61C2341:	54-74	1979-2086..99	NAP	g2104457	246	104	8.00E-29	31	45		(Z95397) unknown [Schizosaccharomyces pombe]
20550	ENU04344	ANI61C9697:	45-67	1967-3156..1168	NAP	g399198	603	183	8.00E-73	38	35		cell division control protein 25 ; SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment) ; (M82964) CDC25 [Saccharomyces kluyveri]
20551	ENU04345	ANI61C4603:	24-44	1965-2740..737	NAP	g3915154	353	83	2.00E-24	33	91		trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (U78320) chitinase [Entamoeba invadens]
20552	ENU04346	ANI61C1932:	35-54	1983-1552..3563	NAP	g1685364	337	113	1.00E-41	33	44		(Z95620) n-acetylglucosaminyl-phosphatidylinositol [Schizosaccharomyces pombe]
20553	ENU04347	ANI61C9831:	41-60	2004-2452..4478	NAP	g2117303	1418	346	e-155	66	90		"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
20554	ENU04348	ANI61C6656:	54-73	2018-3133..1105	NAP	g2506921	161	55	0.000001	32	43		"ferric reductase transmembrane component 2 precursor ; ferric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae) ; (X75950) ORF5, F711 [Saccharomyces cerevisiae] ; (Z28220) ORF YKL220c [Saccharomyces cerevisiae] ; ORF 5 [Saccharomyces cerevisiae] "
20555	ENU04349	ANI61C5227:	22-52	1984-3425..3954	NAP	g728744		53	0.000007				auxin-induced protein PCNT115 ; auxin-induced protein - common tobacco ; (X56267) auxin-induced protein [Nicotiana tabacum] (AL049628) putative exporter [Streptomyces coelicolor]
20556	ENU04350	ANI61C1039	56-77	2022-0:4698..2668	NAP	g4585598		65	2.00E-35				"ferric reductase transmembrane component 2 precursor - yeast (Saccharomyces cerevisiae) ; (X75950) ORF5, F711 [Saccharomyces cerevisiae] ; (Z28220) ORF YKL220c [Saccharomyces cerevisiae] ; ORF 5 [Saccharomyces cerevisiae] "
20557	ENU04351	ANI61C1023	45-64	2036-4:2074..22	NAP	g549758	157	119	6.00E-26	28	36		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20558	ENU04352	ANI61C9133:	54-73	2053-2073	NAP		g3650375	586	254	2.00E-66	37	55	(AL031740) putative mitochondrial translation system component [Schizosaccharomyces pombe]
		393..2453											
20559	ENU04353	ANI61C2779:	68-89	2079-2099	NAP		g4528		360	0	58	88	(X54316) GTP-binding protein [Saccharomyces cerevisiae]
		2459..2351											
20560	ENU04354	ANI61C1106	40-59	2054-2073	NAP		g3182972	794	217	e-127	47	68	probable coatomer gamma subunit (gamma-coat protein) (gamma-COP) ; (Z95396) putative coatomer gamma subunit [Schizosaccharomyces pombe]
		7:3274..1719											
20561	ENU04355	ANI61C1103	26-49	2041-2063	NAP		g2645229	442	195	8.00E-49	36	39	(U78597) kinesin light chain [Plectonema boryanum]
		1:2700..5209											
20562	ENU04356	ANI61C9409:	23-45	2031-2060	NAP		g131782	956	239	9.00E-89	32	52	DNA repair protein RAD50 (153 KID protein) ; RAD50 protein - yeast (Saccharomyces cerevisiae) ; (X14814) 153 KD protein (AA 1 - 1312) [Saccharomyces cerevisiae] ; (X96722) ORF N0872 [Saccharomyces cerevisiae] ; (Z71526) ORF YNL250w [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]
		480..2560											
20563	ENU04357	ANI61C439:5	70-89	2092-2112	NAP		g2258125	520	209	1.00E-59	33	95	(AL021746) phosphatidylserine decarboxylase [Schizosaccharomyces pombe]
		373..5887											
20564	ENU04358	ANI61C8264:	46-67	2074-2109	NAP		g2842521	730	322	6.00E-87	50	100	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
		1449..3554											
20565	ENU04359	ANI61C4603:	26-61	2108-2128	NAP		g3915154	353	83	2.00E-24	33	87	(AL021816) hypothetical protein [Schizosaccharomyces pombe]
		2881..737											
20566	ENU04360	ANI61C1060:	23-42	2143-2162	NAP		g2879870		59	0.000000			SpoC1-C1C protein - Emericella nidulans ; (M83571) SpoC1-C1C [Emericella nidulans]
		2378..196											
20567	ENU04361	ANI61C9302:	68-92	2183-2212	NAP		g283343	304	80	1.00E-17	58	16	
		2590..1817											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20568	ENU04362	ANI61C1076	61-80	2318-	NAP		g1174987	1186	166	3.00E-61	45	20	vacuolar protein sorting-associated protein VPS35 ; vacuolar protein-sorting protein VPS35 - yeast (Saccharomyces cerevisiae) ; (Z49429)
		9:1972..4306		2350									ORF YJL154c [Saccharomyces cerevisiae]
20569	ENU04363	ANI61C216:3	35-55	2322-	NAP		g1352937	48	45	0.002	25	28	hypothetical 39.9 KD protein in HOM6-PMT4 intergenic region ; probable membrane protein YJIR141w - yeast (Saccharomyces cerevisiae) ; (Z49641) ORF YJIR141w [Saccharomyces cerevisiae]
		135..785		2343									
20570	ENU04364	ANI61C5788:	49-68	2330-	NAP		g3618207	721	320	3.00E-86	33	88	(AL031579) conserved hypothetical protein [Schizosaccharomyces pombe]
		2376..22		2361									DNA repair protein RAD9 ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; (X58231) rad9 protein [Schizosaccharomyces pombe] ; (X64648) rad9 [Schizosaccharomyces pombe] ; (X77276) rad9 [Schizosaccharomyces pombe]
20571	ENU04365	ANI61C1001	66-87	2359-	NAP		g131816	189	64	6.00E-16			
		4:243..2606		2385									
20572	ENU04366	ANI61C9256:	60-80	2362-	NAP		g3915154		75	2.00E-31			
		4444..4770		2381									
20573	ENU04367	ANI61C4216:	58-77	2391-	NAP		g3024061	3393	545	0	85	97	6-phosphofructokinase (phosphofructokinase) (phosphohexokinase) ; (Z79690) phosphofructokinase [Aspergillus niger]
		3367..970		2410									
20574	ENU04368	ANI61C1048	47-72	2372-	NAP		g1175379	541	111	2.00E-44	44	27	hypothetical 88.2 KD protein C2F7.18C in chromosome I (U13644) F56D2.5 gene product [Caenorhabditis elegans]
		2:4278..4010		2403									
20575	ENU04369	ANI61C3090:	22-48	2413-	NAP		g1945502	98	82	2.00E-14	34	6	
		650..3116		2445									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20576	ENJU04370	ANI61C9380:	70-89	2490-2510	NAP		g1175371	138	80	5.00E-14	31	22	hypothetical 71.9 KD protein C2F7.08C in chromosome I; hypothetical protein SPAC2F7.08c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe]
20577	ENJU04371	ANI61C9639:	44-75	2490-2516	NAP		g731864	383	176	4.00E-43	25	65	hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YTL120w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
20578	ENJU04372	ANI61C3273:	34-53	2497-2517	NAP		g2465152	240	95	2.00E-18	40	13	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
20579	ENJU04373	ANI61C450:2	43-64	2552-2571	NAP		g3930517	1333	455	e-127	40	86	(AF059906) ubiquitin fusion degradation protein-2 [Schizosaccharomyces pombe]
20580	ENJU04374	ANI61C9792:	24-45	2547-2566	NAP		g730221	3335	788	0	67	81	[Schizosaccharomyces pombe] 2-oxoglutarate dehydrogenase E1 component precursor (alpha-ketoglutarate dehydrogenase) ; oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - yeast (Saccharomyces cerevisiae) ; (Z46833) 2-oxoglutarate dehydrogenase E1 component [Saccharomyces cerevisiae]
20581	ENJU04375	ANI61C1144	64-85	2639-2658	NAP		g549038	133	71	1.00E-13			"transcription initiation factor III, alpha subunit (TFIIIE-alpha) (transcription factor A large subunit) (factor A 66 KD subunit) ; transcription initiation factor III chain TFA1 - yeast (Saccharomyces cerevisiae) ; (Z28028) ORF YKL028w [Saccharomyces cerevisiae] ; (U12825) transcription factor TFIIIE, large subunit [Saccharomyces cerevisiae] " (AB018297) KIAA0754 protein [Homo sapiens]
20582	ENJU04376	ANI61C8159:	70-89	2659-2682	NAP		g3882229	85	46	0.001	26	21	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20583	ENU04377	ANI61C4130:	22-41	2608-3177..520	NAP		g3005592	548	166	7.00E-40	34	27	(AF051911) telomerase reverse transcriptase; mTERT [Mus musculus] ; (AF073311) telomerase catalytic subunit [Mus musculus]
20584	ENU04378	ANI61C9698:	56-75	2651-3605..2478	NAP		g1723845	377	171	3.00E-41	34	45	putative ATP-dependent RNA helicase YGL064C ; hypothetical protein YGL064c - yeast (Saccharomyces cerevisiae) ; (Z72586) ORF YGL064c [Saccharomyces cerevisiae]
20585	ENU04379	ANI61C1132:	72-94	2676-155..2820	NAP		g3136048	2024	362	5.00E-99	50	64	(AL023592) putative helicase [Schizosaccharomyces pombe]
20586	ENU04380	ANI61C8590:	22-55	2689-1848..4579	NAP		g4507071	509	229	5.00E-59	33	43	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 ; HIP116 protein - human ; (L34673) ATPase [Homo sapiens] "
20587	ENU04381	ANI61C8661:	71-90	2828-50..2869	NAP		g4263786	850	225	e-100	37	86	"(AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana] "
20588	ENU04382	ANI61C3919:	51-70	2813-554..3384	NAP		g4502869	1191	176	e-105	43	64	"chloride channel 3 ; chloride channel protein 3, long form - human ; (X78520) chloride channel 3 [Homo sapiens] "
20589	ENU04383	ANI61C9577:	38-57	2971-3062..68	NAP		g3116148	1166	196	e-133	37	62	(AL023290) putative ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20590	ENU04384	ANI61C3260:	26-46	631-655	NAP		g1513174	66	87	9.00E-17	22	43	(U65488) fumocumarin-inducible cytochrome P450 [Papilio polyxenes]
20591	ENU04385	ANI61C1511:			NAP		g2113796	807	196	1.00E-57	59	54	(X94399) cAMP-dependent protein kinase catalytic subunit [Aspergillus niger]
20592	ENU04386	ANI61C6899:	222-240	531-552	NAP		g832882	351	116	1.00E-25	57	100	(L42454) EF-hand protein [Schizosaccharomyces pombe]
20593	ENU04387	ANI61C9048:			NAP		g3116134	882	219	2.00E-56	42	10	(AL023288) hypothetical protein [Schizosaccharomyces pombe]
20594	ENU04388	ANI61C2436:	35-54	632-651	NAP		g1078673	545	83	3.00E-34	60	22	gamma-adaptin - smut fungus (Ustilago maydis) [Ustilago maydis]
20595	ENU04389	ANI61C4421:	34-60	539-561	NAP		g2094863	306	171	3.00E-42	43	19	(Z95334) putative helicase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20596	ENU04390	ANI61C291:7	42-61	578-603	NAP		g2501165	134	79	2.00E-14	32	28	hypothetical 59.6 KD protein in DSK2-CAT8 intergenic region [Saccharomyces cerevisiae]
		480..6857											sterigmatocystin 7-O-methyltransferase precursor [Aspergillus parasiticus]
20597	ENU04391	ANI61C1032	70-88	516-536	NAP		g2498702	86	70	1.00E-11	37	31	(Z83319) similar to ABC transporters; cDNA EST EMBL:D67233 comes from this gene; cDNA EST EMBL:ID67486 comes from this gene; cDNA EST yk385d1.5 comes from this gene; cDNA EST yk398a5.5 comes from this gene; cDNA EST yk398a5.3 co...
		0:4040..4598											
20598	ENU04392	ANI61C1073:	71-90	579-598	NAP		g3879319	431	177	5.00E-44	44	29	
		1..662											
20599	ENU04393	ANI61C5507:	122-139	442-461	NAP		g2408049	136	46	0.0001	29	8	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
		3945..3369											"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
20600	ENU04394	ANI61C3342:	114-133	372-391	NAP		g731024	295	145	2.00E-34	46	38	elongation factor 1-alpha (EF-1-alpha) [Sulfolobus solfataricus]
		1..470											(AL023288) hypothetical dolichyl-phosphate beta-glucosyltransferase protein [Schizosaccharomyces pombe]
20601	ENU04395	ANI61C8781:	23-43	728-747	NAP		g729397	616	260	8.00E-69	41	64	hypothetical 23.9 KD protein in THI5-AGP3 intergenic region [Saccharomyces cerevisiae]
		1035..1											(U30376) Lipomyces kononenkoae subsp. spenceri
20602	ENU04396	ANI61C5009:	114-133	331-358	NAP		g3116140	276	124	2.00E-28	48	38	amylase [Lipomyces kononenkoae]
		1..392											hypothetical 85.4 KD protein C14C4.11 in chromosome I [Schizosaccharomyces pombe]
20603	ENU04397	ANI61S1051:	22-44	261-280	NAP		g1175960	223	97	9.00E-20	53	43	(L41834) nuclear protein [Ensis minor]
		298..604											hypothetical 54.9 KD protein in CBR5-NOT3 intergenic region [Saccharomyces cerevisiae]
20604	ENU04398	ANI61C8380:	22-47	394-414	NAP		g1173537	285	140	5.00E-33	42	28	
		2017..1526											
20605	ENU04399	ANI61C5287:	59-86	454-479	NAP		g3183344	276	105	2.00E-22	37	22	
		84..543											
20606	ENU04400	ANI61S1675:			NAP		g786117	180	51	0.00001	24	55	
		1..835											
20607	ENU04401	ANI61C6597:	52-71	805-829	NAP		g731799	405	129	2.00E-29	38	48	
		10548..9385											

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20608	ENU04402	ANT61C9383:	97-116	709-730	NAP		g586521	303	143	2.00E-33	36	29	hypothetical 86.4 KD protein in PHOS-VPS15 intergenic region
		6240..7174											[Saccharomyces cerevisiae]
20609	ENU04403	ANT61C1091	24-51	801-828	NAP		g3261632	498	116	3.00E-28	46	42	(Z79700) acdD2 [Mycobacterium tuberculosis]
		2:1357..1											"phosphoenolpyruvate synthase (pyruvate,water dikinase) (PEP synthase) [Synecocystis sp.]"
20610	ENU04404	ANT61C4623:	27-46	660-679	NAP		g2499460	1545	267	9.00E-76	54	33	(AB014886) typeII DNA topoisomerase [Emmericella nidulans]
		1815..1											sodium transport ATPase 5 [Saccharomyces cerevisiae]
20611	ENU04405	ANT61C1654:	25-52	726-744	NAP		g3172113	1585	522	e-148	97	16	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]
		1010..1											(AL008967) hypothetical protein Rv2750 [Mycobacterium tuberculosis]
20612	ENU04406	ANT61C1070	35-54	790-811	NAP		g3121791	701	162	2.00E-63	53	23	cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi]
20613	ENU04407	ANT61S1450:	7:639..1826		NAP		g3037018	302			36	97	(AL031907) putative cystine-rich transcriptional regulator
		850..174											[Schizosaccharomyces pombe]
20614	ENU04408	ANT61C5938:	264..1155		NAP		g2624272	56	69	3.00E-11	27	89	salivary proline-rich protein PO (allele M) (contains: peptide P-D) [Homo sapiens]
20615	ENU04409	ANT61C1002	22-48	808-829	NAP		g1706177	754	111	6.00E-24	29	27	"neutral trehalase (alpha,alpha-trehalase) (alpha,alpha-trehalose glucosylhydrolase) [Emmericella nidulans]"
20616	ENU04410	ANT61C3739:	29-48	756-781	NAP		g3766365	756	155	3.00E-37	39	23	abaA protein - Emmericella nidulans [Emmericella nidulans]
		1..1223											hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20617	ENU04411	ANT61S974:9	2..551		NAP		g1709793	151	60	0.000000	29	69	(AF036707) RAD6 [Candida albicans]
		1..2156											
20618	ENU04412	ANT61C8633:	25-52	802-829	NAP		g3929388	3438	221	e-140	99	35	hypothetical 58.1 KD protein in PET117-CEM1 intergenic region [Saccharomyces cerevisiae]
		1..2156											
20619	ENU04413	ANT61C7207:	2146..1628		NAP		g482275	661	266	5.00E-71	79	21	41-2 protein antigen precursor [Plasmodium falciparum]
20620	ENU04414	ANT61C3378:	28-49	723-749	NAP		g731689	578	164	7.00E-40	30	7	
		1304..1											
20621	ENU04415	ANT61C1036	39-58	390-413	NAP		g3273562	425	145	3.00E-34	81	59	
		0:514..1											
20622	ENU04416	ANT61C7198:	1588..1082		NAP		g1723597	318	136	1.00E-31	42	32	
		1588..1082											
20623	ENU04417	ANT61C7472:	26-53	310-329	NAP		g112925	127	71	7.00E-12	30	88	
		1962..1577											

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20624	ENU04418	AN161S4602:	90-108	530-547	NAP		g465511	359	136	2.00E-31	41	33	hypothetical 73.8 KD protein in SAS3-SEC17 intergenic region [Saccharomyces cerevisiae]
		665..1											allantoicase [Saccharomyces cerevisiae]
20625	ENU04419	AN161C3410:	110-137	804-827	NAP		g728828	496	219	3.00E-56	52	49	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
		2232..1354					g2408036	291	117	7.00E-26	35	50	carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56)
20626	ENU04420	AN161C2027:	171-190	347-366	NAP		g423793	75	58	0.000000	35	45	[Pseudomonas sp.]
		1..578								05			(X97346) FCYX [Saccharomyces cerevisiae]
20627	ENU04421	AN161C7678:	22-47	429-448	NAP		g1321944	224	54	0.000001	26	47	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
		7628..7174					g4218005	263	46	0.0002	27	36	"(AC004849) similar to several hypothetical proteins: U70849 (PID:g1572765), U00043 (PID:g470341), Z50070 (PID:g899462), AL033127 (PID:g3821335), and P40034 (PID:g731464) [Homo sapiens]" (AL034490) similar to yeast ngg1-interacting factor 3 [Schizosaccharomyces pombe]
20628	ENU04422	AN161C5312:	22-48	804-823	NAP		g3980554	227	110	6.00E-24	34	63	[Saccharomyces cerevisiae]
		1..1093											
20629	ENU04423	AN161S2268:			NAP								
		1..784											
20630	ENU04424	AN161S3044:	98-117	412-435	NAP								
		1..528											
20631	ENU04425	AN161C3082:	22-46	459-477	NAP		g4008560	215	88	5.00E-17	57	45	hypothetical 73.8 KD protein in SAS3-SEC17 intergenic region [Saccharomyces cerevisiae]
		366..833											
20632	ENU04426	AN161C5001:	90-109	717-736	NAP		g1705828	2423	530	e-150	99	26	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
		1459..1											
20633	ENU04427	AN161C8508:	23-50	804-829	NAP		g549725	520	189	2.00E-47			carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56)
		1020..2041											
20634	ENU04428	AN161C1064	22-41	805-829	NAP		g3493539	1740	431	e-120	99	69	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
		4:1..1254											
20635	ENU04429	AN161C7169:	43-62	626-653	NAP		g476807	365	87	8.00E-34	38	51	carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56)
		755..1											
20636	ENU04430	AN161C7108:	29-56	806-828	NAP		g2131329	388	87	8.00E-35	32	98	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
		2551..3462											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20637	ENU04431	ANT61C1554: 1480..1			NAP		g1351183	806	136	2.00E-44	43	38	"tyrosyl-TRNA synthetase, mitochondrial precursor (tyrosine--TRNA ligase) (TYRRS) [Neurospora crassa]"
20638	ENU04432	ANT61C9626: 22-41 2931..4989		792-814	NAP		g3702631	2007	406	e-113	68	36	(AL031824) protein transport protein sec23 homolog [Schizosaccharomyces pombe]
20639	ENU04433	ANT61S953: 6 14..1	182-204	567-593	NAP		g3647341	556	237	6.00E-62	58	21	(AL031644) RAD16 nucleotide excision repair protein homolog [Schizosaccharomyces pombe]
20640	ENU04434	ANT61C2676: 22-47 1204..1	712-739		NAP		g2654106	1074	201	4.00E-51	74	39	(AF034260) protein kinase NRC-2 [Neurospora crassa]
20641	ENU04435	ANT61C4833: 1060..1			NAP		g4027860	1541	242	e-125	92	38	(U47540) Tama [Emeticella nidulans]
20642	ENU04436	ANT61C5942: 38-57 1632..399	778-797		NAP		g3183172	874	124	2.00E-52	41	56	"probable threonyl-TRNA synthetase, mitochondrial precursor (threonine--TRNA ligase) (THRRS) [Schizosaccharomyces pombe]"
20643	ENU04437	ANT61C528: 6 22-49 252..8036	809-828		NAP		g2131739	572	107	1.00E-22	38	36	hypothetical protein YLR002c - yeast [Saccharomyces cerevisiae]
20644	ENU04438	ANT61C7264: 22-43 2976..1666	802-829		NAP		g3318897	725	158	4.00E-38	39	36	[Saccharomyces cerevisiae]
20645	ENU04439	ANT61C1397: 80-100 901..1	719-738		NAP		g3834343	1429	468	e-131	95	17	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum []" (X05204) atom polypeptide [Emeticella nidulans]
20646	ENU04440	ANT61C5143: 44-70 718..166	513-532		NAP		g1620896	620	251	2.00E-66	76	59	(D87956) protein involved in sexual development [Schizosaccharomyces pombe]
20647	ENU04441	ANT61C3620: 144-164 1549..1228	280-301		NAP		g4507229	238	104	2.00E-22	44	20	Succinic semialdehyde dehydrogenase [Homo sapiens]
20648	ENU04442	ANT61C6334: 22-44 4081..4982	722-749		NAP		g448109	216	101	7.00E-21	34	51	6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
20649	ENU04443	ANT61C3534: 27-46 3454..1931	799-826		NAP		g3722	498	69	3.00E-19	31	39	(X52633) GAP1 protein (AA 1-601) [Saccharomyces cerevisiae]
20650	ENU04444	ANT61C9310: 22-47 1086..2744	726-749		NAP		g114988	2453	480	e-135	95	22	kinesin-like protein BIMC [Emeticella nidulans]
20651	ENU04445	ANT61C5922: 1467..1			NAP		g3183348	408	136	2.00E-31	35	52	hypothetical 60.1 KD protein C23C11.06C in chromosome I [Schizosaccharomyces pombe]

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20652	ENU04446	AN161C6611:	121-140	409-428	NAP		g3451071	247	80	2.00E-16	45	20	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]
20653	ENU04447	1..516 AN161C6297:	26-49	711-730	NAP		g3451463	344	113	2.00E-32	34	57	(AL031349) hypothetical protein [Schizosaccharomyces pombe]
20654	ENU04448	2531..3687 AN161C1107	185-204	617-641	NAP		g3914212	470	188	5.00E-47	49	19	5-oxoprolinase (5-oxo-L-prolinase) (pyroglutaminase) (5-opase) [Rattus norvegicus]
20655	ENU04449	1:1..831 AN161C181:2	22-49	705-730	NAP		g1805251	198	104	1.00E-21	27	41	(U58946) transposase [Aspergillus awamori]
20656	ENU04450	89..1636 AN161C5884:			NAP		g340613	183	38	0.092	27	78	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
20657	ENU04451	2133..2763 AN161C4283:	27-54	450-469	NAP		g2330797	199	71	1.00E-17	37	62	(Z98601) zinc finger protein [Schizosaccharomyces pombe]
20658	ENU04452	12005..10799 AN161C1138:	22-49	804-829	NAP		g3882339	82	139	2.00E-32	33	18	(AB018352) KIAA0809 protein [Homo sapiens]
20659	ENU04453	542..1 AN161S3751:	36-59	467-486	NAP		g4454043	916	333	7.00E-91	97	28	(AL035394) putative receptor kinase [Arabidopsis thaliana]
20660	ENU04454	781..1 AN161C2071:	106-127	671-690	NAP		g731805	463	192	2.00E-48	45	26	SYG1 protein [Saccharomyces cerevisiae]
20661	ENU04455	684..1 AN161C2856:	118-138	628-655	NAP		g1806628	488	115	1.00E-51	49	50	(U79250) glycerol-3-phosphate dehydrogenase [Homo sapiens]
20662	ENU04456	1..434 AN161C6770:	102-122	392-413	NAP		g1708835	188	71	3.00E-12	40	48	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20663	ENU04457	557..1 AN161C2510:	43-62	416-437	NAP		g2313520	165	85	5.00E-16	30	45	(AE000557) cyclopropane fatty acid synthase (cfa) [Helicobacter pylori 26695]
20664	ENU04458	458..2116 AN161C910:2			NAP		g2330815	137	73	7.00E-13	41	36	(Z98602) purine nucleotide binding protein fe5 [Schizosaccharomyces pombe]
20665	ENU04459	1749..197 AN161C8051:	44-63	803-826	NAP		g586312	641	80	3.00E-21	33	43	hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region [Saccharomyces cerevisiae]

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20666	ENU04460	ANI61C2836: 653..1378			NAP		g1175939	331	86	1.00E-32	40	58	hypothetical 41.9 KD protein in HAC1-CAK1 intergenic region [Saccharomyces cerevisiae]
20667	ENU04461	ANI61C2759: 1..716			NAP		g2492763	395	141	8.00E-38	48	67	hypothetical oxidoreductase in MRP144-MTF1 intergenic region [Saccharomyces cerevisiae]
20668	ENU04462	ANI61C1083 5:3653..3984	30-49	282-301	NAP		g1483145	93	36	0.002	29	97	(D64008) Cytochrome b5 [Ascaris suum]
20669	ENU04463	ANI61C1020 8:1..3278	29-56	804-829	NAP		g1723687	754	129	2.00E-29			hypothetical 140.5 KD protein in CTT1-PRP31 intergenic region [Saccharomyces cerevisiae]
20670	ENU04464	ANI61C4296: 1465..856	203-222	465-484	NAP		g3242972	416	109	1.00E-23	54	25	(AF069523) heat shock protein Hsp88 [Neurospora crassa]
20671	ENU04465	ANI61C6540: 1520..2718	45-64	778-797	NAP		g3218400	425	145	2.00E-40	38	75	(AL023860) ser-thr protein kinase [Schizosaccharomyces pombe]
20672	ENU04466	ANI61C4932: 720..3626	22-46	801-828	NAP		g731882	293	101	9.00E-21			hypothetical 195.1 KD protein in DNA43-UBI1 intergenic region [Saccharomyces cerevisiae]
20673	ENU04467	ANI61C1926: 1987..1581	105-132	366-386	NAP		g3687497	168	66	2.00E-12	44	67	(AL031788) putative mitochondrial inner membrane protease subunit 2 [Schizosaccharomyces pombe]
20674	ENU04468	ANI61C8052: 755..2503	22-48	720-744	NAP		g4502323	585	168	6.00E-41	40	17	"ATPase, Cu++ transporting, beta polypeptide (Wilson disease) [Homo sapiens]"
20675	ENU04469	ANI61S1734: 1..854			NAP		g100687	405	37	0.16	41	74	hydroxyproline-rich glycoprotein - rice [Oryza sativa]
20676	ENU04470	ANI61C724:2 882..1	22-45	807-826	NAP		g2493965	2089	317	5.00E-86	58	20	xanthine dehydrogenase (purine hydroxylase J) [Emicella nidulans]
20677	ENU04471	ANI61C1117 1:1..795	110-129	683-706	NAP		g2668553	311	89	5.00E-26	33	18	(U62929) multidrug resistance protein 1 [Filobasidiella neoformans]
20678	ENU04472	ANI61C1823: 1..1738	22-48	748-767	NAP		g2342601	738	137	9.00E-32	29	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20679	ENU04473	ANI61C5324: 1589..1	43-62	722-741	NAP		g3043376	1653	240	e-100	75	42	(AJ005258) amyR [Aspergillus oryzae]

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20680	ENJU04474	ANI61C6771:	24-44	675-697	NAP		g3879362	341	116	1.00E-25	33	52	"(Z81113) similar to DnaI, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST yk447h4.5 comes from this gene; cDNA EST yk474e4.5 c... ["]
20681	ENJU04475	ANI61C1089	215-234	464-484	NAP		g3139137	800	308	7.00E-85	84	22	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
20682	ENJU04476	ANI61S4441:	554..1		NAP		g4835793	148	77	8.00E-14			"(AC007296) Similar to gb U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF00076 RNA recognition motif domains. ESTs gb T44278, gb K65195, gb N65904, gb H37499, gb R90487, gb N95952, gb T4427... ["]
20683	ENJU04477	ANI61C9025:	37-56	792-812	NAP		g3540219	1169	130	6.00E-59	49	22	(D87686) KIAA0017 protein [Homo sapiens]
20684	ENJU04478	ANI61S1996:	1337..1		NAP		g2135765	221	44	0.00002	35	8	"mucin 2 precursor, intestinal - human (fragments) ["]
20685	ENJU04479	ANI61C2726:	102-121	466-486	NAP		g1711467	277	122	2.00E-27	34	43	dibenzothiophene desulfurization enzyme A [Rhodococcus sp.]
20686	ENJU04480	ANI61S2694:	38-65	403-429	NAP		g1938424	285	122	1.00E-27	51	13	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
20687	ENJU04481	ANI61C7219:	2951..2457		NAP		g2624312	413	105	1.00E-40	53	40	(AL008967) lrp1 [Mycobacterium tuberculosis]
20688	ENJU04482	ANI61S4608:	209-228	362-386	NAP		g4884833	322	103	7.00E-27			(AF131877) amino-deoxyarabinheptulosonate-7-phosphate synthase [Streptomyces collinus]
20689	ENJU04483	ANI61C9107:	22-45	807-829	NAP		g4507813	185	82	7.00E-15			UDP-glucose dehydrogenase [Homo sapiens]
20690	ENJU04484	ANI61C4377:	30-51	583-610	NAP		g2132651	309	84	2.00E-26	32	35	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
20691	ENJU04485	ANI61S591:3	41..767		NAP		g501027	147	31	4.6	33	99	(U01849) ORF2 [Trypanosoma brucei]

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20692	ENU04486	ANI61C7389:	22-45	636-663	NAP		g2133317	1829	407	e-113	67	38	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 78K chain precursor - Neurospora crassa [Neurospora crassa] (AL021925) hypothetical protein Rv2263 [Mycobacterium tuberculosis] serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) [Schizosaccharomyces pombe]
20693	ENU04487	ANI61C2578:	26-45	809-829	NAP		g2909569	118	40	0.000003			
20694	ENU04488	ANI61C8776:	26-45	795-815	NAP		g1346422	1459	317	8.00E-86	60	46	
20695	ENU04489	ANI61C510:1	24-46	777-796	NAP		g1730738	805	85	2.00E-19	38	35	actin-like protein ARP5 [Saccharomyces cerevisiae]
20696	ENU04490	ANI61C1122			NAP		g2239223	347	77	2.00E-13	40	98	(Z97210) hypothetical protein [Schizosaccharomyces pombe]
20697	ENU04491	ANI61C3235:	33-52	755-780	NAP		g114971	983	96	1.00E-36	34	32	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]
20698	ENU04492	ANI61C415:2	22-49	615-642	NAP		g1706177	186	62	1.00E-13	34	21	cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi] (Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis]
20699	ENU04493	ANI61S851:7			NAP		g2633966	304	102	3.00E-21	35	20	hypothetical 81.8 KD protein in YPT52-DBP7 intergenic region [Saccharomyces cerevisiae]
20700	ENU04494	ANI61C3482:	22-45	648-669	NAP		g549770	377	79	3.00E-22			translation initiation factor EIF-2B alpha subunit (EIF-2B GDP-GTP exchange factor) (guanine nucleotide exchange factor subunit GCN3) (GCD complex subunit GCN3) (transcriptional activator GCN3) [Saccharomyces cerevisiae]
20701	ENU04495	ANI61C7:378	54-73	804-829	NAP		g121065	548	196	2.00E-49			(AJ007564) Slx2 [Yarrowia lipolytica]
20702	ENU04496	ANI61C8363:	41-61	712-735	NAP		g3820457	817	214	7.00E-55	47	27	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20703	ENU04497	ANI61S1437:	47-66	307-326	NAP		g3885836	265	96	2.00E-19	39	28	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["] (AC000133) ORF [Emmericella nidulans]
20704	ENU04498	ANI61C4370:	37-56	655-679	NAP		g3318897	362	138	7.00E-32	44	31	
20705	ENU04499	ANI61C1120	25-51	510-529	NAP		g1870215	1027	291	2.00E-78	95	53	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20706	ENU04500	ANI61C1014	37-56	718-739	NAP		g2342601	827	286	2.00E-76	53	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20707	ENU04501	ANI61C443:1	26-50	567-586	NAP		g3834343	1013	394	e-109	98	13	(X05204) arom polypeptide [Emericella nidulans]
20708	ENU04502	ANI61C5958: 614..1100	59-78	457-479	NAP		g1293655	410	178	3.00E-44	55	25	(U51327) versicolorin B synthase [Aspergillus parasiticus]
20709	ENU04503	ANI61C7613: 1814..2650	32-51	706-725	NAP		g730506	101	95	7.00E-19	22	63	nuclear division RFT1 protein [Kluveromyces lactis]
20710	ENU04504	ANI61C1839: 13..658	24-47	592-612	NAP		g3608397	83	68	5.00E-11	32	52	(AF071085) putative dTDP-4-keto-L-rhamnose reductase [Enterococcus faecalis]
20711	ENU04505	ANI61C5791: 587..1	58-84	531-550	NAP		g1293655	292	125	3.00E-28	41	29	(U51327) versicolorin B synthase [Aspergillus parasiticus]
20712	ENU04506	ANI61C262:4	54-73	798-820	NAP		g710551	282	76	6.00E-18	29	15	(L40632) ankyrin 3 [Mus musculus]
20713	ENU04507	ANI61C7276: 3527..4344			NAP		g1708836	255	136	2.00E-31	35	98	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilitis]"
20714	ENU04508	ANI61C1144	61-80	514-538	NAP		g2811058	369	139	1.00E-32	42	51	hypothetical 39.5 KD protein in SIGZ-CSN intergenic region [Bacillus subtilis]
20715	ENU04509	ANI61C1164: 493..1695	22-45	803-829	NAP		g131769	1624	320	7.00E-87	97	70	QUTG protein []
20716	ENU04510	ANI61C1065	30-51	719-738	NAP		g3810843	2437	274	5.00E-73	65	25	"(AL032684) putative yeast cell division control protein 68 homolog, putative transcriptional activator [Schizosaccharomyces pombe]"
20717	ENU04511	ANI61S3760: 1..597	26-45	515-534	NAP		g3319372	547	133	1.00E-30	52	17	"(AF077409) similar to reverse transcriptases (PFam: rvt_hmm, score: 60.13) [Arabidopsis thaliana]"
20718	ENU04512	ANI61C7330: 1..2372	69-88	791-810	NAP		g114967	1244	227	7.00E-59	45	33	beta-glucosidase (gentibiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Agrobacterium tumefaciens]
20719	ENU04513	ANI61C8930: 1243..1956	26-45	483-502	NAP		g3395586	234	113	1.00E-24	42	29	(AL031179) similarity to phosphomannomutases [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20720	ENU04514	AN161C1385: 1258..1	22-42	704-731	NAP		g2467275	484	143	1.00E-33	32	56	(Z99759) serine/threonine-protein kinase [Schizosaccharomyces pombe] (AL033389) putative allantoin permease [Schizosaccharomyces pombe]
20721	ENU04515	AN161C1019: 9:2148..1067	25-52	792-816	NAP		g3850093	138	48	0.00006	30	42	
20722	ENU04516	AN161C1039: 7:1265..1	70-89	618-637	NAP		g1711561	582	126	2.00E-28	39	45	sugar transporter STL1 [Saccharomyces cerevisiae]
20723	ENU04517	AN161C7331: 4557..3583	24-43	764-783	NAP		g127568	298	124	9.00E-28	31	86	interferon-induced GTP-binding protein MX [Perca fluviatilis]
20724	ENU04518	AN161C8161: 4359..7310	22-46	721-740	NAP		g731689	1445	313	9.00E-85	51	7	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae] (V00650) URF 1 [Emmericella nidulans]
20725	ENU04519	AN161C1040: 5:4687..4196			NAP		g12688	626	182	1.00E-58	89	46	
20726	ENU04520	AN161C9790: 1..3423	29-56	802-829	NAP		g731871	1132	153	1.00E-36	32	11	hypothetical 269.9 KD protein in FKHI-MET18 intergenic region [Saccharomyces cerevisiae] (AL031854) hypothetical protein [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe] (AL022537) putative protein [Arabidopsis thaliana] (AL023706) hypothetical protein [Schizosaccharomyces pombe]
20727	ENU04521	AN161C1128: 5:1107..1	23-43	725-747	NAP		g3738194	664	153	1.00E-46	42	40	
20728	ENU04522	AN161C5443: 2914..1767	27-54	804-824	NAP		g2342601	618	206	2.00E-52	40	5	
20729	ENU04523	AN161C1558: 180..1075	22-48	805-829	NAP		g2388903	671	229	2.00E-59	53	49	
20730	ENU04524	AN161C6309: 1351..2378	52-71	770-788	NAP		g3063700	160	78	5.00E-15	32	15	
20731	ENU04525	AN161C5366: 147..1179	22-40	657-676	NAP		g3169096	785	204	6.00E-52	46	46	
20732	ENU04526	AN161C7102: 1002..1648	72-93	604-626	NAP		g1942383	154	82	3.00E-15	40	31	
20733	ENU04527	AN161S4490: 153..507	213-231	356-375	NAP		g1244642	89	51	0.000005	32	43	
20734	ENU04528	AN161C9993: 1511..3934	27-46	801-828	NAP		g1175408	612	34	0.033			
20735	ENU04529	AN161C4851: 1350..2018	59-78	602-626	NAP		g3550602	257	118	5.00E-26	36	22	

(Z99759) serine/threonine-protein kinase [Schizosaccharomyces pombe] (AL033389) putative allantoin permease [Schizosaccharomyces pombe]

sugar transporter STL1 [Saccharomyces cerevisiae]

interferon-induced GTP-binding protein MX [Perca fluviatilis]

hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae] (V00650) URF 1 [Emmericella nidulans]

hypothetical 269.9 KD protein in FKHI-MET18 intergenic region [Saccharomyces cerevisiae] (AL031854) hypothetical protein [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe] (AL022537) putative protein [Arabidopsis thaliana] (AL023706) hypothetical protein [Schizosaccharomyces pombe]

[Schizosaccharomyces pombe]

Human 17-Beta-Hydroxysteroid-Dehydrogenase Type 1 Complexed With 17-Beta-Estradiol [] (U40374) aminoglycoside 3'-phosphotransferase [Cloning vector pMH30]

hypothetical 107.3 KD TRP-ASP repeats containing protein C31A2.14 in chromosome I [Schizosaccharomyces pombe] (AJ006710) phosphatidylinositol 3-kinase [Rattus norvegicus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20736	ENU04530	ANI61C3177:	23-48	770-789	NAP		g3914053	2015	426	e-119	76	30	DNA mismatch repair protein MSH2 [Neurospora crassa]
20737	ENU04531	1..1604 ANI61C1056:	35-55	531-558	NAP		g2501152	291	134	4.00E-31	48	33	threonine synthase [Schizosaccharomyces pombe]
20738	ENU04532	1..580 ANI61S4655:			NAP		g2131314	127	41	0.000000	37	37	hypothetical protein YD8142A.01 - yeast (Saccharomyces cerevisiae) (fragment) []
20739	ENU04533	ANI61C1355:	22-48	303-324	NAP		g1870215	851	342	9.00E-94	99	46	(AC000133) ORF [Emmericella nidulans]
20740	ENU04534	500..1 ANI61C5665:	22-48	805-824	NAP		g3150253	819	176	9.00E-52	42	24	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
20741	ENU04535	1..1756 ANI61C3240:	54-73	521-540	NAP		g120625	456	180	7.00E-45	60	100	G10 protein [Xenopus laevis]
20742	ENU04536	3384..3956 ANI61S3332:	47-67	198-223	NAP		g1706202	269	100	3.00E-21	54	47	cutinase precursor (L1) [Aspergillus oryzae]
20743	ENU04537	1..306 ANI61C9348:	122-143	333-359	NAP		g2911462	398	107	2.00E-37	73	17	(AF046923) serine/threonine protein kinase [Colletotrichum trifolii]
20744	ENU04538	1..380 ANI61C4409:	22-49	765-784	NAP		g4176523	341	104	6.00E-22	29	45	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
20745	ENU04539	813..2276 ANI61C9831:	22-44	623-642	NAP		g3581903	480	124	9.00E-28	35	38	(AL031545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20746	ENU04540	1646..1 ANI61C7608:	37-61	724-749	NAP		g4102980	121	42	0.005	20	49	(AF019082) virulent strain associated lipoprotein [Borrelia burgdorferi]
20747	ENU04541	884..1 ANI61C1617:	22-49	454-479	NAP		g464991	142	80	8.00E-15	40	43	ubiquitin carboxyl-terminal hydrolase YUHI (ubiquitin thioesterase) [Saccharomyces cerevisiae]
20748	ENU04542	1230..1561 ANI61C8017:	39-66	424-446	NAP		g4758430	256	93	1.00E-24			geranylgeranyl diphosphate synthase [Homo sapiens]
20749	ENU04543	547..1 ANI61C4194:	22-45	374-393	NAP		g1168953	76	54	0.000000	32	37	citrate lyase beta chain (citrate) (citryl-CoA lyase subunit) [Klebsiella pneumoniae]
20750	ENU04544	2114..2587 ANI61S2295:			NAP		g100753	167	46	0.000000	36	66	hydroxyproline-rich glycoprotein - sorghum [Sorghum bicolor]
20751	ENU04545	1..567 ANI61C7450:	23-44	807-829	NAP		g1256839	868	191	4.00E-73	63	52	(U53329) Ran1-like protein kinase [Fusarium solani f. sp. pisi]
20752	ENU04546	1431..2454 ANI61C3751:	68-87	416-435	NAP		g4902874	112	48	0.00004			"(AJ242575) oxide-reductase enzyme, putative [Sinorhizobium meliloti]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20753	ENJU04547	AN161C1853:	25-52	411-438	NAP		g3914278	264	122	1.00E-27	55	34	pectate lyase B precursor [Glomerella cingulata]
20754	ENJU04548	AN161C5321: 1.459 1554..2523	22-49	805-829	NAP		g3183173	591	187	6.00E-48	52	53	"seryl-TRNA synthetase, cytoplasmic (serine--TRNA ligase) (SERRS) [Schizosaccharomyces pombe]"
20755	ENJU04549	AN161C1011 6:1..710	24-47	481-499	NAP		g1834342	1043	248	e-106	92	15	(Z68905) ATP-binding cassette multidrug transporter [Emmericella nidulans]
20756	ENJU04550	AN161C1045 1:7120..8069			NAP		g3560208	274	95	7.00E-19	33	34	(AL031536) putative transcription factor of the GCS1-GLO3-SPS18 family [Schizosaccharomyces pombe]
20757	ENJU04551	AN161C2588: 748..1	22-49	628-647	NAP		g130117	815	218	3.00E-79	69	39	phosphate-repressible phosphate permease [Neurospora crassa]
20758	ENJU04552	AN161C5294: 996..455	22-46	498-521	NAP		g2501434	162	103	2.00E-22	30	92	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]
20759	ENJU04553	AN161C6129: 423..856	72-99	412-431	NAP		g730443	80	47	0.000000	34	70	quinone oxidoreductase (NADPH:quinone reductase) (zeta-crystallin homolog protein) []
20760	ENJU04554	AN161C1614: 1643..72	56-75	777-796	NAP		g3646379	1450	199	8.00E-95	75	42	(AJ001540) phenylacetyl-CoA ligase [Penicillium chrysogenum]
20761	ENJU04555	AN161C5779: 4080..7040	71-90	773-799	NAP		g2443355	723	108	4.00E-23			(AB003395) ent-Kaurene synthase [Phaeosphaeria sp. L487]
20762	ENJU04556	AN161C1114 1:866..1	23-42	788-815	NAP		g2625138	224	116	1.00E-25	34	14	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
20763	ENJU04557	AN161C7681: 1..2435	22-49	757-780	NAP		g1817584	917	117	8.00E-26	28	19	(Y08991) adaptor protein [Homo sapiens]
20764	ENJU04558	AN161C1919: 860..1	221-240	765-784	NAP		g4165293	962	341	2.00E-99	71	28	(X58824) cdc21 protein [Schizosaccharomyces pombe]
20765	ENJU04559	AN161C1065 5:930..1	26-45	767-786	NAP		g1346521	1027	317	8.00E-86	78	62	S-adenosylmethionine synthetase (methionine adenosyltransferase) (ADOMET synthetase) [Neurospora crassa]
20766	ENJU04560	AN161C2670: 1204..1	101-120	610-631	NAP		g604369	928	215	6.00E-70	53	34	(U17857) hMLH1 gene product [Homo sapiens]
20767	ENJU04561	AN161C4238: 1645..2569	22-42	772-793	NAP		g3023682	998	332	9.00E-94	79	30	elongation factor 2 (EF-2) [Candida albicans]

Sequence Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20768	ENU04562	ANI61S2955: 1..531			NAP		g4218005	140	43	0.002	25	25	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20769	ENU04563	ANI61C1957: 422..1763	22-41	771-795	NAP		g461623	1173	92	2.00E-36	68	21	beta-galactosidase precursor (lactase) [Aspergillus niger]
20770	ENU04564	ANI61S3141: 666..1	182-209	612-631	NAP		g2062165	797	330	6.00E-90	87	38	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
20771	ENU04565	ANI61C3056: 3300..1880	33-60	801-820	NAP		g3850089	772	183	6.00E-61	52	62	(AL033389) putative yeast cell division cycle CDC50 homolog
20772	ENU04566	ANI61C8012: 5408..4491	22-45	810-829	NAP		g2842699	518	173	2.00E-42	54	43	[Schizosaccharomyces pombe] putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
20773	ENU04567	ANI61S3854: 586..90	168-193	399-418	NAP		g3417425	202	53	5.00E-14	36	50	(AL031261) conserved hypothetical protein [Schizosaccharomyces pombe]
20774	ENU04568	ANI61C1100: 0:8321..9087	33-53	598-622	NAP		g643443	769	225	1.00E-78	72	39	(U08104) PHOG [Penicillium chrysogenum]
20775	ENU04569	ANI61C1131: 8:1..839	103-120	795-817	NAP		g1723773	335	144	7.00E-34	36	39	hypothetical 81.2 KD protein in MIES1-FOL2 intergenic region [Saccharomyces cerevisiae]
20776	ENU04570	ANI61S2538: 671..1	220-247	585-605	NAP		g1723448	242	120	1.00E-26	43	31	hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]
20777	ENU04571	ANI61C5097: 525..1	97-118	482-503	NAP		g2370479	146	71	7.00E-12	29	21	(Z98849) putative centromere protein [Schizosaccharomyces pombe]
20778	ENU04572	ANI61C2309: 1195..1	22-46	762-780	NAP		g544368	215	75	4.00E-14	29	51	galactose-proton symport (galactose transporter) [Escherichia coli]
20779	ENU04573	ANI61C9634: 642..1942	22-46	810-829	NAP		g2661622	640	145	4.00E-46	48	65	(AL009197) hypothetical protein phosphatase [Schizosaccharomyces pombe]
20780	ENU04574	ANI61C9830: 1643..363	33-52	683-702	NAP		g1729868	1503	367	e-101	72	53	"probable T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta) [Schizosaccharomyces pombe]"
20781	ENU04575	ANI61S3302: 567..1	180-207	443-470	NAP		g1397290	139	44	4.00E-11	47	67	(U61949) Similar to cytidine deaminase. [Caenorhabditis elegans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20782	ENU04576	AN161C3245:	22-42	709-735	NAP		g2342601	1176	183	1.00E-45	35	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20783	ENU04577	AN161C7535:	2557..1		NAP		g4481947	211	65	4.00E-21	36	99	(AL035637) hypothetical protein. [Schizosaccharomyces pombe]
20784	ENU04578	AN161C1091	33-52	784-803	NAP		g4454039	482	169	2.00E-41	47	31	(AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
20785	ENU04579	AN161C6944:	38-57	781-803	NAP		g3777495	1275	284	7.00E-76	65	27	(U92083) calcium transporting ATPase [Pichia angusta]
20786	ENU04580	AN161C7384:	23-46	704-729	NAP		g128397	962	334	3.00E-91	99	100	nuclear movement protein NUDC [Emmericella nidulans]
20787	ENU04581	AN161C7182:	3181..3930		NAP		g1870209	235	74	8.00E-13	46	30	(AC000133) ORF [Emmericella nidulans]
20788	ENU04582	AN161C1122	27-54	761-780	NAP		g4836423	138	34	1.4			(AF119670) integral membrane protein [Magnaporthe grisea]
20789	ENU04583	AN161C7682:	78-105	749-776	NAP		g4164428	473	205	5.00E-52	49	19	(AL035247) putative pre-mrna splicing factor ma helicase [Schizosaccharomyces pombe]
20790	ENU04584	AN161C8016:	22-44	767-794	NAP		g3901117	970	135	2.00E-44	38	45	(AJ012752) maltose permease [Saccharomyces cerevisiae]
20791	ENU04585	AN161C1556:	66-85	772-791	NAP		g1723187	505	80	3.00E-14	41	24	112.3 KD protein in PYK1-SNCl intergenic region [Saccharomyces cerevisiae]
20792	ENU04586	AN161C5421:	118-137	528-546	NAP		g1805262	336	147	6.00E-35	35	10	"(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
20793	ENU04587	AN161C6728:	85-111	630-649	NAP		g418345	129	72	4.00E-12	39	46	probable methionyl-TRNA formyltransferase precursor [Saccharomyces cerevisiae]
20794	ENU04588	AN161C5679:	22-47	723-742	NAP		g189036	121	71	1.00E-11	19	20	(M31013) nonmuscle myosin heavy chain (NMHC) [Homo sapiens]
20795	ENU04589	AN161C2763:	55-74	307-331	NAP		g3264834	279	118	2.00E-26	44	33	(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermiis]
20796	ENU04590	AN161C7721:	23-44	803-829	NAP		g2673947	287	98	1.00E-22	31	20	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
20797	ENU04591	AN161C1672:	23-50	430-449	NAP		g3859681	485	128	2.00E-49	50	60	(AL033503) transcription regulatory protein [Candida albicans]
20798	ENU04592	AN161C9504:	49-72	480-504	NAP		g465847	336	83	4.00E-33			hypothetical 66.5 KD protein F02A9.5 in chromosome III []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20799	ENU04593	ANI61C9338:	22-45	711-737	NAP		g2276359	1861	273	1.00E-72	38	11	(Z97992) putative phosphatidylinositol 3-kinase [Schizosaccharomyces pombe]
20800	ENU04594	ANI61C6660:	45-64	453-477	NAP		g42931	138	131	3.00E-30	31	100	(X56175) ORF 2 (AA 1 - 109) [Escherichia coli]
20801	ENU04595	ANI61C9395:	106-128	389-414	NAP		g1709760	271	87	1.00E-21	50	47	putative proteasome component PRE6 (macropain subunit) (multicatalytic endopeptidase complex subunit) [Schizosaccharomyces pombe]
20802	ENU04596	ANI61C6006:	22-43	709-736	NAP		g1255430	348	125	4.00E-28	37	71	(U53155) No definition line found [Caenorhabditis elegans]
20803	ENU04597	ANI61C7769:			NAP		g3873958	152	92	6.00E-18	26	79	(Z81458) similar to transposable element [Caenorhabditis elegans]
20804	ENU04598	ANI61C4415:	22-44	698-720	NAP		g4506221	665	60	2.00E-31	40	50	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 [Homo sapiens]"
20805	ENU04599	ANI61C5780:	23-47	518-545	NAP		g2501434	521	125	3.00E-53	63	100	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]
20806	ENU04600	ANI61C7849:	30-57	712-731	NAP		g3947746	527	220	1.00E-56	56	29	(AJ009960) DNA photolyase [Trichoderma harzianum]
20807	ENU04601	ANI61C7563:	31-50	334-360	NAP		g3309657	372	159	1.00E-38	60	15	(AF074944) RRM3/PIF1 helicase homolog [Schizosaccharomyces pombe]
20808	ENU04602	ANI61C1080	25-44	774-794	NAP		g102827	63	72	4.00E-12			alpha-latrotoxin precursor - black widow spider [Latrodectus tredecimguttatus]
20809	ENU04603	ANI61C6782:	26-45	778-805	NAP		g731421	377	98	2.00E-34	38	47	hypothetical 53.3 KD protein in HXT8-CAN1 intergenic region [Saccharomyces cerevisiae]
20810	ENU04604	ANI61C4065:	218-238	385-406	NAP		g1723643	217	78	4.00E-20	41	33	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region [Saccharomyces cerevisiae]
20811	ENU04605	ANI61C5853:	22-45	807-826	NAP		g3738190	706	196	2.00E-49	43	82	(AL031854) putative ras related GTP-binding protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20812	ENU04606	ANI61C1054	39-56	724-746	NAP		g2956769	1614	169	9.00E-60	54	21	(AL022103) phosphatidylinositol phosphate phosphatase; synaptojanin-like [Schizosaccharomyces pombe]
20813	ENU04607	ANI61C7324: 4754..5464	50-69	670-690	NAP		g2408075	436	188	4.00E-47	41	98	(Z99167) hypothetical conserved protein [Schizosaccharomyces pombe]
20814	ENU04608	ANI61C2440: 1..643	186-213	589-608	NAP		g2132014	175	92	3.00E-18	37	39	hypothetical protein YOL124c - yeast [Saccharomyces cerevisiae]
20815	ENU04609	ANI61S1755: 1..588			NAP		g3413504	91	44	0.0007	22	4	[Saccharomyces cerevisiae] (Y16563) Bassoon [Rattus norvegicus]
20816	ENU04610	ANI61C4426: 844..1	41-64	717-743	NAP		g2147805	319	161	5.00E-39	36	33	NarB protein - Oscillatoria chalybea [Oscillatoria chalybea]
20817	ENU04611	ANI61C3356: 976..1	27-48	723-749	NAP		g1708850	222	93	3.00E-18	38	34	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae]
20818	ENU04612	ANI61C4165: 3186..2199	28-47	774-793	NAP		g417318	589	185	3.00E-46	44	59	MSS51 protein [Saccharomyces cerevisiae]
20819	ENU04613	ANI61C1138 1:971..1478	27-46	398-416	NAP		g1172568	198	80	6.00E-17	48	73	low molecular weight phosphotyrosine protein phosphatase (low molecular weight cytosolic acid phosphatase) (PTPASE) (small tyrosine phosphatase) [Schizosaccharomyces pombe]
20820	ENU04614	ANI61C5427: 1940..1520	209-228	366-385	NAP		g1549231	121	38	0.000003	31	18	(D50497) chloride channel (ClC-5) [Rattus rattus]
20821	ENU04615	ANI61C1005 7:2999..584	23-47	800-822	NAP		g2132992	242	86	3.00E-16	27	25	probable membrane protein YPL183c - yeast [Saccharomyces cerevisiae]
20822	ENU04616	ANI61C1355: 2053..2529	203-222	459-478	NAP		g1870229	817	300	3.00E-81	97	100	[Saccharomyces cerevisiae] (AC000133) ORF [Emmericella nidulans]
20823	ENU04617	ANI61C5998: 7885..4728	22-42	802-821	NAP		g1166378	525	86	3.00E-16			"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" (U58946) transposase [Aspergillus awamori]
20824	ENU04618	ANI61C1102 6:1..629	107-127	506-527	NAP		g1805251	250	120	9.00E-27	35	37	(AJ001421) Rer1 protein [Homo sapiens]
20825	ENU04619	ANI61C7487: 243..1014	22-43	713-740	NAP		g2385369	466	146	9.00E-41	53	98	(U20323) ankyrin-like protein [Saccharomyces cerevisiae]
20826	ENU04620	ANI61C2085: 952..441	22-48	460-479	NAP		g665573	64	44	0.0006	31	98	emniatin synthetase - fungus (Fusarium scirpi) [Fusarium scirpi]
20827	ENU04621	ANI61C3624: 5678..1	35-54	630-649	NAP		g481866	2935	223	8.00E-62	44	8	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20828	ENJU04622	ANI61C4110:	73-100	295-317	NAP		g2130022	117	66	1.00E-10	35	37	aldose reductase homolog - wild oat [Avena fatua]
20829	ENJU04623	ANI61C3096:	23-43	777-800	NAP		g2132857	116	41	0.014			probable membrane protein YOL158c - yeast [Saccharomyces cerevisiae]
20830	ENJU04624	ANI61C5542:	22-49	429-454	NAP		g137024	321	116	1.00E-25			[Saccharomyces cerevisiae] uridylylate kinase (UK) (uridine monophosphate kinase) (UMP kinase) [Saccharomyces cerevisiae]
20831	ENJU04625	ANI61C3542:	42-61	803-829	NAP		g2499558	386	120	1.00E-26			hypothetical 84.2 KD protein SLR0473 [Synecocystis sp.]
20832	ENJU04626	ANI61C2155:	27-46	722-741	NAP		g1084969	1548	399	e-129	97	42	sulfate adenylyltransferase (EC 2.7.7.4) - Emericella nidulans [Emericella nidulans]
20833	ENJU04627	ANI61C5633:	102-129	586-612	NAP		g3929349	659	244	4.00E-64	54	47	C-14 sterol reductase (sterol C14-reductase) [Nectria haematococca]
20834	ENJU04628	ANI61S4409:	29-56	272-295	NAP		g3549662	558	230	3.00E-60	96	23	(AL031394) hypothetical protein [Arabidopsis thaliana]
20835	ENJU04629	ANI61C681:	6 22-45	525-552	NAP		g2132903	385	174	6.00E-43	55	23	probable membrane protein YOR165w - yeast [Saccharomyces cerevisiae]
20836	ENJU04630	ANI61C6221:	41-62	407-434	NAP		g115689	306	132	2.00E-30	60	38	[Saccharomyces cerevisiae] nuclear protein SNF4 (regulatory protein CAT3) [Saccharomyces cerevisiae]
20837	ENJU04631	ANI61C4344:	22-46	790-809	NAP		g2104447	961	169	2.00E-41	39	47	(Z95396) heat shock protein 70 homolog [Schizosaccharomyces pombe]
20838	ENJU04632	ANI61C9952:	219-245	614-639	NAP		g2507475	595	242	3.00E-63	46	16	paired amphipathic helix protein [Saccharomyces cerevisiae] (U34998) Rad9 [Coprinus cinereus]
20839	ENJU04633	ANI61C5160:	68-87	784-803	NAP		g13533390	167	68	1.00E-10			meiotic recombination protein REC14 [Schizosaccharomyces pombe]
20840	ENJU04634	ANI61C4215:	22-45	807-829	NAP		g2498838	508	78	2.00E-42	47	72	hypothetical 20.9 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20841	ENJU04635	ANI61C6750:			NAP		g731690	152	87	9.00E-17	40	100	RAS suppressor protein 1 (RSU-1) (RSP-1 protein) (RSP-1) [Homo sapiens]
20842	ENJU04636	ANI61C8558:	28-47	455-479	NAP		g2498866	84	58	0.000000	37	36	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20843	ENU04637	AN161C9157: 26-45	537-556		NAP		g4027860	858	194	6.00E-49	98	24	(U47540) Tama [Emericella nidulans]
20844	ENU04638	AN161C8418: 1549..1857			NAP		g122094	461	157	5.00E-38	92	83	histone H4.2 [Emericella nidulans]
20845	ENU04639	AN161C1129 7:1..1664	96-119	725-749	NAP		g1546072	707	148	5.00E-35	35	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
20846	ENU04640	AN161C1103 4:3908..5575	23-50	793-820	NAP		g3656	447	118	4.00E-26	28	53	(X55713) putative cytochrome P450 [Saccharomyces cerevisiae]
20847	ENU04641	AN161C1269: 3063..1220	22-46	804-829	NAP		g2196560	165	32	4			(AB004690) Mif6 [Schizosaccharomyces pombe]
20848	ENU04642	AN161C4393: 1..785	72-91	742-759	NAP		g120777	660	257	6.00E-68	50	53	succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
20849	ENU04643	AN161C3785: 1270..1	24-51	724-749	NAP		g2226061	716	226	1.00E-58	46	51	(AF005040) folypolyglutamate synthetase; PPGS [Neurospora crassa]
20850	ENU04644	AN161C8146: 469..1	102-124	454-479	NAP		g1749638	387	157	5.00E-38	62	53	"(D89215) similar to Saccharomyces cerevisiae transaldolase, SWISS-PROT Accession Number P15019 [Schizosaccharomyces pombe]"
20851	ENU04645	AN161C3784: 637..1	47-66	509-533	NAP		g2326237	60	66	1.00E-17	26	63	(AC004684) putative ribitol dehydrogenase [Arabidopsis thaliana]
20852	ENU04646	AN161C8433: 1..377	24-43	332-356	NAP		g1172766	328	146	8.00E-35			adenylosuccinate synthetase (IMP--aspartate ligase) [Saccharomyces cerevisiae]
20853	ENU04647	AN161C8966: 5392..6501	44-63	711-730	NAP		g2132445	435	86	3.00E-16	40	27	probable membrane protein YDL148c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
20854	ENU04648	AN161C9765: 1..1767	29-48	775-798	NAP		g1723249	2140	257	e-103	67	23	hypothetical 137.2 KD protein C27F1.09C in chromosome I [Schizosaccharomyces pombe]
20855	ENU04649	AN161C5247: 3740..5201	40-59	667-686	NAP		g2499017	1022	173	7.00E-64	49	49	"alpha.alpha-trehalose-phosphate synthase (UDP-forming) 1 (trehalose-6-phosphate synthase) (UDP-glucose-glucosephosphate glucosyltransferase) [Aspergillus niger]"
20856	ENU04650	AN161C1061 8:121..892	22-48	725-751	NAP		g4154667	126	48	0.000000	29	71	(AE001454) fructose-BISphosphate aldolase [Helicobacter pylori 199]
20857	ENU04651	AN161C388:9 35..1	22-44	672-691	NAP		g757832	187	69	2.00E-16	30	44	(Z37980) hypothetical 4-hydroxyphenylacetate permease [Escherichia coli]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20858	ENJU04652	ANI61S3598:			NAP		g3913423	356	95	4.00E-19	48	59	S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC)
		1..644											(SAMDC) [Nicotiana tabacum]
20859	ENJU04653	ANI61C9728:	67-86	788-807	NAP		g135503	1230	438	e-122	93	58	tubulin gamma chain [Emmericella nidulans]
		1..897											putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emmericella nidulans]
20860	ENJU04654	ANI61C7518:	28-47	729-748	NAP		g2492661	2917	579	e-165	96	12	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
		373..2142											pyruvate decarboxylase [Emmericella nidulans]
20861	ENJU04655	ANI61S1593:			NAP		g283032	141	34	0.002	29	55	2-deoxy-D-glucuronate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Bacillus subtilis]
		1..606											"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"
20862	ENJU04656	ANI61S51:1..556			NAP		g2501326	555	212	6.00E-55	72	29	(AL031907) conserved hypothetical protein [Schizosaccharomyces pombe]
20863	ENJU04657	ANI61C1227:	22-49	806-827	NAP		g1730031	511	190	1.00E-47	50	98	(AE000934) unknown [Methanobacterium thermoautotrophicum]
		1831..968											"(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana]"
20864	ENJU04658	ANI61C5694:	102-129	667-692	NAP		g1169440	1343	531	e-150	97	6	(AC000133) ORF [Emmericella nidulans]
		1..808											sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei) []
20865	ENJU04659	ANI61C5170:	51-71	710-732	NAP		g3766378	225	52	6.00E-10	42	100	"hydroxyquinol 1,2-dioxygenase - Pseudomonas cepacia [Burkholderia cepacia]"
		1373..621											(AL021838) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
20866	ENJU04660	ANI61C9574:	23-50	449-468	NAP		g2622925	91	66	2.00E-10	28	67	
		1187..1572											
20867	ENJU04661	ANI61C3829:	34-60	443-466	NAP		g4115913	129	82	1.00E-19	34	41	
		1..498											
20868	ENJU04662	ANI61C1010			NAP		g1870209	414	106	2.00E-22	33	50	
		5:1221..1											
20869	ENJU04663	ANI61S3791:			NAP		g2133632	118	48	0.00008	20	20	
		1..845											
20870	ENJU04664	ANI61C3055:	22-44	377-398	NAP		g2120651	244	100	1.00E-20	47	38	
		2351..2686											
20871	ENJU04665	ANI61C8620:	43-62	784-804	NAP		g2894281	872	257	5.00E-68	46	36	
		4660..6246											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20872	ENU04666	ANI61S1089:	1..536		NAP		g2117904	150	69	3.00E-11	34	48	ribose-phosphate pyrophosphokinase (EC 2.7.6.1) PRS1 - yeast (Candida albicans) []
20873	ENU04667	ANI61C7703:	22-47	797-821	NAP		g1063421	581	74	5.00E-18	33	43	(L48797) toxin pump [Cochliobolus carbonum]
20874	ENU04668	ANI61C1106	66-89	589-614	NAP		g729075	326	95	5.00E-19	52	99	cell division control protein 31 [Saccharomyces cerevisiae]
20875	ENU04669	ANI61C313:1	116-137	435-457	NAP		g1083855	133	79	2.00E-14	33	1	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum] (AF010263) tartrate dehydrogenase [Agrobacterium vitis]
20876	ENU04670	ANI61C6199:			NAP		g2305218	501	129	3.00E-50	54	59	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]
20877	ENU04671	ANI61C1123	22-49	700-727	NAP		g2673951	671	79	3.00E-16	31	18	hypothetical 23.1 KD protein in SHP1-PTC3 intergenic region
20878	ENU04672	ANI61C4534:	102-121	621-640	NAP		g465516	260	105	1.00E-25	48	74	[Saccharomyces cerevisiae] (AF078790) No definition line found [Caenorhabditis elegans]
20879	ENU04673	ANI61S2960:	1..547		NAP		g3329623	189	41	0.0003	24	53	probable membrane protein YOR271c - yeast (Saccharomyces cerevisiae)
20880	ENU04674	ANI61C3402:	115-134	615-634	NAP		g2132933	722	191	3.00E-60	60	72	[Saccharomyces cerevisiae]
20881	ENU04675	ANI61S4333:	29-48	436-455	NAP		g542225	448	136	7.00E-32	66	42	ribosomal protein L4.e - fission yeast (Schizosaccharomyces pombe) []
20882	ENU04676	ANI61C1943:	102-124	360-381	NAP		g1705917	550	222	1.00E-57	57	11	probable clathrin heavy chain [Schizosaccharomyces pombe]
20883	ENU04677	ANI61C9505:	71-98	540-567	NAP		g4049509	232	106	1.00E-22	31	24	(AL034563) elongation factor g [Schizosaccharomyces pombe]
20884	ENU04678	ANI61C1094	41-60	626-643	NAP		g2132968	1222	135	4.00E-31	33	22	probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
20885	ENU04679	ANI61C1049	112-131	805-829	NAP		g4107287	223	61	8.00E-15	32	45	[Saccharomyces cerevisiae] (AL035076) putative allantoin permease [Schizosaccharomyces pombe]
20886	ENU04680	ANI61C9717:	27-46	785-812	NAP		g4098647	751	257	7.00E-68	51	56	"(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]" (AL035064) queuine tRNA-ribosyltransferase
20887	ENU04681	ANI61C9944:	23-47	629-648	NAP		g4106673	796	171	3.00E-85	66	59	[Schizosaccharomyces pombe]

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20888	ENU04682	ANI61C7199:	68-87	306-325	NAP		g730917	307	78	1.00E-18			"T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta) [Saccharomyces cerevisiae]"
20889	ENU04683	ANI61C1075	24-44	803-829	NAP		g1723251	417	70	3.00E-15	29	59	hypothetical 50.9 KD protein C3F10.06C in chromosome I [Schizosaccharomyces pombe]
20890	ENU04684	ANI61C2651:	22-49	785-805	NAP		g3123261	154	70	2.00E-11			meiotic recombination protein REC12 [Schizosaccharomyces pombe]
20891	ENU04685	ANI61C9331:	22-41	732-749	NAP		g1063421	519	108	1.00E-28	44	40	(L48797) toxin pump [Cochliobolus carbonum]
20892	ENU04686	ANI61S29:1..654			NAP		g2635181	553	213	7.00E-55	56	70	(Z99117) similar to protease [Bacillus subtilis]
20893	ENU04687	ANI61C9880:	22-41	808-829	NAP		g2498765	469	107	1.00E-28			peroxisomal membrane protein PEX16 (peroxin-16) [Yarrowia lipolytica]
20894	ENU04688	ANI61C891:1	51-69	457-481	NAP		g1805251	124	73	1.00E-16	30	29	(U58946) transposase [Aspergillus awamori]
20895	ENU04689	ANI61C3704:	69-89	805-823	NAP		g4586103	199	67	1.00E-22	33	76	(AL049638) putative protein [Arabidopsis thaliana]
20896	ENU04690	ANI61C758:3	22-48	714-741	NAP		g2497080	1119	125	5.00E-30	32	16	hypothetical 171.1 KD protein in YL16A-DAK1 intergenic region [Saccharomyces cerevisiae]
20897	ENU04691	ANI61S2532:			NAP		g2119707	127	40	0.01	32	61	proline-rich protein precursor - rat [] [Saccharomyces cerevisiae]
20898	ENU04692	ANI61C883:8	22-45	456-479	NAP		g1176053	156	90	1.00E-19	34	50	hypothetical 33.3 KD protein in ADE3-SER2 intergenic region [Saccharomyces cerevisiae]
20899	ENU04693	ANI61C2209:	22-42	719-738	NAP		g1077575	182	62	0.000000	27	41	hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
20900	ENU04694	ANI61C9811:	31-50	767-786	NAP		g120777	947	310	1.00E-83	56	58	[Saccharomyces cerevisiae] succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
20901	ENU04695	ANI61C8000:	41-60	727-749	NAP		g1703361	998	370	e-102			"ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-L-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-... [Neurospora crassa]"

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20902	ENU04696	ANI61C7533: 22-46	3582..4673	805-829	NAP		g3850084	370	87	2.00E-16	36	75	(AL033338) alcohol dehydrogenase [Schizosaccharomyces pombe]
20903	ENU04697	ANI61C6751: 120-147	294-316		NAP		g3150262	196	80	5.00E-15	38	32	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
20904	ENU04698	ANI61C6031: 30-54	647-673		NAP		g113314	1311	482	e-135	96	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
20905	ENU04699	ANI61C1084 51-70	714-733		NAP		g2132014	611	233	1.00E-60	45	61	hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae)
20906	ENU04700	ANI61C201:1 94-113	308-335		NAP		g2131347	264	68	2.00E-11	52	19	hypothetical protein YDL153c - yeast (Saccharomyces cerevisiae)
20907	ENU04701	ANI61C4912: 49-72	600-627		NAP		g3122266	603	171	4.00E-60	65	56	[Saccharomyces cerevisiae] eukaryotic translation initiation factor 3 delta subunit (EIF-3 delta) [Schizosaccharomyces pombe]
20908	ENU04702	ANI61C7350: 199-218	594-617		NAP		g2507129	395	112	3.00E-24	40	36	transporter protein SME1/ESP1 [Saccharomyces cerevisiae]
20909	ENU04703	ANI61C2646: 1..595			NAP		g4127832	306	140	8.00E-33	39	37	(Y17243) cytochrome P450 [Gibberella fujikuroi]
20910	ENU04704	ANI61C1132 23-43	703-729		NAP		g464369	221	78	8.00E-23	32	35	phenol 2-monooxygenase (phenol hydroxylase) [Trichosporon cutaneum]
20911	ENU04705	ANI61C7309: 71-92	460-483		NAP		g2956774	62	48	0.00003	27	72	(AL022103) hypothetical protein. [Schizosaccharomyces pombe]
20912	ENU04706	ANI61C332:1 81-99	421-438		NAP		g585251	318	134	4.00E-31	43	36	polyketide synthase HETM [Anabaena sp.]
20913	ENU04707	ANI61C101:1 22-46	801-828		NAP		g1870209	283	87	8.00E-24	32	50	(AC000133) ORF [Emmericella nidulans]
20914	ENU04708	ANI61C3232: 25-45	720-747		NAP		g2492658	3245	541	e-153	97	14	putative strigamocystin biosynthesis fatty acid synthase beta subunit [Emmericella nidulans]
20915	ENU04709	ANI61C1335: 48-70	349-368		NAP		g585668	413	152	1.00E-36	62	34	polygalacturonase precursor (PG) (pectinase) [Gibberella fujikuroi]
20916	ENU04710	ANI61C1053 0:722..1			NAP		g2133039	447	198	5.00E-50	48	15	probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)
20917	ENU04711	ANI61C4364: 30-49	725-747		NAP		g2342601	814	123	2.00E-27	30	5	[Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20918	ENU04712	ANI6IS2752: 1..605			NAP		g4760549	77	53	0.000001			(AB019494) IDN3 [Homo sapiens]
20919	ENU04713	ANI6IC7196: 22-49		777-804	NAP		g3859775	415	111	2.00E-31	52	53	(Z54328) putative aminopeptidase p [Schizosaccharomyces pombe]
20920	ENU04714	ANI6IC9312: 22-46		802-829	NAP		g3915187	556	132	3.00E-30	33	14	probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N- recognin) []
20921	ENU04715	ANI6IC9006: 42-61		697-716	NAP		g83716	3301	404	e-141	95	32	regulatory protein alcR - Emericella nidulans [Emericella nidulans]
20922	ENU04716	ANI6IC1084 4996..7003	22-44	623-643	NAP		g416965	658	50	3.00E-21	37	7	"erythronolide synthase, modules 1 and 2 (ORF 1) (6-deoxyerythronolide B synthase 1) (DEBS 1) []"
20923	ENU04717	ANI6IC6533: 22-48		727-749	NAP		g1175451	842	152	3.00E-36			hypothetical protein C22F3.14C in chromosome I []
20924	ENU04718	ANI6IC5137: 88-110		741-760	NAP		g3702632	592	137	3.00E-63	43	41	(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]
20925	ENU04719	ANI6IC419:1 23-46		412-431	NAP		g1172542	388	168	3.00E-41	47	22	dolichyl-phosphate-mannose--protein mannosyltransferase 4 [Saccharomyces cerevisiae]
20926	ENU04720	ANI6IC8353: 26-45		776-794	NAP		g122805	311	109	3.00E-23	30	53	6-hydroxy-D-nicotine oxidase (6-HDNO) [Arthrobacter oxidans]
20927	ENU04721	ANI6IC3877: 1384..1			NAP		g3122851	2113	284	e-134	89	41	sulfur metabolite repression control protein [Emericella nidulans]
20928	ENU04722	ANI6IC8873: 8184..7035			NAP		g1175441	458	83	3.00E-15	27	31	hypothetical 98.4 KD protein C24H6.13 in chromosome I [Schizosaccharomyces pombe]
20929	ENU04723	ANI6IC1126 4:323..1	102-123	448-475	NAP		g4204352	396	166	1.00E-40	78	64	[Schizosaccharomyces pombe] (U07366) eIF-5A [Candida albicans]
20930	ENU04724	ANI6IC4166: 121-140		505-524	NAP		g1076211	227	45	0.0006	28	43	hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii]
20931	ENU04725	ANI6IC6980: 22-44		561-582	NAP		g2213560	369	164	4.00E-40	44	98	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20932	ENU04726	ANI6IC9955: 22-49		760-783	NAP		g534844	501	184	7.00E-46	55	39	(U13672) beta-glucosidase [Candida wickerhamii]
20933	ENU04727	ANI6IC1013 2:1954..2613	23-50	538-558	NAP		g2105430	316	145	4.00E-34	45	17	(U97079) U5-116KD [Mus musculus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20934	ENU04728	ANT61S4589: 1..553			NAP		g82698	177	47	0.00008	35	54	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
20935	ENU04729	ANT61C1053 5:2480..3612	45-64	792-819	NAP		g416643	231	65	7.00E-10	32	58	aristolochene synthase (sesquiterpene cyclase) (AS) [Penicillium roqueforti] (AC004521) unknown protein
20936	ENU04730	ANT61C9379: 3315..2805	23-50	467-490	NAP		g3128203	134	63	0.000000	36	75	[Arabidopsis thaliana]
20937	ENU04731	ANT61C4278: 2535..1838	22-42	652-671	NAP		g3915405	146	79	4.00E-14	37	96	hypothetical 17.5 KD protein in chromosome II [Schizosaccharomyces pombe]
20938	ENU04732	ANT61C1110 3:5478..4766	105-125	643-665	NAP		g3925752	276	68	1.00E-22	41	58	(AL034352) putative signal transduction protein [Schizosaccharomyces pombe]
20939	ENU04733	ANT61S3754: 1..508	31-56	371-390	NAP		g2911045	695	187	2.00E-73	95	51	(AL021961) putative protein [Arabidopsis thaliana]
20940	ENU04734	ANT61C9298: 818..1			NAP		g1401057	158	104	1.00E-21	25	14	(U40375) Supr16h [Mus musculus]
20941	ENU04735	ANT61S3133: 1..565	46-65	427-450	NAP		g4105798	164	99	2.00E-20	36	43	(AF049930) PGP237-11 [Petunia x hybrida]
20942	ENU04736	ANT61C7989: 640..179	71-89	418-441	NAP		g3880413	160	66	1.00E-10	33	46	(Z81137) Similarity to Yeast YIP1 protein (SW:P53039); cDNA EST EMBL:701608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene; ... []
20943	ENU04737	ANT61C5949: 1..816	55-75	594-612	NAP		g2493011	323	151	5.00E-36	37	13	probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae] (AF116827) unknown [Homo sapiens]
20944	ENU04738	ANT61C9477: 1..1752	30-49	806-829	NAP		g4768831	418	38	0.12			(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]
20945	ENU04739	ANT61C1110 7:9439..8176	28-47	769-796	NAP		g4455787	886	195	4.00E-52	52	66	hypothetical 48.1 KD protein in TUB1-CPR3 intergenic region [Saccharomyces cerevisiae]
20946	ENU04740	ANT61C5813: 272..1145	41-60	734-761	NAP		g1730621	585	223	1.00E-61	57	56	putative enoyl-CoA hydratase [Mycobacterium leprae]
20947	ENU04741	ANT61C6657: 1283..1644	33-52	422-445	NAP		g1706567	89	59	0.000000	25	40	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20948	ENU04742	ANI61C5440:	90-109	748-767	NAP		g728743	1212	322	e-103			"6-phosphogluconate dehydrogenase, decarboxylating 1 [Saccharomyces cerevisiae]"
20949	ENU04743	ANI61C3035:	105-130	416-443	NAP		g4056553	133	86	1.00E-16	39	20	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
20950	ENU04744	ANI61C5064:	37-56	804-829	NAP		g231714	212	99	5.00E-20	36	24	CDC21 protein []
20951	ENU04745	ANI61C7394:	107-126	401-420	NAP		g125155	283	127	4.00E-29	41	71	Adenylate kinase 2 (ATP-AMP transphosphorylase) [Saccharomyces cerevisiae]
20952	ENU04746	ANI61C1243:	105-125	349-371	NAP		g114251	175	51	1.00E-12	41	40	L-asparaginase I (L-asparagine amidohydrolase I) [Escherichia coli]
20953	ENU04747	ANI61C5328:	24-45	762-786	NAP		g3560207	361	89	3.00E-17	35	46	(AL031536) fmx1p. [Schizosaccharomyces pombe]
20954	ENU04748	ANI61C8350:	22-44	766-788	NAP		g2791647	470	89	4.00E-17	31	42	(AL021287) hypothetical protein RV3049c [Mycobacterium tuberculosis]
20955	ENU04749	ANI61S1354:			NAP		g1079170	137	52	0.000006	31	61	larval glue protein Lgp-3 precursor - fruit fly [Drosophila virilis]
20956	ENU04750	ANI61C9637:	41-60	791-812	NAP		g4154817	480	107	1.00E-47	42	87	[Drosophila virilis] (AE001466) putative [Helicobacter pylori J99] (AB007770) translation elongation factor 1 alpha [Aspergillus oryzae]
20957	ENU04751	ANI61C7698:	22-49	723-746	NAP		g4521247	1397	494	e-139	92	57	delta-(L-alpha-aminoacidipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
20958	ENU04752	ANI61C291:1			NAP		g113314	1686	492	e-141	93	7	(Z99120) similar to Na+/nucleoside cotransporter [Bacillus subtilis] hypothetical hydrolase/peptidase Y4TM [Rhizobium sp. NGR234]
20959	ENU04753	ANI61C1116	22-48	763-783	NAP		g2635715	530	111	1.00E-35	41	63	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
20960	ENU04754	ANI61C7546:	31-51	807-828	NAP		g2497952	221	98	1.00E-19			(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
20961	ENU04755	ANI61S4137:			NAP		g283032	161	32	0.013	35	59	(U81165) MOD-E [Podospira anserina]
20962	ENU04756	ANI61C936:6	49-68	494-515	NAP		g3560228	423	157	6.00E-43	50	61	
20963	ENU04757	ANI61C1316:	47-73	725-747	NAP		g2804612	1030	238	2.00E-89	83	37	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20964	ENU04758	ANI6IS4517: 1..440	24-47	373-393	NAP		g2330857	411	175	2.00E-43	60	10	phosphoribosylformylglycinamide synthase [Schizosaccharomyces pombe]
20965	ENU04759	ANI6IC3920: 22-46	723-746		NAP		g3650404	1579	148	4.00E-35	42	28	(AL031739) eukaryotic translation initiation factor 3 subunit [Schizosaccharomyces pombe]
20966	ENU04760	ANI6IC9383: 1..3966	24-51	807-826	NAP		g416765	1139	164	5.00E-40	27	13	general negative regulator of transcription subunit 1 [Saccharomyces cerevisiae]
20967	ENU04761	ANI6IC8310: 378..1	106-125	459-479	NAP		g1703347	311	85	8.00E-26	51	67	adenine phosphoribosyltransferase 1 (APRT 1) [Saccharomyces cerevisiae]
20968	ENU04762	ANI6IS2708: 1..750			NAP		g2493749	132	36	0.21	23	14	240 KD protein of rod photoreceptor CNG-channel [Bos taurus]
20969	ENU04763	ANI6IC3037: 575..1	23-45	519-546	NAP		g1352954	224	96	2.00E-19	35	25	hypothetical 77.7 KD protein in CCT3-CCT8 intergenic region [Saccharomyces cerevisiae]
20970	ENU04764	ANI6IC1117: 3:924..214	220-238	638-657	NAP		g136682	333	140	8.00E-33	39	99	ubiquitin carboxyl-terminal hydrolase isozyme L3 (UCH-L3) (ubiquitin thiolesterase L3) [Homo sapiens]
20971	ENU04765	ANI6IC6434: 2648..1866	23-44	712-731	NAP		g1076802	75	46	0.0003			extensin-like protein - maize [Zea mays]
20972	ENU04766	ANI6IC26:81 7..1	222-244	736-763	NAP		g1705828	1119	298	3.00E-85	95	23	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emmericella nidulans]
20973	ENU04767	ANI6IC8888: 282..1609	25-52	713-737	NAP		g730755	837	129	2.00E-50	54	45	transporter protein SMF2 [Saccharomyces cerevisiae]
20974	ENU04768	ANI6IC4526: 1314..1	22-45	809-828	NAP		g3650406	754	199	1.00E-50	47	26	(AL031739) 26S proteasome regulatory subunit [Schizosaccharomyces pombe]
20975	ENU04769	ANI6IC1120: 11172..12742	22-44	714-731	NAP		g125727	701	141	1.00E-39			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase [Kluyveromyces lactis])
20976	ENU04770	ANI6IC7885: 1238..835	102-122	334-353	NAP		g1711623	159	38	0.000000	41	11	"alanyl-TRNA synthetase, cytoplasmic (alanine--TRNA ligase) (ALARS) [Saccharomyces cerevisiae]"
20977	ENU04771	ANI6IC6793: 1..648	59-78	571-591	NAP		g3135013	755	302	1.00E-81	68	24	(AJ005963) 100 kDa protein [Ajiellomyces capsulatus]
20978	ENU04772	ANI6IC7746: 4718..4215	95-114	451-478	NAP		g1351714	190	73	1.00E-12	25	33	putative transporter C1D3.18C [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20979	ENU04773	ANI61C1049:	48-69	588-615	NAP		g3288709	996	277	e-109	89	15	(AB010442) PMR1 [Penicillium digitatum]
20980	ENU04774	ANI61C8780:	48-65	799-826	NAP		g130333	554	154	6.00E-37	47	68	pectin lyase D precursor (PLD) (pectin lyase I) (PLI) [Aspergillus niger]
20981	ENU04775	ANI61C1252:	114-133	435-462	NAP		g400069	841	261	5.00E-87			insertion element IS1 protein INSB [Escherichia coli]
20982	ENU04776	ANI61C1269:	496..1		NAP		g2145993	125	69	4.00E-11	28	97	yfcA protein - Mycobacterium leprae [Mycobacterium leprae]
20983	ENU04777	ANI61C9834:	65-84	798-816	NAP		g3402279	702	156	1.00E-54	49	78	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]
20984	ENU04778	ANI61C3653:	121-140	342-361	NAP		g134920	101	47	0.00008	26	30	sulfated surface glycoprotein 185 (SSG 185) [Volvox carter]
20985	ENU04779	ANI61C6617:	23-42	576-595	NAP		g1079456	471	192	2.00E-49	60	62	"actin-capping protein beta chain, splice form 2 - chicken [Gallus gallus]"
20986	ENU04780	ANI61S1139:	1..586		NAP		g1572721	133	38	0.044	31	13	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
20987	ENU04781	ANI61C8129:	22-46	621-640	NAP		g730240	249	142	3.00E-33	34	54	osmotic growth protein 1 [Saccharomyces cerevisiae]
20988	ENU04782	ANI61C1094	186-204	729-748	NAP		g3560228	476	98	7.00E-31	43	77	(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
20989	ENU04783	ANI61C7234:	1296..1		NAP		g2499716	1440	303	e-109	83	55	"exopolysaccharuronase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
20990	ENU04784	ANI61C9604:	6879..6438		NAP		g729650	258	98	3.00E-20	44	30	"exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase) [Penicillium janthinellum]"
20991	ENU04785	ANI61C6076:	22-45	496-515	NAP		g1197667	96	31	5.1	29	98	(U46857) vitellogenin [Anolis pulchellus]
20992	ENU04786	ANI61C5316:	68-87	362-381	NAP		g1174622	227	84	5.00E-16	52	19	"T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta) [Saccharomyces cerevisiae]"
20993	ENU04787	ANI61C9088:	111-130	532-555	NAP		g2826168	193	57	0.000000	36	42	(AB010714) salicylate hydroxylase [Pseudomonas putida]

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20994	ENU04788	ANT61C5537: 22-43	456-479	NAP			g729763	198	101	4.00E-21	38	80	30 KD heat shock protein [Emericella nidulans]
20995	ENU04789	ANT61C753:7 22-49	702-721	NAP			g1083855	150	92	4.00E-18	26	1	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum]
20996	ENU04790	ANT61C1830: 107-129	802-821	NAP			g2501686	919	349	3.00E-95	59	16	hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region [Saccharomyces cerevisiae]
20997	ENU04791	ANT61C8954: 93-112	556-579	NAP			g3978466	462	108	1.00E-47	45	29	(AF086822) dihydroxyacetone synthase [Candida boidinii]
20998	ENU04792	ANT61C1899: 35-54	805-829	NAP			g2501202	1767	272	e-108	75	51	protein disulfide isomerase precursor (PD) [Aspergillus niger]
20999	ENU04793	ANT61C3322: 164-183	454-479	NAP			g1722894	379	159	9.00E-39	52	42	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-l-arabinofuranosidase (arabinosidase) [Bacteroides ovatus]"
21000	ENU04794	ANT61C1684: 22-41	781-808	NAP			g2330829	557	170	1.00E-41	40	18	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
21001	ENU04795	ANT61C1574: 120-137	492-511	NAP			g2293194	99	57	0.000000	28	41	(AF008220) yreR [Bacillus subtilis]
21002	ENU04796	ANT61C1236: 22-45	766-792	NAP			g125462	1460	573	e-163			"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3)I) [Cloning vector pHIND2.2]"
21003	ENU04797	ANT61C5865: 108-127	724-750	NAP			g2492799	589	161	8.00E-58	44	72	putative sterigmatocystin biosynthesis dehydrogenase STCV [Emericella nidulans]
21004	ENU04798	ANT61C1994: 29-51	370-389	NAP			g4884104	110	57	0.000000			(AL050060) hypothetical protein [Homo sapiens]
21005	ENU04799	ANT61S1320: 1..590		NAP			g3874243	147	50	0.00002	20	50	(Z70204) similar to PHD-finger.; cDNA EST EMBL:100556 comes from this gene; cDNA EST yk3447.5 comes from this gene [Caenorhabditis elegans]
21006	ENU04800	ANT61C1743: 24-44	733-755	NAP			g3261605	699	185	3.00E-61	45	14	(Z74697) ppsA [Mycobacterium tuberculosis]
21007	ENU04801	ANT61C911: 22-48	776-797	NAP			g2894293	507	105	6.00E-28	35	47	(AL021837) hypothetical protein [Schizosaccharomyces pombe]

Database "Schizosaccharomyces"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21008	ENU04802	ANT61C8612:	102-125	294-314	NAP		g2239205	198	90	5.00E-18	37	48	(Z97209) hypothetical protein [Schizosaccharomyces pombe]
21009	ENU04803	ANT61C8663:	28-49	806-828	NAP		g134854	269	92	4.00E-18	27	19	transcription initiation protein SPT6 [Saccharomyces cerevisiae]
21010	ENU04804	ANT61C1850:	25-52	720-747	NAP		g1805251	849	272	3.00E-72	54	50	(U58946) transposase [Aspergillus awamori]
21011	ENU04805	ANT61C5897:	33-52	590-617	NAP		g1870216	1136	416	e-116	100	100	(AC000133) f4p06 [Emericella nidulans]
21012	ENU04806	ANT61C9479:	22-44	792-818	NAP		g4056553	300	94	1.00E-18	39	34	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
21013	ENU04807	ANT61C1226:	101-120	424-444	NAP		g1710045	274	106	2.00E-22	38	21	mitochondrial respiratory chain complexes assembly protein RCA1 (TAT-binding homolog 12) [Saccharomyces cerevisiae]
21014	ENU04808	ANT61C6000:	22-47	806-827	NAP		g2842516	484	88	7.00E-17			(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe]
21015	ENU04809	ANT61C7282:	22-49	376-399	NAP		g3150141	504	128	2.00E-48	73	51	(AL023594) 40s ribosomal protein s4 type [Schizosaccharomyces pombe]
21016	ENU04810	ANT61C1158:	43-63	791-810	NAP		g1911743	1514	320	e-103	84	65	(S83229) beta-isopropylmalate dehydrogenase=isozyme [Aspergillus niger]
21017	ENU04811	ANT61C7741:	22-42	697-724	NAP		g1705679	2474	226	5.00E-99	78	31	cell division control protein 48 [Saccharomyces cerevisiae]
21018	ENU04812	ANT61C3249:	52-70	774-793	NAP		g1078072	247	85	8.00E-16	32	41	probable membrane protein YLR324w - yeast [Saccharomyces cerevisiae]
21019	ENU04813	ANT61C7670:	50-69	772-791	NAP		g3043376	261	60	0.000000			[Saccharomyces cerevisiae]
21020	ENU04814	ANT61C6680:	30-47	482-507	NAP		g4099032	892	176	8.00E-74	96	58	(AJ005258) anyR [Aspergillus oryzae]
21021	ENU04815	ANT61S2301:	71-90	363-386	NAP		g1175364	183	82	2.00E-15	39	46	(U82084) unknown [Bacteriophage SFX]
21022	ENU04816	ANT61C9378:	23-45	775-802	NAP		g2132860	280	45	0.000000	42	91	hypothetical 28.0 KD protein C13C5.04 in chromosome I [Schizosaccharomyces pombe]
		472..1418							6				probable membrane protein YOL162w - yeast [Saccharomyces cerevisiae]
													[Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21023	ENU04817	ANI61C9378: 1..456	22-48	407-434	NAP		g2132861	363	84	2.00E-29	51	75	probable membrane protein YOL163w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21024	ENU04818	ANI61C1114: 4:516..1	32-51	398-415	NAP		g2222786	422	108	3.00E-23	63	69	(Z97185) hypothetical protein [Schizosaccharomyces pombe]
21025	ENU04819	ANI61C2562: 1533..2108	51-70	449-468	NAP		g131768	569	211	3.00E-54	60	35	quinate permease (quinate transporter) [Emmericella nidulans]
21026	ENU04820	ANI61C1106: 5:1224..1	30-49	670-691	NAP		g3183329	713	136	6.00E-53	57	52	hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]
21027	ENU04821	ANI61C1024: 9:9831..9292	94-115	494-519	NAP		g1293655	113	70	1.00E-11	26	27	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21028	ENU04822	ANI61S1471: 631..28			NAP		g418604	857	328	2.00E-93	89	64	hypothetical 35.6 KD protein in RPME-TDK intergenic region (ORFP) []
21029	ENU04823	ANI61C8903: 1..1199	102-125	803-829	NAP		g232152	1231	421	e-132	97	51	G2/mitotic-specific cyclin B [Emmericella nidulans]
21030	ENU04824	ANI61C7756: 1187..1	22-49	618-643	NAP		g3451467	569	212	4.00E-54	45	45	(AL031349) putative cystathionine gamma-synthase [Schizosaccharomyces pombe]
21031	ENU04825	ANI61C4392: 822..1	22-43	697-715	NAP		g3947592	448	121	2.00E-46			"(AL034364) similar to homogenisate 1,2-dioxygenase (EC 1.13.11.5) (homogenisicase) (homogenisate oxygenase) (homogenistic acid oxidase); cDNA EST yk385c12.5 comes from this gene; cDNA EST EMBL:D73328 comes from this gene; cD... []"
21032	ENU04826	ANI61S1672: 1..695			NAP		g2119707	77	55	0.000000	27	80	proline-rich protein precursor - rat []
21033	ENU04827	ANI61C1097: 5:812..1721	71-90	805-829	NAP		g2496731	881	336	1.00E-91	67	92	hypothetical 30.2 KD protein Y4OV [Rhizobium sp. NGR234]
21034	ENU04828	ANI61C3908: 798..1409	22-44	485-511	NAP		g586485	242	145	3.00E-34	35	50	hypothetical 45.5 KD protein in FIG1-GIP1 intergenic region [Saccharomyces cerevisiae]
21035	ENU04829	ANI61S49:1..530			NAP		g416876	238	47	5.00E-11	38	60	dihydrodipicolinate synthase (DHDPs) (vegetative protein 81) (VEG81) [Bacillus subtilis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21036	ENU04830	ANI61C1518:	22-43	659-678	NAP		g1168464	1254	212	2.00E-78	57	53	monamine oxidase N (MAO-N) [Aspergillus niger]
21037	ENU04831	ANI61C1133:	217-236	715-740	NAP		g118381	1019	228	6.00E-59	56	58	ornithine decarboxylase (ODC) [Neurospora crassa]
21038	ENU04832	ANI61C4437:	22-43	440-462	NAP		g4583351	113	64	5.00E-10	27	30	(AF114167) lysosomal pepstatin insensitive protease [Canis familiaris]
21039	ENU04833	ANI61C2465:	57-76	795-815	NAP		g1546072	1287	147	1.00E-34	40	9	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21040	ENU04834	ANI61C9269:	26-53	808-829	NAP		g1805251	718	249	3.00E-65	44	51	(U58946) transposase [Aspergillus awamori]
21041	ENU04835	ANI61C9769:	102-127	526-551	NAP		g1870212	903	278	2.00E-74	94	97	(AC000133) ORF [Emmericella nidulans]
21042	ENU04836	ANI61C6563:	121-144	378-405	NAP		g1351598	398	167	5.00E-41	47	31	hypothetical 59.6 KD protein C4G8.07C in chromosome I [Schizosaccharomyces pombe]
21043	ENU04837	ANI61C6365:	39-57	728-749	NAP		g2342601	2803	145	3.00E-34	37	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21044	ENU04838	ANI61C2860:	161-187	714-740	NAP		g1346361	269	142	1.00E-35	41	32	serine/threonine-protein kinase SHK2 [Schizosaccharomyces pombe]
21045	ENU04839	ANI61C9769:	22-47	591-610	NAP		g1870213	1021	254	e-108	97	99	(AC000133) ORF [Emmericella nidulans]
21046	ENU04840	ANI61C1028	60-79	443-461	NAP		g609350	549	228	3.00E-59	63	22	(U15099) methionine synthase [Saccharomyces cerevisiae]
21047	ENU04841	ANI61C1045	105-132	426-447	NAP		g1709181	288	117	2.00E-27	39	27	high affinity methionine permease [Saccharomyces cerevisiae]
21048	ENU04842	ANI61C2802:	43-62	775-794	NAP		g4056555	849	86	3.00E-16			(AL034583) putative mitochondrial atp-dependent ma helicase precursor [Schizosaccharomyces pombe]
21049	ENU04843	ANI61S4378:			NAP		g1079170	144	31	0.04	31	69	larval glue protein Lgp-3 precursor - fruit fly (Drosophila virilis) [Drosophila virilis]
21050	ENU04844	ANI61C2758:	105-131	523-546	NAP		g2133266	875	319	1.00E-86	96	16	chromosome scaffold protein sudA - Emmericella nidulans [Emmericella nidulans]
21051	ENU04845	ANI61C5221:	22-45	806-828	NAP		g3282216	540	56	0.000000			(U68716) polyketide synthase homolog [Botryotinia fuckeliana]
21052	ENU04846	ANI61C1008	35-54	497-519	NAP		g135649	263	75	2.00E-13	41	31	"2,4-dichlorophenol 6-monoxygenase (2,4-dichlorophenol hydroxylase) (2,4-DCP hydroxylase) [Plasmid pJP4]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21053	ENU04847	ANI61C9706:	22-48	725-747	NAP		g1805262	3278	103	2.00E-45	39	13	"(U75347) fatty acid synthase, beta subunit [Emerticella nidulans]"
21054	ENU04848	ANI61C3226:	58-77	676-695	NAP		g1723578	359	96	3.00E-29	50	60	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
21055	ENU04849	ANI61C1235:	22-49	783-810	NAP		g4557168	1419	530	e-150	97	99	(AF104442) inhibitor resistant beta lactamase TEM-54 [Escherichia coli]
21056	ENU04850	ANI61S1182:	924..72		NAP		g3153821	177	34	0.99	26	29	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21057	ENU04851	ANI61C7768:	24-51	468-492	NAP		g3005097	502	109	2.00E-48	67	99	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]"
21058	ENU04852	ANI61C4396:	55-76	768-787	NAP		g1293655	416	155	4.00E-37	41	37	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21059	ENU04853	ANI61C1049	22-46	775-802	NAP		g1834340	4837	489	e-138	95	18	(Z68904) ATP-binding cassette multidrug transporter [Emerticella nidulans]
21060	ENU04854	ANI61C6622:	81-100	479-500	NAP		g131768	555	226	9.00E-59	60	34	quinate permease (quinate transporter) [Emerticella nidulans]
21061	ENU04855	ANI61S1397:	552..1		NAP		g140011	497	182	1.00E-45	85	30	mitochondrial ribosomal protein S5 [Emerticella nidulans]
21062	ENU04856	ANI61C1122	122-144	458-482	NAP		g2493391	359	155	1.00E-37	49	38	probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) [Emerticella nidulans]
21063	ENU04857	ANI61C9762:	78-97	305-331	NAP		g731700	228	104	2.00E-22	41	31	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region [Saccharomyces cerevisiae]
21064	ENU04858	ANI61C957.1	102-125	516-543	NAP		g1703456	520	219	2.00E-56	52	18	cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21065	ENU04859	ANI61C3989:	55-74	724-743	NAP		g1293655	332	78	8.00E-31	36	38	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21066	ENU04860	ANI61C5606:	66-85	760-786	NAP		g4106374	910	178	1.00E-89	73	46	(AF069777) mitogen-activated protein kinase kinase CPK1 [Cryphonectria parasitica]
21067	ENU04861	ANI61S4332:	397..1		NAP		g3170523	637	258	1.00E-68	99	10	(AF053883) coatomer alpha subunit [Emerticella nidulans]
21068	ENU04862	ANI61C9112:	22-48	725-752	NAP		g464738	138	58	0.000000			translocation protein SEC66 (HSS1 protein) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21069	ENU04863	ANI61C320:1			NAP		g940860	461	147	8.00E-35	51	29	(X90565) MYO2 [Saccharomyces cerevisiae]
21070	ENU04864	ANI61C6479: 744..2877	97-116	651-672	NAP		g1749498	176	95	5.00E-19	28	77	(D89145) similar to Saccharomyces cerevisiae ORF YGL092W
21071	ENU04865	ANI61C7648: 1..428	27-50	373-400	NAP		g1170421	180	60	3.00E-13	40	21	[Schizosaccharomyces pombe] HUS2 protein [Saccharomyces cerevisiae]
21072	ENU04866	ANI61C7910: 2260..1			NAP		g113314	3671	454	e-136	89	7	delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emertella nidulans]
21073	ENU04867	ANI61C1224: 1..844	64-91	638-663	NAP		g462071	797	290	7.00E-85			"fatty acid synthase, subunit beta [Yarrowia lipolytica]"
21074	ENU04868	ANI61C9303: 4520..2714	27-54	805-829	NAP		g4755188	521	73	8.00E-24			(AC007018) unknown protein [Arabidopsis thaliana]
21075	ENU04869	ANI61C2783: 1067..2183	22-44	677-695	NAP		g2414579	545	216	1.00E-55	49	44	(Z99292) flavoprotein [Schizosaccharomyces pombe]
21076	ENU04870	ANI61C1014 6:1022..265	50-69	635-657	NAP		g1730743	387	183	9.00E-46	46	77	hypothetical 34.9 KD protein in MSK1-PDA2 intergenic region [Saccharomyces cerevisiae]
21077	ENU04871	ANI61C3868: 3311..3872	22-49	436-461	NAP		g2494018	214	89	3.00E-17	35	79	maltose O-acetyltransferase [maltose transacetylase] [Escherichia coli]
21078	ENU04872	ANI61C1035 4:592..1	22-49	515-534	NAP		g2315274	419	76	1.00E-32	49	51	(Y11113) endoglucanase IV [Hypocrea jecorina]
21079	ENU04873	ANI61C8581: 3239..4082	22-42	799-819	NAP		g3980401	213	127	7.00E-29	33	97	(AC004561) putative tropinone reductase [Arabidopsis thaliana]
21080	ENU04874	ANI61C27:1.. 2171	24-51	715-742	NAP		g586352	1238	134	1.00E-30	34	22	hypothetical 124.0 KD protein in PCS60-ABD1 intergenic region [Saccharomyces cerevisiae]
21081	ENU04875	ANI61C1053 5:4916..3815	185-204	810-829	NAP		g2851424	181	100	1.00E-20	25	75	hypothetical 37.5 KD protein in DEGA-NPRB intergenic region [Bacillus subtilis]
21082	ENU04876	ANI61C7988: 770..1	40-59	665-691	NAP		g1175361	150	55	0.000000	29	51	hypothetical 48.5 KD protein C13C5.02 in chromosome I [Schizosaccharomyces pombe]
21083	ENU04877	ANI61C1202: 1..1694	22-41	786-808	NAP		g2342601	790	166	2.00E-40	37	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21084	ENU04878	ANI61C5153: 216..1177	40-59	768-787	NAP		g1706176	977	316	2.00E-85	71	25	cutinase transcription factor 1 alpha [Fusarium solani f. sp. pisi]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21085	ENU04879	ANI61C6712: 22-49	722-749		NAP		g10709997	726	48	0.0001			DNA repair protein RAD18 [Schizosaccharomyces pombe]
21086	ENU04880	ANI61C499:7 2698..1	806-829		NAP		g2909648	548	157	5.00E-47	53	95	(AL021943) echA5 [Mycobacterium tuberculosis]
21087	ENU04881	ANI61C4145: 64-90	485-504		NAP		g1078626	954	346	5.00E-95	99	12	bind protein - Emericella nidulans [Emericella nidulans]
21088	ENU04882	ANI61C7661: 102-123	291-310		NAP		g464435	303	126	6.00E-29	53	26	acid phosphatase precursor [Aspergillus niger]
21089	ENU04883	ANI61C6082: 68-87	804-826		NAP		g1805261	645	166	1.00E-44	40	13	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21090	ENU04884	ANI61S373:1. 42-61	257-276		NAP		g2392764	335	141	4.00E-34	78	17	(AC002534) hypothetical protein [Arabidopsis thaliana]
21091	ENU04885	ANI61C3838: 23-46	807-826		NAP		g3806120	2179	466	e-130	96	23	(AF097728) pyruvate carboxylase [Aspergillus terreus]
21092	ENU04886	ANI61C1035 45..1417	791-810		NAP		g3335173	373	71	1.00E-17			(AF071202) ABC transporter MOAT-B [Homo sapiens]
21093	ENU04887	ANI61C4237: 31-50	807-829		NAP		g1870208	2438	114	7.00E-25	99	58	(AC000133) ORF [Emmericella nidulans]
21094	ENU04888	ANI61C1042 0:5573..4046	810-829		NAP		g2495217	1971	436	e-121	78	57	glucokinase (glucose kinase) (GLK) [Aspergillus niger]
21095	ENU04889	ANI61C5224: 23-50	801-827		NAP		g1077569	1088	208	3.00E-75	53	37	probable membrane protein YDR109c - yeast [Saccharomyces cerevisiae]
21096	ENU04890	ANI61C3404: 22-48	790-810		NAP		g2131132	213	90	1.00E-17	24	19	[Saccharomyces cerevisiae] UDPglucose--glycoprotein glucosephosphotransferase (EC 2.7.8.19) - fission yeast
21097	ENU04891	ANI61C2738: 35-54	780-805		NAP		g4160575	539	122	2.00E-49	53	42	(Schizosaccharomyces pombe) [Schizosaccharomyces pombe] (AL035226) putative structure specific recognition protein, possible chromatin-associated HMG protein
21098	ENU04892	ANI61C1038 0:3069..3813	702-721		NAP		g1730665	121	67	2.00E-10	29	91	[Schizosaccharomyces pombe] hypothetical 25.3 KD protein in TTM23-ARE2 intergenic region [Saccharomyces cerevisiae]
21099	ENU04893	ANI61C2329: 30-54	795-820		NAP		g4507295	250	85	4.00E-16	28	99	syntaxin 7 [Homo sapiens]

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21100	ENU04894	AN161C1038	22-46	535-562	NAP		g3790261	371	160	1.00E-38	43	65	(AL031966) putative quinone oxidoreductase [Schizosaccharomyces pombe]
21101	ENU04895	AN161S1377	70-89	378-397	NAP		g2494062	740	292	8.00E-79	98	51	hypothetical 30.8 KD protein in GIP-FDRA intergenic region [Escherichia coli]
21102	ENU04896	AN161C1013	22-49	766-789	NAP		g3873546	1129	190	6.00E-75	57	66	(AL033534) acetyl-coa acetyltransferase [Schizosaccharomyces pombe]
21103	ENU04897	AN161C1117	105-128	377-401	NAP		g129302	329	132	2.00E-30	43	47	D-amino acid oxidase (DAMOX) (DAO) (DAAO) [Nectria haematococca]
21104	ENU04898	AN161C4968	22-48	769-788	NAP		g135139	1151	348	3.00E-95	57	47	"lysyl-TRNA synthetase, cytoplasmic (lysine--TRNA ligase) (LYSRS) [Saccharomyces cerevisiae]"
21105	ENU04899	AN161C6717	27-46	806-829	NAP		g3660282	574	88	9.00E-30	39	54	"Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm ["]
21106	ENU04900	AN161C6446	22-48	706-730	NAP		g1077167	152	73	3.00E-12	23	53	hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21107	ENU04901	AN161C989	1	63-86	NAP		g1546072	903	55	0.000000	21	9	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21108	ENU04902	AN161C4177	22-44	428-447	NAP		g141305	472	172	6.00E-47			YPT1-related protein 2 [Schizosaccharomyces pombe]
21109	ENU04903	AN161C7502	27-50	795-822	NAP		g1351721	1692	296	2.00E-85	56	10	putative translational activator C18G6.05C (GCN1 homolog) [Schizosaccharomyces pombe]
21110	ENU04904	AN161C7090	23-43	794-813	NAP		g3170246	1708	398	e-128	98	49	(AF043230) trehalose-6-phosphate synthase subunit 1 [Emmericella nidulans]
21111	ENU04905	AN161C4732	96-115	302-321	NAP		g3287841	94	54	0.000000	30	19	glucose oxidase precursor (glucose oxyhydraz) (GOD) (beta-D-glucose:oxygen 1-oxido-reductase) [Talaromyces flavus]
21112	ENU04906	AN161C5835			NAP		g3283373	230	82	4.00E-15	30	28	(AF067650) sarcosine dehydrogenase [Rattus norvegicus]

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21113	ENU04907	ANT61C6337:	71-90	800-819	NAP		g3451309	427	140	6.00E-45	40	95	(AL031324) transcription initiation factor IIIe beta subunit (TFIIE-beta)
		25..904											[Schizosaccharomyces pombe]
21114	ENU04908	ANT61C6864:	22-48	804-824	NAP		g4063002	937	228	4.00E-59	42	35	(AB021703) fr [Neurospora crassa]
		2562..4261											(Z97052) putative ubiquinone biosynthesis methyltransferase
21115	ENU04909	ANT61S4630:			NAP		g2213547	201	95	1.00E-19	46	33	[Schizosaccharomyces pombe]
		561..258											[Schizosaccharomyces pombe]
21116	ENU04910	ANT61C4391:	33-52	411-430	NAP		g1723516	327	144	4.00E-34	59	53	(Z97052) putative ubiquinone biosynthesis methyltransferase
		5103..4750											[Schizosaccharomyces pombe]
21117	ENU04911	ANT61C1164:	31-53	247-266	NAP		g101797	469	195	8.00E-50	85	33	hypothetical 24.4 KD protein
		2089..1757											C22E12.02 in chromosome I
21118	ENU04912	ANT61C8818:	122-142	397-416	NAP		g3170523	546	191	2.00E-48	94	10	[Schizosaccharomyces pombe]
		4250..3805											quinate 5-dehydrogenase (EC 1.1.1.24)
21119	ENU04913	ANT61C2376:	30-49	786-805	NAP		g2497129	446	111	6.00E-24	38	72	- Emericella nidulans []
		159..1272											(AF053883) coatomer alpha subunit
21120	ENU04914	ANT61C3368:	22-41	800-827	NAP		g1351682	425	82	3.00E-16	28	48	[Emmericella nidulans]
		3477..1762											hypothetical 38.2 KD protein in SUB1-ARGR1 intergenic region
21121	ENU04915	ANT61C9569:	24-43	804-829	NAP		g1154950	129	47	2.00E-11	27	35	[Saccharomyces cerevisiae]
		2051..741											hypothetical 53.5 KD protein
21122	ENU04916	ANT61C8170:	28-47	775-794	NAP		g2147662	1979	238	4.00E-62	46	12	CIF5.07C in chromosome I
		1..2682											[Schizosaccharomyces pombe]
21123	ENU04917	ANT61C6409:	95-114	551-577	NAP		g730338	774	289	1.00E-77	67	36	(X94769) choline dehydrogenase
		678..1											[Rattus rattus]
21124	ENU04918	ANT61C9456:	46-65	734-757	NAP		g1173091	497	171	4.00E-42	49	63	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]
		1444..667											lysophospholipase precursor (phospholipase B) [Penicillium chrysogenum]
21125	ENU04919	ANT61C9369:	84-106	500-527	NAP		g1703371	253	93	8.00E-24	43	22	ran GTPASE activating protein 1 (RNAI protein) [Schizosaccharomyces pombe]
		1..548											sterol O-acyltransferase 2 (sterol-ester synthase 2) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21126	ENU04920	AN161C7770:	72-91	689-710	NAP		g1352918	517	179	6.00E-45	44	55	CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PSEP 1) (A-factor converting enzyme) [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
21127	ENU04921	AN161C8438:	37-56	745-764	NAP		g4499843	609	91	2.00E-19	38	53	(L47346) alpha-glucoside permease [Saccharomyces cerevisiae] (U32375) tartrate dehydrogenase [Agrobacterium vitis] (AL023534) putative methionine aminopeptidase 1 [Schizosaccharomyces pombe] (AL031179) atp synthase delta chain family; oligomycin sensitivity conferring protein [Schizosaccharomyces pombe] 4-carboxymuconolactone decarboxylase (CMD) [Acinetobacter calcoaceticus]
21132	ENU04926	AN161C2478:	22-48	454-478	NAP		g118292	258	109	1.00E-23	38	100	hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (AC005313) unknown protein [Arabidopsis thaliana]
21133	ENU04927	AN161C4431:	27-46	807-828	NAP		g2132120	139	175	5.00E-43	27	19	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment) [Schizosaccharomyces pombe] ORF5 - Alcaigenes eutrophus [Ralstonia eutrophus]
21134	ENU04928	AN161C6376:	22-47	805-828	NAP		g3548818	348	134	1.00E-30	37	64	"dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glied) [Neurospora crassa]"
21135	ENU04929	AN161C8026:	26-45	613-632	NAP		g2130442	1140	129	5.00E-34	33	29	putative folypolyglutamate synthase (folypoly-gamma-glutamate synthetase) (FPGS) [Saccharomyces cerevisiae]
21136	ENU04930	AN161C5280:	40-59	605-624	NAP		g2120955	387	175	2.00E-43	46	67	
21137	ENU04931	AN161C7663:	24-43	704-731	NAP		g2493479	860	196	2.00E-49	47	21	
21138	ENU04932	AN161S996:	1. 28-48	249-273	NAP		g2494589	129	58	0.000000	37	22	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21139	ENU04933	ANI61C1866: 1576..1092	42-61	436-463	NAP		g2997731	650	222	1.00E-57	68	48	(AF054512) endoglucanase V [Aspergillus aculeatus]
21140	ENU04934	ANI61C7308: 113-132	524-543		NAP		g2117031	538	190	7.00E-51	62	37	(X94220) rhamnoglucuronase [Aspergillus niger]
21141	ENU04935	ANI61C6373: 1..637	22-49	680-702	NAP		g1546072	828	75	7.00E-13			(U68040) polyketide synthase [Cochliobolus heterostrophus]
21142	ENU04936	ANI61C1004: 3:4535..1974	22-47	809-829	NAP		g2465160	1351	92	5.00E-38	41	24	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
21143	ENU04937	ANI61C6032: 1..657	152-171	533-558	NAP		g1723241	167	72	4.00E-12	29	29	hypothetical 60.7 KD protein C26A3.15C in chromosome I [Schizosaccharomyces pombe]
21144	ENU04938	ANI61C3309: 2809..1386	27-46	768-787	NAP		g2440206	1169	155	7.00E-59	56	33	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
21145	ENU04939	ANI61C9915: 906..1	58-81	805-825	NAP		g1169440	1451	321	e-150	97	6	"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"
21146	ENU04940	ANI61C4247: 1..1862	23-45	752-778	NAP		g2342601	1009	261	6.00E-69	47	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21147	ENU04941	ANI61C3772: 1125..814	72-91	253-272	NAP		g549657	284	98	2.00E-20	54	24	hypothetical 49.0 KD protein UFD4-CAP1 intergenic region [Saccharomyces cerevisiae]
21148	ENU04942	ANI61C7930: 1..1336	44-63	611-632	NAP		g3334134	203	48	0.00006	30	36	chromatin assembly factor 1 P90 subunit (CAF-1 90 KD subunit) (RAP1 localization factor 2) [Saccharomyces cerevisiae]
21149	ENU04943	ANI61C9002: 1069..579	57-76	447-466	NAP		g3687473	191	52	2.00E-10	44	99	(AL031798) WD repeat protein [Schizosaccharomyces pombe]
21150	ENU04944	ANI61S3829: 1..529			NAP		g758803	90	46	0.0001	24	33	(U23828) peritrophin-95 precursor [Lucilia cuprina]
21151	ENU04945	ANI61C4391: 2057..1	22-40	712-731	NAP		g3114719	949	72	4.00E-12	38	13	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckelliana]
21152	ENU04946	ANI61C1720: 1181..1	116-138	721-748	NAP		g2791647	409	82	9.00E-23	29	48	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
21153	ENU04947	ANI61C1069: 1:1..435	22-48	383-402	NAP		g2132249	348	123	6.00E-28	56	72	hypothetical protein YPL252c - yeast [Saccharomyces cerevisiae]
21154	ENU04948	ANI61S3700: 457..1	113-132	408-428	NAP		g2462832	700	184	6.00E-69	92	26	(AF000657) similar to Bacillus Cota [Arabidopsis thaliana]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21155	ENU04949	AN161C8568: 22-45	453-475	NAP		g4176522	291	136	2.00E-31	30	47	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
21156	ENU04950	AN161C8225: 39-62	806-829	NAP		g3264834	810	109	1.00E-45	46	77	(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermiis]
21157	ENU04951	AN161C4401: 22-43	663-690	NAP		g1351102	282	124	2.00E-34	44	53	putative agmatinase precursor (agmatine ureohydrolase) (AUH) [Schizosaccharomyces pombe]
21158	ENU04952	AN161S4151: 31-51	245-271	NAP		g4514357	215	82	1.00E-17	35	100	(AB013376) unknown [Bacillus halodurans]
21159	ENU04953	AN161C1075: 197-216	568-587	NAP		g730745	327	132	2.00E-30	38	17	osomolarity two-component system protein SLN1 [Saccharomyces cerevisiae]
21160	ENU04954	AN161C279:1 111-129	501-526	NAP		g3319315	271	104	5.00E-22	49	15	(AF074951) cellobiose dehydrogenase [Thielavia heterothalica]
21161	ENU04955	AN161C1025: 23-48	428-447	NAP		g1723260	396	173	8.00E-43	52	27	hypothetical GTP-binding protein C3F10.16C in chromosome I [Schizosaccharomyces pombe]
21162	ENU04956	AN161C9690: 27-54	688-715	NAP		g1166378	569	111	8.00E-24	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" (AF095741) unknown [Rattus norvegicus]
21163	ENU04957	AN161C1050: 32-51	472-491	NAP		g3747107	96	67	1.00E-10	35	38	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis]
21164	ENU04958	AN161C7276: 6137..5602		NAP		g3912991	237	110	8.00E-24	39	19	coat assembly complex beta adaptin subunit [Rattus norvegicus]
21165	ENU04959	AN161C5836: 56-77	597-624	NAP		g4557469	620	185	4.00E-66			hypothetical 62.3 KD protein in PTP3-ILV1 intergenic region [Saccharomyces cerevisiae]
21166	ENU04960	AN161C5110: 22-43	712-731	NAP		g731485	811	159	5.00E-73	51	48	(D64006) Ap-4-A phosphoriylase II [Synechocystis sp.]
21167	ENU04961	AN161C5433: 687..1068		NAP		g1001338	87	65	2.00E-12	27	50	hypothetical 36.4 KD protein in POP2-HOL1 intergenic region [Saccharomyces cerevisiae]
21168	ENU04962	AN161C3958: 79-98	370-389	NAP		g1730686	96	39	0.014	25	45	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21169	ENU04963	AN161C84:10 22-41	712-731	NAP		g2132651	712	249	3.00E-65	42	48	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]
21170	ENU04964	AN161S1096: 38-57	445-464	NAP		g2673951	655	210	3.00E-58	66	16	

Seq num	Seq id	Contig source	5 pos	3 pos	Primer	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21171	ENU04965	ANI61C5094:	107-126	353-372		NAP		g584806	431	180	4.00E-45	62	23	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21172	ENU04966	ANI61C3659:	48-68	291-310		NAP		g849206	519	213	4.00E-55	74	26	(U28373) Etf1p: Elongation factor 2 (Swiss Prot. accession number P32324). Note that the entire gene is not included in this cosmid.
21173	ENU04967	ANI61C2382:	49-76	614-641		NAP		g1351604	150	52	2.00E-10	26	66	[Saccharomyces cerevisiae] hypothetical 40.0 KD protein C4G8.14C in chromosome I []
21174	ENU04968	ANI61C1180:	22-47	684-709		NAP		g2408064	161	94	9.00E-19	29	23	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
21175	ENU04969	ANI61C2243:	22-41	728-749		NAP		g2408021	352	120	1.00E-26	37	41	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21176	ENU04970	ANI61C2141:	22-43	658-677		NAP		g4249560	1044	268	1.00E-90	72	51	(AB003109) beta-glucosidase [Hunnicola grisea var. thermoides]
21177	ENU04971	ANI61C9921:	24-51	539-565		NAP		g549643	191	79	3.00E-14	33	18	hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region [Saccharomyces cerevisiae]
21178	ENU04972	ANI61C2170:	23-42	714-740		NAP		g1709064	782	314	5.00E-85	57	75	MNN9 protein [Candida albicans]
21179	ENU04973	ANI61C7073:	68-88	360-381		NAP		g454438	317	111	2.00E-30	60	10	(L28110) LON gene of S. cerevisiae is downstream of the HAP 3 gene; Putative ATP-binding motif bp 1960 to bp 1986.; Putative catalytic site serine of serine proteases from bp 3109 to bp 3111 [Saccharomyces cerevisiae]
21180	ENU04974	ANI61C1121	52-71	601-628		NAP		g731024	387	138	3.00E-32	40	49	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
21181	ENU04975	ANI61C2031:	69-96	356-383		NAP		g2687850	120	77	9.00E-14	24	25	(Y15839) fatty acid transporter protein [Coeliobolus heterotrophus]
21182	ENU04976	ANI61S4631:				NAP		g4589850	142	62	0.000000	32	26	(AB025967) chorogenin Hminor [Oryzias latipes]
21183	ENU04977	ANI61C7290:				NAP		g2072023	420	138	3.00E-32	53	100	(U93506) symbiosis-related protein [Laccaria bicolor]
21184	ENU04978	ANI61C6657:	103-123	421-440		NAP		g1073534	185	89	2.00E-17	39	43	incB protein - Escherichia coli [Escherichia coli]

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21185	ENU04979	ANT61C1051	28-55	807-829	NAP		g10855432	147	38	0.07			mucin (clone PGM-2A) - pig [Sus scrofa]
21186	ENU04980	ANT61C7282: 2:5237..3644	31-58	465-489	NAP		g4262216	336	138	2.00E-32	35	64	(AC006161) putative DNA binding protein [Arabidopsis thaliana]
21187	ENU04981	ANT61S1306: 554..1			NAP		g4218005	179	49	0.00003	21	31	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21188	ENU04982	ANT61C1082	116-135	662-686	NAP		g4538673	116	70	1.00E-11	26	57	"(AL049474) putative lipid metabolism protein, sphingomyelinase family similarity [Schizosaccharomyces pombe]"
21189	ENU04983	ANT61C1252: 729..1091	36-55	418-436	NAP		g773414	434	183	8.00E-46	92	66	(U23751) beta galactosidase [Cloning vector pBBR1MCS-5]
21190	ENU04984	ANT61C439:9			NAP		g2330831	228	108	3.00E-23	26	53	(Z98530) myo-inositol transporter [Schizosaccharomyces pombe]
21191	ENU04985	ANT61C8782: 319..9705	29-50	720-739	NAP		g1351343	1615	547	e-155	98	26	positive regulator of purine utilisation [Emeticella nidulans]
21192	ENU04986	ANT61C295:6	157-184	797-824	NAP		g2648302	278	103	2.00E-32	44	86	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
21193	ENU04987	ANT61C6797: 1073..1	62-81	715-735	NAP		g2146821	548	91	1.00E-17	36	39	alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) []
21194	ENU04988	ANT61C346:8	139-166	433-452	NAP		g3136049	132	63	0.000000	36	38	(AL023592) putative phosphatidylinositol- glycan-class c protein [Schizosaccharomyces pombe]
21195	ENU04989	ANT61C7116: 2155..1			NAP		g2599548	1110	223	1.00E-57	40	34	(AF029346) chloride channel protein 3 [Oryctolagus cuniculus]
21196	ENU04990	ANT61C4598: 441..1	22-42	437-461	NAP		g1651554	745	294	2.00E-79	98	65	(D90748) Spermidine/putrescine transport system permease protein PotB. [Escherichia coli]
21197	ENU04991	ANT61C5425: 724..1	96-115	597-616	NAP		g2492660	334	129	2.00E-29	36	11	afatoxin biosynthesis polyketide synthase (PKS) [Aspergillus parasiticus]
21198	ENU04992	ANT61C8486: 2325..3743	22-42	807-829	NAP		g1176339	671	209	2.00E-53	43	60	hypothetical 50.8 KID protein in MIR1-STE18 intergenic region [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21199	ENU04993	ANI61C948:1..580			NAP		g2190551	170	108	4.00E-23	28	38	"(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb Z71181). ESTs
21200	ENU04994	ANI61C4231: 1926..2480	22-41	414-435	NAP		g3859773	141	73	1.00E-12	32	20	gb H36844.gb AA394956 come from this gene. [Arabidopsis thaliana]"
21201	ENU04995	ANI61C6504: 1220..1	65-84	729-747	NAP		g728850	110	35	0.61			(Z98598) hypothetical protein [Schizosaccharomyces pombe]"
													"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase)
													[Saccharomyces cerevisiae var. diastaticus]"
21202	ENU04996	ANI61C1933: 1..571			NAP		g4249560	560	225	2.00E-58	66	34	(AB003109) beta-glucosidase [Humicola grisea var. thermoidae]"
21203	ENU04997	ANI61C6870: 1120..1	22-49	806-829	NAP		g2388995	360	148	4.00E-35	36	56	(Z98981) hypothetical protein [Schizosaccharomyces pombe]"
21204	ENU04998	ANI61S913:1..754			NAP		g107749	124	71	1.00E-11	27	34	synapsin I splice form a - human []"
21205	ENU04999	ANI61C2450: 1269..1	74-93	712-731	NAP		g1360744	340	84	3.00E-25	34	14	"ankyrin 1, erythrocyte form 3 - human []"
21206	ENU05000	ANI61S719:4 91..1	23-41	451-470	NAP		g2656001	211	92	2.00E-18	39	20	(Z98977) hypothetical protein [Schizosaccharomyces pombe]"
21207	ENU05001	ANI61C1120 5:9128..8237	22-49	802-829	NAP		g3879734	269	79	2.00E-18	38	93	(Z93388) predicted using GeneFinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727... []"
21208	ENU05002	ANI61C7395: 906..2125	22-47	744-764	NAP		g1723736	720	187	7.00E-47	43	43	hypothetical 68.3 KD protein in PDX1-SNG1 intergenic region [Saccharomyces cerevisiae]"
21209	ENU05003	ANI61C3250: 1100..1	60-79	726-743	NAP		g2625138	574	233	1.00E-60	39	17	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]"
21210	ENU05004	ANI61C5872: 1..969	22-42	804-829	NAP		g2492658	1336	314	7.00E-85	99	12	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emmericella nidulans]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21211	ENU05005	ANT61C9398: 666..1	102-124	523-547	NAP		g2851654	282	71	4.00E-22	43	31	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21212	ENU05006	ANT61C1139: 3:2741..4047	22-47	795-814	NAP		g2498757	378	96	3.00E-19	31	52	peroxisomal membrane protein PAS2 (peroxin-3) [Pichia pastoris]
21213	ENU05007	ANT61C5990: 1689..1400	102-124	250-267	NAP		g2499716	206	94	3.00E-19	45	22	"exopolygalacturonase precursor (exoPg) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
21214	ENU05008	ANT61C5102: 1..502	139-163	426-445	NAP		g3116147	179	67	2.00E-14	34	27	(AL023290) amino acid permease [Schizosaccharomyces pombe]
21215	ENU05009	ANT61C1061: 3:945..1	26-46	722-749	NAP		g730745	63	48	0.00006	27	16	osomolarly two-component system protein SLN1 [Saccharomyces cerevisiae]
21216	ENU05010	ANT61C5586: 1296..2033			NAP		g101797	1141	455	e-127	91	74	quinate 5-dehydrogenase (EC 1.1.1.24) - Emericella nidulans []
21217	ENU05011	ANT61C1129: 2:2645..2267	164-183	336-358	NAP		g417321	189	83	8.00E-16	46	33	methylentetrahydrofolate dehydrogenase (NAD+) [Saccharomyces cerevisiae]
21218	ENU05012	ANT61C1543: 928..625			NAP		g1870219	78	45	0.0002	30	99	(AC000133) ORF [Emericella nidulans]
21219	ENU05013	ANT61C8821: 1284..376	24-50	791-818	NAP		g2498849	263	123	1.00E-27	33	86	replication factor-A protein 2 (single-stranded DNA-binding protein P30 subunit) [Schizosaccharomyces pombe]
21220	ENU05014	ANT61C7941: 928..1	118-137	719-736	NAP		g2257514	387	157	6.00E-40	38	51	(AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
21221	ENU05015	ANT61C5148: 1..550	110-129	454-473	NAP		g2493491	44	46	0.0002	25	92	hypothetical protein MJ0304 [Methanococcus jannaschii]
21222	ENU05016	ANT61C7063: 3083..1			NAP		g2342601	1262	77	1.00E-13	27	4	(X89442) peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21223	ENU05017	ANI61C2576: 3088..4293	24-44	786-805	NAP		g1711573	610	156	6.00E-46	48	76	"probable succinyl-CoA ligase (GDP-forming), alpha-chain precursor (succinyl-CoA synthetase, alpha chain) (SCS-alpha) ["]
21224	ENU05018	ANI61S335:5 39..1	63-90	486-509	NAP		g3860271	877	353	7.00E-97	97	20	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
21225	ENU05019	ANI61C1118 5:657..1	22-45	525-548	NAP		g585169	422	129	4.00E-45	49	27	UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase)
21226	ENU05020	ANI61C9007: 1.605	102-125	558-584	NAP		g730017	282	83	5.00E-20	50	26	[Saccharomyces cerevisiae] cystathionine gamma-synthase (O-succinylhomoserine (thiol)-lyase) [probable ATP-dependent DNA helicase C4H3.05 [Schizosaccharomyces pombe]
21227	ENU05021	ANI61C1183: 2222..1	68-87	717-736	NAP		g1723281	1051	122	3.00E-27	33	29	hypothetical 95.4 KD protein in SEC4-MSH4 intergenic region [Saccharomyces cerevisiae]
21228	ENU05022	ANI61C8411: 754..2343	30-57	779-799	NAP		g1175914	811	248	4.00E-65	42	34	(AF015561) RO10 [Neurospora crassa]
21229	ENU05023	ANI61C1834: 1947..2749	104-131	756-782	NAP		g2353165	186	46	0.0002	34	97	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emeticella nidulans]
21230	ENU05024	ANI61S578:6 24..1			NAP		g1705828	157	69	9.00E-12	33	18	(AL021246) echA14 [Mycobacterium tuberculosis]
21231	ENU05025	ANI61C1040 4:1486..565	41-60	795-822	NAP		g2791526	118	41	0.000000	32	63	putative tartarate transporter [Agrobacterium vitis]
21232	ENU05026	ANI61C1120 1:1734..2597	22-48	781-802	NAP		g4033481	233	69	2.00E-20	29	53	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
21233	ENU05027	ANI61C3812: 545..1	22-49	503-524	NAP		g3522935	63	57	0.000000	25	59	HOS3 protein [Saccharomyces cerevisiae]
21234	ENU05028	ANI61C2852: 1883..1	84-103	714-736	NAP		g2833193	594	85	6.00E-16	28	34	(AF009417) cytochrome P450 [Myrothecium roridum]
21235	ENU05029	ANI61C5843: 1..941	61-81	806-829	NAP		g2267601	306	120	1.00E-26	33	47	(Y17243) cytochrome P450 [Gibberella fujikuroi]
21236	ENU05030	ANI61C626:1 233..1	80-99	718-735	NAP		g4127832	601	144	6.00E-47	41	51	hypothetical 118.6 KD protein C29E6.03C in chromosome I [Schizosaccharomyces pombe]
21237	ENU05031	ANI61C8459: 9479..5897	33-53	805-828	NAP		g1351618	585	67	1.00E-10			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21238	ENU05032	ANI61C1121: 4754..3724	22-42	802-829	NAP		g124871	489	151	6.00E-46	40	87	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) [Kluyveromyces lactis]
21239	ENU05033	ANI61C4611: 1755..1	28-47	728-747	NAP		g3417410	1275	252	2.00E-66	50	31	(AL031261) sulfate permease [Schizosaccharomyces pombe]
21240	ENU05034	ANI61C1027: 8:2501..4162	22-48	782-808	NAP		g1870209	2360	476	e-134	85	51	(AC000133) ORF [Emeticella nidulans]
21241	ENU05035	ANI61C1047: 1:862..1278	33-52	413-432	NAP		g4056552	379	114	2.00E-36	59	43	(AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]
21242	ENU05036	ANI61C8687: 2011..1	43-62	626-645	NAP		g3912991	2086	419	e-116	67	33	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis]
21243	ENU05037	ANI61C7437: 1159..637	102-126	454-473	NAP		g2980827	114	80	8.00E-15	41	32	(AL022172) protein kinase [Schizosaccharomyces pombe]
21244	ENU05038	ANI61C6321: 3230..2423	62-80	747-766	NAP		g1680605	442	100	1.00E-42	52	99	(S59774) RNA polymerase subunit [Saccharomyces cerevisiae]
21245	ENU05039	ANI61C2198: 983..1	141-162	718-745	NAP		g547861	611	246	2.00E-64	48	32	ATP-dependent protease LA 2 [Myxococcus xanthus]
21246	ENU05040	ANI61C4414: 259..1253	22-46	801-828	NAP		g1730705	400	90	6.00E-38	42	92	hypothetical 27.5 KD protein in SPO1-SIS1 intergenic region [Saccharomyces cerevisiae]
21247	ENU05041	ANI61C6703: 3118..4359	51-73	805-829	NAP		g3261634	474	171	7.00E-42	42	40	(Z79700) hypothetical protein Rv0976c [Mycobacterium tuberculosis]
21248	ENU05042	ANI61C1053: 3:1539..2879	22-42	616-634	NAP		g3080527	872	206	2.00E-52	43	65	(AL022600) putative mannose-1-phosphate gaunyl transferase [Schizosaccharomyces pombe]
21249	ENU05043	ANI61S1767: 1..595	39-58	457-478	NAP		g539079	698	285	2.00E-76	70	16	peroxisomal assembly protein 5 - yeast [Pichia pastoris] []
21250	ENU05044	ANI61S3339: 1..831			NAP		g1076802	116	37	0.000002	30	21	extensin-like protein - maize [Zea mays]
21251	ENU05045	ANI61C1089: 7:1..972	66-85	711-731	NAP		g731288	185	64	0.000000	25	35	hypothetical 87.5 KD protein in ACS1-GCV3 intergenic region [Saccharomyces cerevisiae]
21252	ENU05046	ANI61C9718: 665..328	25-48	292-316	NAP		g4100190	153	87	5.00E-17	40	26	"(U95181) 2,5 dihydroxyphenylacetate oxidase [Caenorhabditis elegans]"
21253	ENU05047	ANI61S371:1..490			NAP		g539218	96	43	0.002	16	30	hypothetical protein YKL201c - yeast [Saccharomyces cerevisiae] []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21254	ENU05048	AN161C8803:	31-50	806-829	NAP		g4502091	410	160	1.00E-38	33	7	"ankyrin 2, neuronal [Homo sapiens]"
21255	ENU05049	AN161C8498:	22-47	808-829	NAP		g4176530	2328	277	3.00E-86	57	22	(AL035263) putative condensin subunit [Schizosaccharomyces pombe]
21256	ENU05050	AN161C1137:	5241..1481		NAP		g4468948	1258	490	e-138	92	49	(X00790) cytochrome oxidase I [Emmericella nidulans]
21257	ENU05051	AN161C4514:	431..1282		NAP		g729967	150	75	1.00E-13	36	39	homocitrate dehydratase [Saccharomyces cerevisiae]
21258	ENU05052	AN161C5723:	23-50	665-692	NAP		g3318897	453	221	4.00E-57	41	42	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["]
21259	ENU05053	AN161C7280:	22-46	802-821	NAP		g3914344	344	128	6.00E-29			3-phyltyase precursor [Bacillus sp.]
21260	ENU05054	AN161C1544:	112-132	711-733	NAP		g2828341	165	98	1.00E-19	30	18	(AB004305) mBLVR [Mus musculus]
21261	ENU05055	AN161C8211:	69-87	747-766	NAP		g1077413	809	260	2.00E-87	66	99	hypothetical protein YLR186w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21262	ENU05056	AN161S9:1..5			NAP		g2465558	162	79	2.00E-14	37	74	(AF011545) YedB [Bacillus subtilis]
21263	ENU05057	AN161C9836:	22-45	804-828	NAP		g1351714	749	154	8.00E-37	34	55	putative transporter C11D3.18C [Schizosaccharomyces pombe]
21264	ENU05058	AN161C8454:	48-68	766-785	NAP		g2132208	739	210	1.00E-53	41	31	hypothetical protein YPL150w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21265	ENU05059	AN161S13:69	157-174	618-645	NAP		g2804470	120	81	7.00E-15	28	16	(AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]
21266	ENU05060	AN161C5161:	34-53	627-647	NAP		g3668157	513	82	5.00E-15			(AL031764) putative exocyst complex component [Schizosaccharomyces pombe]
21267	ENU05061	AN161C229:1	33-59	624-643	NAP		g419963	226	73	3.00E-12	44	83	snRNP protein B - fruit fly (Drosophila melanogaster) [Drosophila melanogaster]
21268	ENU05062	AN161C728:2			NAP		g3025214	231	80	1.00E-17	36	36	hypothetical 65.9 KD protein in SSP120-HAP1 intergenic region [Saccharomyces cerevisiae]
21269	ENU05063	AN161C9372:	115-134	388-407	NAP		g2146853	325	90	1.00E-17	45	32	alpha-galactosidase (EC 3.2.1.22) III precursor - fungus (Trichoderma reesei) [Hypocrea jecorina]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21270	ENU05064	AN161C6066:	192-211	455-479		NAP		g83697	633	254	4.00E-67	83	100	catabolic 3-dehydrogenase - Emericella nidulans [Emericella nidulans]
21271	ENU05065	AN161C1113	64-82	786-804		NAP		g2507475	365	93	2.00E-18	36	9	Paired amphipathic helix protein [Saccharomyces cerevisiae]
21272	ENU05066	AN161C3518:	210-237	571-598		NAP		g538067	157	44	0.0008	29	14	(M77661) putative pol polyprotein [Magnaporthe grisea]
21273	ENU05067	AN161C9741:	55-74	794-813		NAP		g2970627	725	289	2.00E-77	50	86	(AF051914) C-4 methyl sterol oxidase [Candida albicans]
21274	ENU05068	AN161C9993:	107-130	673-699		NAP		g1723552	325	130	1.00E-29	44	62	putative mitochondrial carrier protein C12B10.09 [Schizosaccharomyces pombe]
21275	ENU05069	AN161C4742:	73-92	621-638		NAP		g3183171	784	318	2.00E-86	61	25	"probable alanyl-tRNA synthetase, cytoplasmic (alanine--tRNA ligase) (ALARS) [Schizosaccharomyces pombe]"
21276	ENU05070	AN161S4634:				NAP		g731584	114	31	6	35	60	hypothetical 17.1 KD protein in PUR5 3region [Saccharomyces cerevisiae]
21277	ENU05071	AN161C6461:	101-120	679-696		NAP		g2626826	170	137	2.00E-32	31	17	(D83967) YrkN [Bacillus subtilis]
21278	ENU05072	AN161C720:	147-66	800-824		NAP		g4505823	640	267	8.00E-71	48	94	pirin [Homo sapiens]
21279	ENU05073	AN161C276:	142-67	765-788		NAP		g2224775	595	226	2.00E-58	43	71	(Z97025) pyruvate carboxylase [Bacillus subtilis]
21280	ENU05074	AN161C9649:	26-45	650-677		NAP		g1546072	555	167	8.00E-41	37	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21281	ENU05075	AN161S1135:				NAP		g4008576	172	53	0.000002	34	37	"(AL034491) similar to yeast transcription initiation factor iif, alpha subunit [Schizosaccharomyces pombe]"
21282	ENU05076	AN161S1439:				NAP		g3329623	156	45	0.0007	17	69	(AF078790) No definition line found [Caenorhabditis elegans]
21283	ENU05077	AN161C1060	94-116	798-817		NAP		g1351343	1530	493	e-149	96	26	positive regulator of purine utilisation [Emericella nidulans]
21284	ENU05078	AN161C8743:				NAP		g3646453	331	138	3.00E-32	38	100	(AL031603) putative succinate dehydrogenase cytochrome b subunit precursor [Schizosaccharomyces pombe]
21285	ENU05079	AN161C7969:				NAP		g208131	126	64	5.00E-10	42	98	(M77169) beta-galactosidase alpha-peptide [Shuttle vector pJIR1457]

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21286	ENU05080	ANT61C9657:	44-63	800-820	NAP		g400269	1494	377	e-104	64	52	Methylmalonate-semialdehyde dehydrogenase precursor (acylating) (MMSDH) [Rattus norvegicus]
21287	ENU05081	ANT61C6968:	28-48	808-829	NAP		g1399263	1443	469	e-131	96	60	(U28383) cystathionine beta-lyase [Emmericella nidulans]
21288	ENU05082	ANT61C1441:	121-141	664-683	NAP		g462168	617	248	3.00E-65	46	9	translational activator GCN1 [Saccharomyces cerevisiae]
21289	ENU05083	ANT61C249:5	93-112	317-344	NAP		g4757128	78	55	0.000000			(AJ238717) ZRP protein [Rattus norvegicus]
21290	ENU05084	ANT61S3273:			NAP		g283032	92	49	0.00003	27	57	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
21291	ENU05085	ANT61C6213:	22-41	805-829	NAP		g3283220	1109	200	1.00E-71	56	51	(AF061241) splicing factor hPRP17 [Homo sapiens]
21292	ENU05086	ANT61C3458:	102-121	666-685	NAP		g2673947	594	226	2.00E-58	52	18	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21293	ENU05087	ANT61S1524:			NAP		g168082	69	48	0.00004	35	17	(M59935) negative-acting regulatory protein [Emmericella nidulans]
21294	ENU05088	ANT61C5043:	38-57	750-769	NAP		g3006156	905	175	6.00E-70	52	52	(AL022299) putative serine palmitoyltransferase [Schizosaccharomyces pombe]
21295	ENU05089	ANT61C1208:			NAP		g4867801	1922	49	0.00004			(AJ132442) phenylacetate 2-hydroxylase [Emmericella nidulans]
21296	ENU05090	ANT61C2406:	118-137	638-658	NAP		g584839	599	239	1.00E-62			beta-glucuronidase (GUS) (beta-D-glucuronoside glucuronosohydrolase) [Escherichia coli]
21297	ENU05091	ANT61C1087			NAP		g2224699	97	67	9.00E-11	27	18	(AB002377) KIAA0379 [Homo sapiens]
21298	ENU05092	ANT61C721:5	65-87	468-492	NAP		g548669	313	151	3.00E-36	44	17	DNA repair protein RAD8 [Schizosaccharomyces pombe]
21299	ENU05093	ANT61C1097	29-56	719-746	NAP		g4481954	1614	363	e-100	74	31	(AL035637) putative protease subunit; chaperonin [Schizosaccharomyces pombe]
21300	ENU05094	ANT61C5311:	22-45	463-482	NAP		g543325	188	92	3.00E-20	33	56	small nuclear ribonucleoprotein U1A - mouse [Mus musculus]
21301	ENU05095	ANT61S3796:			NAP		g4490609	361	109	6.00E-28	53	22	(AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]
21302	ENU05096	ANT61S2956:	35-53	287-306	NAP		g2956768	109	45	0.00001	29	33	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21303	ENU05097	AN161C9512: 1490..2267	23-50	736-757	NAP		g3183392	386	92	2.00E-36	45	99	hypothetical 24.1 KD protein C17A5.08 in chromosome I precursor [Schizosaccharomyces pombe] (Z99107) yeta [Bacillus subtilis]
21304	ENU05098	AN161C6112: 983..1	26-45	722-749	NAP		g2633022	585	225	4.00E-58	43	31	hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii] (AF007865) bacitracin synthetase 1; BacA [Bacillus licheniformis] (AF052061) polygalacturonase [Ophiostoma novo-ulmi] (L35487) mannanase [Aspergillus aculeatus] putative sterigmatocystin biosynthesis ketoreductase STCE [Emericella nidulans] (AF059534) severin kinase [Dictyostelium discoideum] proline-rich protein MRP2 - mouse (fragment) [] hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii] (Y07919) beta-prime-adaptin protein [Mus musculus] transcription elongation factor S-II (TFIIS) [Schizosaccharomyces pombe] (Z99531) ubiquitin system protein [Schizosaccharomyces pombe] ARP2/3 complex 20 KD subunit (P20-ARC) [Homo sapiens] (AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum] hypothetical 49.1 KD protein C11D3.06 in chromosome I [Schizosaccharomyces pombe]
21305	ENU05099	AN161C3343: 6378..5998	22-49	420-439	NAP		g1076211	101	33	1.6			
21306	ENU05100	AN161C1093: 4:2210..344	22-44	808-829	NAP		g2982194	494	163	1.00E-39	38	5	
21307	ENU05101	AN161C9439: 102-123	414-438	NAP			g2967835	312	70	1.00E-27	55	34	
21308	ENU05102	AN161C1118: 6:6780..6338	104-130	396-422	NAP		g558311	294	132	9.00E-31	52	34	
21309	ENU05103	AN161C7701: 1654..687	59-76	773-792	NAP		g2492756	1193	372	e-102	95	92	
21310	ENU05104	AN161C2235: 3153..1469	45-64	799-826	NAP		g3075511	823	58	0.000000	27	49	
21311	ENU05105	AN161C5581: 1..502			NAP		g91209	123	57	0.000000	29	67	
21312	ENU05106	AN161C9514: 1675..1088	118-138	525-552	NAP		g1076211	60	43	0.001	27	34	
21313	ENU05107	AN161C4192: 2141..1	42-61	722-749	NAP		g2398720	1362	271	4.00E-72	51	27	
21314	ENU05108	AN161C2192: 892..390	40-58	431-450	NAP		g1351227	385	148	2.00E-35	43	57	
21315	ENU05109	AN161C1130: 1:1..2848	48-71	782-806	NAP		g2440180	473	32	6.9			
21316	ENU05110	AN161C7737: 1616..1089	60-80	484-507	NAP		g3121766	329	128	8.00E-30	72	68	
21317	ENU05111	AN161S2227: 1..755			NAP		g4063042	154	39	0.033	30	11	
21318	ENU05112	AN161C123:9: 66..1	24-43	794-813	NAP		g1351703	856	284	7.00E-76	56	58	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21319	ENU05113	ANI61C5332: 1091..2649	27-46	802-829	NAP		g4033486	299	75	7.00E-13			putative tartrate transporter [Agrobacterium vitis]
21320	ENU05114	ANI61C4918: 1107..1	22-44	724-749	NAP		g1352677	1333	369	e-101	91	37	serine/threonine protein phosphatase 2B catalytic subunit (calmodulin-dependent calcineurin A subunit) [Emmericella nidulans] (AB001995) Tel1p [Schizosaccharomyces pombe]
21321	ENU05115	ANI61C3944: 3311..1	23-50	797-817	NAP		g3764029	825	168	6.00E-53	43	9	emopamil-binding protein - human [Homo sapiens]
21322	ENU05116	ANI61C8015: 35..834	69-88	756-775	NAP		g1362793	263	69	5.00E-11	33	99	(X98690) Pristinamycin I synthase 2 [Streptomyces pristinaespiralis]
21323	ENU05117	ANI61C5643: 1526..2246	27-45	671-694	NAP		g1483603	128	105	3.00E-22	36	8	(X89442) peptidase synthetase [Metarhizium anisopliae]
21324	ENU05118	ANI61C3986: 925..1	41-60	776-796	NAP		g2342601	437	188	5.00E-47	34	5	"(Z98978) SPAC27E2.06c, putative methionyl-tRNA synthetase, le n:539aa, similar eg. to YGR171C, SYMM_YEAST, P22438, methi onyl-tRNA synthetase; mitochondrial, (575aa), fasta scores, opt:396, E0:0, (39.9% identity in 546 aa o...]"
21325	ENU05119	ANI61C8013: 1411..3361	45-71	805-829	NAP		g2388946	958	85	2.00E-33	36	48	putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emmericella nidulans]
21326	ENU05120	ANI61C2723: 1..998	34-53	735-754	NAP		g2492661	1471	440	e-123	97	11	(U20808) auxin-induced protein [Vigna radiata]
21327	ENU05121	ANI61S2128: 94..537	107-125	390-407	NAP		g1184121	130	66	1.00E-10	31	46	DNA-directed RNA polymerase I 190 KD polypeptide (A190) [Saccharomyces cerevisiae]
21328	ENU05122	ANI61C1070: 6:2792..1	23-47	656-683	NAP		g2507346	1768	335	2.00E-91	54	16	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
21329	ENU05123	ANI61C4506: 496..1	102-128	453-472	NAP		g1790870	214	75	4.00E-13	44	50	(AL021070) ppsB [Mycobacterium tuberculosis]
21330	ENU05124	ANI61C4658: 1919..3382	23-43	799-823	NAP		g3261497	676	232	3.00E-60	43	18	(AC002292) Phosphatidylinositol 3-kinase [Arabidopsis thaliana]
21331	ENU05125	ANI61C4699: 489..1			NAP		g2462752	404	167	5.00E-41	51	20	hypothetical 83.4 KD protein in DSK2-CAT8 intergenic region [Saccharomyces cerevisiae]
21332	ENU05126	ANI61C4285: 2701..4130	42-61	765-784	NAP		g2497216	610	244	5.00E-64	49	35	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21333	ENU05127	ANT61C7878:	22-42	528-547	NAP		g1945326	184	91	5.00E-18	27	13	(Z72902) ORF YGR116w [Saccharomyces cerevisiae]
21334	ENU05128	ANT61S1312:			NAP		g1572721	137	41	0.008	28	15	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21335	ENU05129	ANT61C4899:	34-53	781-800	NAP		g57554	201	101	5.00E-21	32	47	(X65296) carboxylesterase [Rattus rattus]
21336	ENU05130	ANT61C3565:	74-93	711-730	NAP		g3913798	1464	439	e-122	72	52	"exoglucanase I precursor (exocellulohydrolase I) (1,4-beta-cellobiohydrolase I) (beta-glucanocellulohydrolase I) [Aspergillus aculeatus]"
21337	ENU05131	ANT61C9214:	218-244	802-829	NAP		g1729921	198	57	0.000000	39	55	Lipase 2 (triacylglycerol lipase) [Saccharomyces cerevisiae]
21338	ENU05132	ANT61S831:1.			NAP		g1176993	383	168	3.00E-41	44	88	hypothetical 26.6 KD sensory transduction protein in IDH 3'region [Bacillus subtilis]
21339	ENU05133	ANT61C4796:	22-47	528-547	NAP		g3915105	474	160	8.00E-39	61	33	threonine dehydratase precursor (threonine deaminase) [Arxula adenivorans]
21340	ENU05134	ANT61C2653:	92-111	540-559	NAP		g1130507	141	83	2.00E-15	31	46	(L41670) fumarylacetoacetate hydrolase [Emmericella nidulans]
21341	ENU05135	ANT61S957.5	188-215	486-513	NAP		g1652748	345	150	5.00E-36	48	65	(D90908) hypothetical protein [Synecocystis sp.]
21342	ENU05136	ANT61C953:7	22-43	653-679	NAP		g417321	527	205	2.00E-52	59	64	methylenetetrahydrofolate dehydrogenase (NAD+)
21343	ENU05137	ANT61C1080	114-133	550-570	NAP		g82852	614	231	3.00E-63	61	45	[Saccharomyces cerevisiae] hypothetical protein (LAC12 3' region) - yeast (Kluyveromyces marxianus var. lactis) [Kluyveromyces lactis]
21344	ENU05138	ANT61C4415:	51-70	537-555	NAP		g549009	201	67	4.00E-21	33	34	probable uroporphyrin-III C-methyltransferase (urogen III methylase) (SUMT) (uroporphyrinogen III methylase) (UROM) [Saccharomyces cerevisiae]
21345	ENU05139	ANT61C55:39	113-132	458-476	NAP		g3378433	233	80	6.00E-19	38	34	(AF079317) flavoprotein subunit p-crezol methylhydroxylase [Sphingomonas aromaticivorans]
21346	ENU05140	ANT61C489:5	118-135	507-528	NAP		g4185903	717	291	2.00E-78	80	32	(AJ132432) fimbria [Gibberella pulicaris]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21347	ENU05141	ANT61C3097:	113-132	625-647	NAP		g417038	640	193	2.00E-64	65	45	transcriptional activator GCN5 [Saccharomyces cerevisiae]
21348	ENU05142	ANT61C1204:	205-228	685-712	NAP		g4539186	192	111	7.00E-24	31	58	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]
21349	ENU05143	ANT61C1041	27-47	662-689	NAP		g731836	448	155	4.00E-50	51	37	probable mannosyltransferase KTR7 [Saccharomyces cerevisiae]
21350	ENU05144	ANT61C4688:	22-40	730-752	NAP		g549443	1580	257	e-126	96	12	condial green pigment synthase [Emertella nidulans]
21351	ENU05145	ANT61C8490:	40-59	773-792	NAP		g112984	1245	158	3.00E-70	68	53	"aspartate aminotransferase, mitochondrial precursor (Transaminase A) (glutamate oxaloacetate transaminase-2) [Mus musculus]" (AL031523) hypothetical protein [Schizosaccharomyces pombe]
21352	ENU05146	ANT61C1856:	22-46	449-476	NAP		g3560223	121	66	1.00E-10	29	48	(AL023776) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
21353	ENU05147	ANT61C3386	22-47	718-744	NAP		g3184060	578	123	6.00E-50	49	26	(AF064069) aryl-alcohol oxidase precursor [Pleurotus eryngii]
21354	ENU05148	ANT61C726:6	22-46	562-581	NAP		g3851524	190	97	1.00E-19	30	32	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
21355	ENU05149	ANT61C2963:	32-59	331-354	NAP		g3850084	156	75	3.00E-13	32	46	(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]
21356	ENU05150	ANT61C8811:	49-68	336-356	NAP		g3702632	300	128	2.00E-29	48	18	hypothetical 33.7 KD protein in ISC10 3region [Saccharomyces cerevisiae]
21357	ENU05151	ANT61C2538:	53-73	410-434	NAP		g731385	165	72	2.00E-12	34	48	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
21358	ENU05152	ANT61S1367:			NAP		g82698	210	45	0.0008	32	70	"(U75347) fatty acid synthase, alpha subunit [Emertella nidulans]"
21359	ENU05153	ANT61C6372:			NAP		g1805261	169	67	9.00E-11	33	9	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucose:oxygen 1-oxido-reductase) [Talaromyces flavus]
21360	ENU05154	ANT61C1057	22-44	700-719	NAP		g3287841	828	187	8.00E-47	63	43	hypothetical 68.5 KD protein in SCS3-SUP44 intergenic region [Saccharomyces cerevisiae]
21361	ENU05155	ANT61C7117:	25-48	375-398	NAP		g1723913	499	209	1.00E-53	63	27	

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21362	ENU05156	ANI61C3955:	120-138	486-505	NAP		g731968	486	203	1.00E-51	50	61	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region [Saccharomyces cerevisiae]
21363	ENU05157	ANI61C4224:	22-43	803-826	NAP		g4557481	761	148	4.00E-35	31	18	canalicular multispecific organic anion transporter [Homo sapiens]
21364	ENU05158	ANI61C7037:	1..1762		NAP		g4154078	195	93	7.00E-26	37	26	(AL035161) putative efflux protein [Streptomyces coelicolor]
21365	ENU05159	ANI61C856:2	57-76	451-470	NAP		g1170131	209	103	7.00E-22	37	35	glucarate dehydratase subunit (GDH) [Pseudomonas putida]
21366	ENU05160	ANI61C8308:	26-46	806-829	NAP		g1351678	130	43	0.003			hypothetical 41.5 KD protein C1F5.03C in chromosome I [Schizosaccharomyces pombe]
21367	ENU05161	ANI61C1012	26-53	723-749	NAP		g82798	844	197	4.00E-71	55	15	DNA-directed RNA polymerase (EC 2.7.7.6) I 189K chain - fission yeast (Schizosaccharomyces pombe) [Schizosaccharomyces pombe]
21368	ENU05162	ANI61S395:5	105-126	442-461	NAP		g4574121	146	85	4.00E-16	32	30	(AF009415) choline dehydrogenase [Staphylococcus xylosum]
21369	ENU05163	ANI61C9793:	22-48	781-803	NAP		g2342601	1701	158	4.00E-38	30	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21370	ENU05164	ANI61C7505:	69-88	774-796	NAP		g1363761	598	73	6.00E-15			probable membrane protein YPR194c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21371	ENU05165	ANI61C2147:	33-52	455-477	NAP		g1723578	296	130	2.00E-30	48	53	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
21372	ENU05166	ANI61C1526:	46-64	803-822	NAP		g4456821	1167	306	5.00E-99	76	56	(AL035548) casein kinase i homolog cki1 [Schizosaccharomyces pombe]
21373	ENU05167	ANI61C8658:	22-43	761-780	NAP		g3183368	810	191	7.00E-59	58	41	hypothetical 64.0 KD protein C20G4.05C in chromosome I [Schizosaccharomyces pombe]
21374	ENU05168	ANI61S2442:			NAP		g1805261	251	94	5.00E-19	43	9	"(U75347) fatty acid synthase, alpha subunit [Emeticella nidulans]"
21375	ENU05169	ANI61C8742:	22-47	728-749	NAP		g4106669	791	225	1.00E-69	73	57	(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
21376	ENU05170	ANI61C6713:	49-68	638-657	NAP		g3402279	415	152	9.00E-40	61	48	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

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21377	ENU05171	ANI61C4226:	25-52	808-829	NAP		g2492658	5056	455	e-148	98	13	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
21378	ENU05172	ANI61S3081:			NAP		g100210	184	41	0.009	34	59	extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum]
21379	ENU05173	ANI61C2460:	103-122	457-479	NAP		g3560221	161	58	8.00E-13	35	42	(AL031523) hypothetical protein [Schizosaccharomyces pombe]
21380	ENU05174	ANI61C8889:	38-57	789-808	NAP		g1800044	187	83	2.00E-15	32	56	(D90890) similar to [Escherichia coli]
21381	ENU05175	ANI61C3669:	46-71	677-695	NAP		g731763	576	245	3.00E-64	51	40	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region [Saccharomyces cerevisiae]
21382	ENU05176	ANI61C1049			NAP		g4218005	136	60	0.000000	19	30	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21383	ENU05177	ANI61S2866:			NAP		g854065	247	34	0.009	38	24	(X83413) U88 [Human herpesvirus 6]
21384	ENU05178	ANI61C2024:			NAP		g3646479	202	56	0.000000	36	100	(AJ010981) putative transposase [Talaromyces stipitatus]
21385	ENU05179	ANI61C9308:	45-64	492-511	NAP		g3878825	354	166	1.00E-40	50	47	(Z70782) similar to sorbitol dehydrogenase; cDNA EST EMBL.T00701 comes from this gene [Caenorhabditis elegans]
21386	ENU05180	ANI61C8487:	22-44	717-744	NAP		g3135994	689	142	4.00E-35	39	18	(AL023589) hypothetical protein [Schizosaccharomyces pombe]
21387	ENU05181	ANI61C518:	8 48-67	706-730	NAP		g1706695	303	114	9.00E-25	36	54	phosphomevalonate kinase [Saccharomyces cerevisiae]
21388	ENU05182	ANI61S4173:	215-233	416-435	NAP		g1351673	322	129	1.00E-29	45	53	hypothetical 37.7 KD protein C1F7.12 in chromosome I [Schizosaccharomyces pombe]
21389	ENU05183	ANI61C1188:	22-41	791-815	NAP		g631954	1952	362	e-119	99	28	chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans [Emericella nidulans]
21390	ENU05184	ANI61C3528:	25-46	414-441	NAP		g2981719	252	106	7.00E-23	38	20	Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone [

Database Connection

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21391	ENU05185	ANT61C6380:	33-52	797-817	NAP		g2342601	653	101	9.00E-21	25	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21392	ENU05186	ANT61S2843:	2296..234		NAP		g1352946	366	136	1.00E-31	49	60	hypothetical 32.6 KD protein in DAL5-TIH11 intergenic region [Saccharomyces cerevisiae]
21393	ENU05187	ANT61C5497:	27-54	808-829	NAP		g2739355	2771	429	e-119	71	25	(AC003972) pNORE1 [Homo sapiens]
21394	ENU05188	ANT61C5368:	22-44	787-806	NAP		g1729996	139	54	9.00E-11	32	75	TOXD protein [Cochliobolus carbonum]
21395	ENU05189	ANT61C9887:	191-218	533-556	NAP		g3875727	225	65	2.00E-22	49	28	(Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]
21396	ENU05190	ANT61C8675:	24-43	725-744	NAP		g3121988	339	112	9.00E-30	34	48	betaine aldehyde dehydrogenase (BADH) []
21397	ENU05191	ANT61C3613:	22-48	332-356	NAP		g1711469	257	116	6.00E-26	47	29	dibenzothioephene desulfurization enzyme C (DBT sulfur dioxygenase) [Rhodococcus sp.]
21398	ENU05192	ANT61C8895:	37-64	723-749	NAP		g102551	926	360	1.00E-98	65	17	kinesin-related protein unc-104 - Caenorhabditis elegans []
21399	ENU05193	ANT61C2996:	75-95	666-685	NAP		g3913980	435	157	9.00E-44	50	49	probable kynureninase (L-kynurenine hydrolase) [Saccharomyces cerevisiae]
21400	ENU05194	ANT61C5409:	71-90	265-284	NAP		g1314705	85	35	0.18	31	33	(U53863) Nopp44/46 [Trypanosoma brucei]
21401	ENU05195	ANT61C1209:	22-44	748-775	NAP		g462739	216	106	3.00E-22	35	34	NPL4 protein [Saccharomyces cerevisiae]
21402	ENU05196	ANT61S3756:	27-47	553-572	NAP		g3482917	544	142	1.00E-51	74	26	"(AC003970) Similar to Glucose-6-phosphate dehydrogenases, [Arabidopsis thaliana]"
21403	ENU05197	ANT61C1055	22-41	788-808	NAP		g1352891	153	95	7.00E-19	24	69	putative glycosyltransferase HOC1 precursor [Saccharomyces cerevisiae]
21404	ENU05198	ANT61C4595:	67-87	492-516	NAP		g417308	457	94	8.00E-32			probable helicase MOT1 []
21405	ENU05199	ANT61C4356:	40-59	600-621	NAP		g481285	356	159	1.00E-38	36	32	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger [Aspergillus niger]
21406	ENU05200	ANT61C3342:	22-41	476-495	NAP		g3219829	178	60	5.00E-15	36	99	Multidrug resistance-associated protein 4 [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21407	ENU05201	ANI61C1135	22-48	497-521	NAP		g481230	148	88	5.00E-17	32	43	L-idiol 2-dehydrogenase (EC 1.1.1.14) precursor - rat [Rattus norvegicus]
21408	ENU05202	ANI61C7939	22-41	519-539	NAP		g3567	217	96	2.00E-20	40	60	(X55731) COX11 (AA 1-277) [Saccharomyces cerevisiae]
21409	ENU05203	ANI61C7448			NAP		g1272506	444	125	7.00E-43	87	100	(D43686) L41 ribosomal protein [Candida maltosa]
21410	ENU05204	ANI61C2343			NAP		g1652639	52	75	3.00E-13	26	12	(D90907) sensory transduction histidine kinase [Synecocystis sp.]
21411	ENU05205	ANI61C1286	65-84	728-747	NAP		g2440190	606	187	1.00E-46	36	18	(Z98602) putative protein transport protein sec7 homolog
21412	ENU05206	ANI61S281	1		NAP		g433011	114	66	2.00E-10	29	53	[Schizosaccharomyces pombe] "(S62929) PRB1L precursor protein=basic proline rich proteins (Ps, PmF, PmS, and Pe) precursor (C-terminal) [Homo sapiens]" (AL031263) putative GTPase-activator protein for Rho-like GTPases
21413	ENU05207	ANI61C5167	221-239	605-624	NAP		g3417437	226	102	3.00E-21	34	64	[Schizosaccharomyces pombe] (U96090) myb-related transcription factor [Strongylocentrotus purpuratus] (U35661) colony 1 [Ophiostoma ulmi]
21414	ENU05208	ANI61C2551	27-47	775-795	NAP		g2072499	148	86	3.00E-16	29	31	hypothetical 72.5 KD protein C2F7.10 in chromosome 1
21415	ENU05209	ANI61C9694	217-238	722-741	NAP		g998355	239	127	8.00E-29	30	33	[Schizosaccharomyces pombe] (Z98977) hypothetical protein [Schizosaccharomyces pombe] (Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
21416	ENU05210	ANI61C9624	22-49	555-581	NAP		g1175373	390	137	6.00E-34	46	29	putative SEC14 cytosolic factor (phosphatidylinositol/phosphatidylcholine transfer protein) (P/PC TP) [Schizosaccharomyces pombe]
21417	ENU05211	ANI61C6114			NAP		g2388934	189	56	0.000000	38	23	NADH-ubiquinone dehydrogenase 24 KD subunit precursor [Neurospora crassa]
21418	ENU05212	ANI61C7669	24-51	730-749	NAP		g3282044	1676	390	e-113	76	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
21419	ENU05213	ANI61C3906			NAP		g1710858	431	182	2.00E-45	50	65	
21420	ENU05214	ANI61C5852	120-139	726-746	NAP		g730212	798	180	2.00E-89	72	90	
21421	ENU05215	ANI61C9289	22-46	807-829	NAP		g538067	523	161	6.00E-39	34	20	

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21422	ENU05216	ANI61C7651: 28-51	833..1	787-806	NAP		g3978134	541	83	6.00E-32	48	24	(U65409) Sla2p [Yarrowia lipolytica]
21423	ENU05217	ANI61C320:1	102-129	654-677	NAP		g2995360	481	99	6.00E-36	56	48	(AL022243) nucleosome assembly protein. [Schizosaccharomyces pombe]
21424	ENU05218	ANI61C6917: 36-57	576..182	348-374	NAP		g4758126	241	62	0.000000	001		"DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome [Homo sapiens]"
21425	ENU05219	ANI61C9553: 23-44	2242..409	801-828	NAP		g118233	452	55	2.00E-19			allantoate permease [Saccharomyces cerevisiae]
21426	ENU05220	ANI61C9720: 45-64	1..1503	810-829	NAP		g1352079	1801	289	e-107	70	30	beta-glucosidase 1 precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosylhydrolase) [Aspergillus aculeatus]
21427	ENU05221	ANI61C2169: 59-78	245..937	562-581	NAP		g4539264	662	241	4.00E-63	58	58	(AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]
21428	ENU05222	ANI61C4363: 27-50	1426..1	711-731	NAP		g417305	702	190	1.00E-47	46	41	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN9)-alpha-mannosidase [Saccharomyces cerevisiae]"
21429	ENU05223	ANI61S1929: 111-134	575..1	521-544	NAP		g113314	891	356	5.00E-98	93	5	delta-(L-alpha-aminoacyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emerticella nidulans]
21430	ENU05224	ANI61C7050: 32-51	3317..4174	757-780	NAP		g2773302	270	179	2.00E-44	35	51	(AF040720) xylosidase/arabinosidase [Selenomonas ruminantium]
21431	ENU05225	ANI61C6970: 22-49	85..1015	797-824	NAP		g543961	210	85	8.00E-16			cell division control protein 14 [Schizosaccharomyces pombe]
21432	ENU05226	ANI61C784:5	61..1	428-455	NAP		g2154997	247	134	3.00E-31	40	26	(Y12503) Man9-mannosidase [Sus scrofa]
21433	ENU05227	ANI61S3090: 1..457	743..1		NAP		g100210	156	37	0.09	32	45	extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum]
21434	ENU05228	ANI61C3808: 101-120	743..1	617-640	NAP		g1363750	204	65	5.00E-20	30	15	hypothetical protein YLR419w - yeast [Saccharomyces cerevisiae]
21435	ENU05229	ANI61C1125	7:485..1	437-456	NAP		g4557587	157	70	4.00E-14	37	32	[Saccharomyces cerevisiae]
21436	ENU05230	ANI61C9186: 59-78	4850..1262	791-810	NAP		g4585936	1397	192	3.00E-48	38	21	funamylacetacetase [Homo sapiens]
													(AC007211) putative helicase [Arabidopsis thaliana]

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21437	ENU05231	ANI61C2296: 4890..5915	22-49	779-801	NAP		g1217600	149	92	3.00E-19	27	48	(D38215) tcr3 [Streptomyces aureofaciens]
21438	ENU05232	ANI61C8809: 310..1320			NAP		g416657	576	162	2.00E-42	52	73	Anti-silencing protein 1 [Saccharomyces cerevisiae]
21439	ENU05233	ANI61C1071: 6:3239..1	64-83	719-738	NAP		g2342601	1457	214	1.00E-57	40	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21440	ENU05234	ANI61C79:28 29..3543	22-46	630-649	NAP		g1174617	494	129	1.00E-42	64	33	"T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon) ["
21441	ENU05235	ANI61C9059: 1..533	99-120	490-512	NAP		g3116126	93	61	0.000000	28	30	(AL023287) Sat1p [Schizosaccharomyces pombe]
21442	ENU05236	ANI61C8724: 1944..3970	22-47	800-827	NAP		g1546072	493	70	2.00E-11			(U68040) polyketide synthase [Cochliobolus heterostrophus]
21443	ENU05237	ANI61C4628: 1..650	108-126	548-567	NAP		g2983756	265	119	2.00E-26	42	40	(AE000735) ATP-dependent protease ATPase subunit clpX [Aquifex aeolicus]
21444	ENU05238	ANI61C4376: 823..1527	22-45	646-673	NAP		g2347143	660	266	1.00E-70	59	99	(U48234) spU2AF23 [Schizosaccharomyces pombe]
21445	ENU05239	ANI61C4928: 1597..1	72-91	781-807	NAP		g2501339	673	207	9.00E-53	51	35	Copper amine oxidase I [Aspergillus niger]
21446	ENU05240	ANI61C9658: 2293..1816	72-89	434-456	NAP		g2132029	150	58	0.000000	37	56	Hypothetical protein YOR004w - yeast (Saccharomyces cerevisiae)
21447	ENU05241	ANI61C4358: 704..1569	31-49	719-738	NAP		g2842699	369	164	5.00E-40	42	50	[Saccharomyces cerevisiae] putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
21448	ENU05242	ANI61C4668: 1..996	38-57	726-747	NAP		g1177622	216	49	0.00004	28	27	(X89715) AOF1001 [Saccharomyces cerevisiae]
21449	ENU05243	ANI61C1134: 8:618..1	22-46	524-548	NAP		g4160578	154	79	2.00E-14	31	54	(AL035218) hypothetical protein [Schizosaccharomyces pombe]
21450	ENU05244	ANI61C639:7 12..322	22-45	452-479	NAP		g731385	158	94	8.00E-19	37	50	hypothetical 33.7 KID protein in ISC10 3region [Saccharomyces cerevisiae]
21451	ENU05245	ANI61C7684: 640..1399	72-91	718-739	NAP		g1175370	177	120	1.00E-26	30	39	hypothetical 68.8 KID protein C2F7.07C in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21452	ENU05246	ANI61C8831: 22-43	458-478		NAP		g2132738	460	175	2.00E-43	61	98	probable membrane protein YNL044w - yeast (Saccharomyces cerevisiae)
		2353..2820											[Saccharomyces cerevisiae]
21453	ENU05247	ANI61C6666: 23-44	490-514		NAP		g2894269	245	117	7.00E-26	32	49	(AL021839) myb family DNA binding protein [Schizosaccharomyces pombe]
		734..1											[Saccharomyces cerevisiae]
21454	ENU05248	ANI61C5501: 23-50	725-748		NAP		g462414	1454	123	8.00E-64	69	45	amino-acid permease INDAl [Trichoderma harzianum]
		605..2159											(AC006250) putative Athila
21455	ENU05249	ANI61S150:5	110-130	376-399	NAP		g4263543	584	229	9.00E-60	85	15	retroelement ORF1 protein
		74..155											[Arabidopsis thaliana]
21456	ENU05250	ANI61S310:5	183-210	340-365	NAP		g3913727	496	142	8.00E-38	98	20	"glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD) [Arabidopsis thaliana]"
		86..201											methionine aminopeptidase 1 precursor (METAP 1) (peptidase M 1) (MAP) [Saccharomyces cerevisiae]
21457	ENU05251	ANI61C5962: 22-48	779-801		NAP		g1351928	292	66	3.00E-25	38	65	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
		1..1303											probable membrane protein YOL163w - yeast (Saccharomyces cerevisiae)
21458	ENU05252	ANI61C6706: 37-54	803-829		NAP		g1166378	515	79	2.00E-25	34	24	[Saccharomyces cerevisiae]
		2398..1											(AF002660) aflatoxin [Aspergillus parasticus]
21459	ENU05253	ANI61C8887: 118-137	372-399		NAP		g2132861	92	45	0.00002	32	56	Periodic tryptophan protein 2 [Saccharomyces cerevisiae]
		1..420											(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
21460	ENU05254	ANI61C1016	27-50	700-723	NAP		g2738309	251	98	8.00E-20	31	51	hypothetical 15.9 KD protein in GFP1-SYG1 intergenic region [Saccharomyces cerevisiae]
		0:827..1											(AB001995) Tel1p [Schizosaccharomyces pombe]
21461	ENU05255	ANI61C6324: 29-56	723-742		NAP		g730431	914	258	6.00E-70	62	27	Myo-inositol-1-phosphate synthase (IPS) [Candida albicans]
		1123..1											(Z98951) hypothetical protein [Schizosaccharomyces pombe]
21462	ENU05256	ANI61C1002: 2743..3805			NAP		g2804298	532	118	3.00E-36	38	51	Candida cylindracea []
		2430..1926											
21463	ENU05257	ANI61C4431: 56-75	460-484		NAP		g731809	182	91	4.00E-18	40	99	
		2430..1926											
21464	ENU05258	ANI61C6829: 110-129	389-416		NAP		g3764029	318	146	6.00E-35	51	5	
		2880..2444											
21465	ENU05259	ANI61C1930: 1240..1			NAP		g1170566	697	172	4.00E-54	47	51	
		1..3275											
21466	ENU05260	ANI61C3261: 22-47	737-759		NAP		g2370466	2515	146	2.00E-34	29	5	
		1..3275											
21467	ENU05261	ANI61C2859: 23-42	785-804		NAP		g1421604	431	177	7.00E-44	40	48	
		99..1099											

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21468	ENU05262	ANI6IC4819: 2775..2475	121-146	256-280	NAP		g3219530	226	106	5.00E-23	52	52	(AJ006688) IgE-binding protein [Aspergillus fumigatus]
21469	ENU05263	ANI6IC1017 5:1..712	172-191	538-557	NAP		g558311	520	118	1.00E-51	57	51	(L35487) mannanase [Aspergillus aculeatus]
21470	ENU05264	ANI6IC9994: 26..1083	22-49	804-829	NAP		g4507293	354	185	3.00E-46	43	81	syntaxin 5A [Homo sapiens]
21471	ENU05265	ANI6IS1430: 1..745			NAP		g4218005	156	62	0.000000	21	35	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21472	ENU05266	ANI6IC746:1 ..380	122-142	337-358	NAP		g418296	268	123	5.00E-28			vacuolar ATP synthase 95 KD subunit (vacuolar ATPase 95 KD subunit) [Saccharomyces cerevisiae]
21473	ENU05267	ANI6IC2820: 629..1	22-44	490-509	NAP		g3169065	219	104	4.00E-22	32	19	(AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]
21474	ENU05268	ANI6IC7326: 1..356	50-75	308-335	NAP		g2499454	219	104	2.00E-22	46	34	pectinesterase precursor (pectin methylesterase) (PE) [Aspergillus aculeatus]
21475	ENU05269	ANI6IC7855: 3027..4065	22-43	801-828	NAP		g2132944	430	183	1.00E-45	40	87	probable membrane protein YOR311c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21476	ENU05270	ANI6IC1495: 1..635	102-126	464-483	NAP		g3850070	575	120	1.00E-56	58	28	(AL033385) transketolase [Schizosaccharomyces pombe]
21477	ENU05271	ANI6IC7628: 1..386	27-52	340-365	NAP		g2905657	323	138	1.00E-32	59	31	(AF047469) arsenite translocating ATPase [Homo sapiens]
21478	ENU05272	ANI6IC7236: 1..584	22-42	541-563	NAP		g1077557	101	55	0.000000	30	26	probable membrane protein YDR061w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21479	ENU05273	ANI6IC7050: 965..2783	22-40	802-829	NAP		g1929089	253	36	0.46			(Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]
21480	ENU05274	ANI6IC5946: 1..992	39-58	789-807	NAP		g4160583	578	218	4.00E-56	50	73	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
21481	ENU05275	ANI6IC8772: 51..569	22-45	456-475	NAP		g2133256	318	129	2.00E-30	68	39	o-pyrocatechuate decarboxylase (EC 4.1.1.46) - Aspergillus niger (fragments) []
21482	ENU05276	ANI6IC1063 3:1017..1	47-66	755-780	NAP		g3130032	378	165	4.00E-40	35	48	(AL023534) major facilitator family transporter [Schizosaccharomyces pombe]

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21483	ENU05277	ANI6IS3800:			NAP		g119712	160	51	0.000009	32	78	extensin precursor (proline-rich glycoprotein) [Zea mays]
21484	ENU05278	ANI6IC4389:	93-112	387-406	NAP		g1652128	102	68	5.00E-11	27	9	(D90903) hypothetical protein [Synechocystis sp.]
21485	ENU05279	ANI6ISS30:5	43-70	396-423	NAP		g538067	149	50	0.000000	29	13	(M77661) putative pol polyprotein [Magnaporthe grisea]
21486	ENU05280	ANI6IC7970:	102-129	278-296	NAP		g442927	246	77	9.00E-17	50	18	Glucose Oxidase (E.C.1.1.3.4) []
21487	ENU05281	ANI6IC255:1	32-51	776-795	NAP		g4704282	236	88	9.00E-17			(AL049728) hypothetical protein [Schizosaccharomyces pombe]
21488	ENU05282	ANI6IC4337:	22-44	806-825	NAP		g3080521	391	149	9.00E-37	38	33	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
21489	ENU05283	ANI6IC9934:	56-75	380-399	NAP		g3123246	548	226	5.00E-59	71	28	serine-type carboxypeptidase F precursor (proteinase F) (CPD-II) [Aspergillus niger]
21490	ENU05284	ANI6IC1103	22-46	771-798	NAP		g1175933	206	92	5.00E-18	33	21	hypothetical 96.7 KID protein in STE2-FRS2 intergenic region [Saccharomyces cerevisiae]
21491	ENU05285	ANI6IC565:3	49-68	803-829	NAP		g1708073	1592	250	7.00E-66	66	45	GMP synthase (glutamine-hydrolysing) (glutamine amidotransferase) (GMP synthetase) [Saccharomyces cerevisiae]
21492	ENU05286	ANI6IC12:18	22-42	714-735	NAP		g4758416	281	121	6.00E-27			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
21493	ENU05287	ANI6IC7103:	54-73	623-650	NAP		g3114278	698	281	3.00E-75	70	99	"Chain J, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution []" (AB011123) KIAA0551 protein [Homo sapiens]
21494	ENU05288	ANI6IC7913:	22-49	515-534	NAP		g3043626	81	34	0.85			(AF009417) cytochrome P450 [Myrothecium roridum]
21495	ENU05289	ANI6IC5607:	70-89	778-801	NAP		g2267601	244	59	1.00E-19	31	44	(X60499) rad15 [Schizosaccharomyces pombe]
21496	ENU05290	ANI6IC9702:	22-48	802-828	NAP		g5022	2884	429	e-119	68	36	HEFM1 protein [Saccharomyces cerevisiae]
21497	ENU05291	ANI6IC1121	28-47	759-784	NAP		g1708195	892	136	2.00E-31	50	22	(U58946) transposase [Aspergillus awamori]
21498	ENU05292	ANI6IC3793:	102-126	388-413	NAP		g1805251	143	52	0.000002	31	25	ATP-dependent bile acid permease [Saccharomyces cerevisiae]
21499	ENU05293	ANI6IC3447:	33-60	722-741	NAP		g3915963	503	154	6.00E-37	36	15	

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21500	ENU05294	ANI61C9040: 1009..1	31-58	723-749	NAP		g3915067	362	100	1.00E-38	41	43	aspartyl-TRNA synthetase (aspartate--TRNA ligase) (ASPRS) [Aquifex aeolicus]
21501	ENU05295	ANI61C1022	66-87	513-532	NAP		g1168269	278	123	1.00E-27	37	50	"arabian endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinamASE A) (ABN A) [Aspergillus niger]"
21502	ENU05296	ANI61C9143: 322..1	145-164	454-479	NAP		g4731167	173	88	3.00E-17			(AF108357) c-myc binding protein MM-1 [Mus musculus]
21503	ENU05297	ANI61C7822: 3976..4512	44-63	477-502	NAP		g4519181	863	188	2.00E-75	98	16	(AB023911) chitin synthase [Emicella nidulans]
21504	ENU05298	ANI61C9203: 3211..802	54-73	778-797	NAP		g2147662	718	116	2.00E-25	28	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]
21505	ENU05299	ANI61C8314: 136..1241	22-45	808-829	NAP		g2501437	432	115	1.00E-27	30	79	DNA damage tolerance protein RHC31 (RAD31 homolog) [Saccharomyces cerevisiae]
21506	ENU05300	ANI61C9664: 520..4543	22-47	724-746	NAP		g2065438	1877	178	4.00E-71	48	19	(Y11989) Wk1 protein [Schizosaccharomyces pombe]
21507	ENU05301	ANI61S3836: 1..901			NAP		g4760549	100	69	3.00E-11			(AB019494) IDN3 [Homo sapiens]
21508	ENU05302	ANI61C7667: 217..840	54-73	537-554	NAP		g1171737	199	76	3.00E-19	43	16	Nonsense-mediated mRNA decay protein 2 (up-frameshift suppressor 2) [Saccharomyces cerevisiae]
21509	ENU05303	ANI61C1021	108-130	447-469	NAP		g4210942	537	222	9.00E-58	65	60	(AF069518) 17beta-hydroxysteroid dehydrogenase [Cochliobolus lunatus]
21510	ENU05304	ANI61C7952: 1472..966	25-44	463-485	NAP		g1723793	212	105	2.00E-22			putative 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase (3beta-HSD) (3-beta-hydroxy-delta(5)-steroid dehydrogenase (3-beta-hydroxy-5-ene steroid dehydrogenase) (progesterone reductase) / steroid delta-isomerase.. [Saccharomyces cerevisiae]
21511	ENU05305	ANI61C3186: 4376..4770	35-62	369-396	NAP		g1723781	83	64	6.00E-10	31	45	hypothetical 34.3 KD protein in TAF145-YOR1 intergenic region [Saccharomyces cerevisiae]

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21512	ENU05306	AN161C1003	63-82	495-512	NAP		g3024443	201	89	2.00E-18	38	52	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) [Zalierion arboricola]
21513	ENU05307	AN161C378.4	22-47	784-803	NAP		g416820	164	75	5.00E-13	22	74	para-hydroxybenzoate--polyprenyltransferase precursor (PHB:polyprenyltransferase) [Saccharomyces cerevisiae]
21514	ENU05308	AN161C3805: 1..1904	67-86	780-799	NAP		g1706176	1345	138	3.00E-32	44	26	[Fusarium solani f. sp. pisi]
21515	ENU05309	AN161C3630: 22-47	803-829	NAP			g538067	790	203	1.00E-51	37	20	(M77661) putative pol polyprotein [Magnaporthe grisea]
21516	ENU05310	AN161C1203: 102-122	387-406	NAP			g1001163	600	137	8.00E-34	81	45	(D64001) hypothetical protein [Synechocystis sp.]
21517	ENU05311	AN161C1698: 22-44	781-807	NAP			g3121995	388	159	5.00E-48	39	26	DOM34 interacting protein 2 [Saccharomyces cerevisiae]
21518	ENU05312	AN161C9662: 36-55	477-496	NAP			g3879850	270	98	6.00E-20	43	100	(Z81592) predicted using GeneFinder [Caenorhabditis elegans]
21519	ENU05313	AN161C1070: 45-64	769-788	NAP			g2959374	712	148	4.00E-35	45	47	(AL022117) putative pre-mrna splicing factor [Schizosaccharomyces pombe]
21520	ENU05314	AN161S1429: 0:1822..483		NAP			g2996650	121	54	0.000000	24	11	(AC004493) KIAA0324 [Homo sapiens]
21521	ENU05315	AN161C2295: 26-45	576-595	NAP			g3411013	484	213	1.00E-54	49	24	(AF000232) protein mannosyltransferase 1 [Candida albicans]
21522	ENU05316	AN161C8866: 63-82	745-765	NAP			g173384	2075	429	e-119	74	26	(L07734) DNA polymerase delta [Schizosaccharomyces pombe]
21523	ENU05317	AN161C8004: 22-48	700-721	NAP			g3080532	404	120	1.00E-26	39	62	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
21524	ENU05318	AN161C914:4 22-47	805-826	NAP			g3878905	180	121	7.00E-27	28	65	(Z46794) similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST EMBL: C08977 comes from this gene; cDNA EST EMBL: C09386 comes from this gene; cDNA EST yk447c11.5 comes from this... []
21525	ENU05319	AN161C5448: 22-48	625-644	NAP			g786117	73	48	0.00007	20	52	(L41834) nuclear protein [Ensis minor]

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21526	ENU05320	ANI61C1071	22-45	790-809	NAP		g549602	195	50	0.000002	32	75	hypothetical 32.0 KD protein in SAP190-SP014 intergenic region [Saccharomyces cerevisiae]
21527	ENU05321	ANI61C2481	61-80	806-829	NAP		g1654028	262	49	0.00005			(Z81360) hypothetical protein Rv1726 [Mycobacterium tuberculosis]
21528	ENU05322	ANI61S2482			NAP		g2465144	86	58	0.000000	32	63	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
21529	ENU05323	ANI61C7829	211-235	626-649	NAP		g2266908	143	86	3.00E-16	38	70	(AE001274) PXNC; L4171.2 [Leishmania major]
21530	ENU05324	ANI61C2803	29-53	386-405	NAP		g1711410	106	64	4.00E-10	27	34	Pristinamycin IIA synthase subunit A (PIIA synthase subunit A) [Streptomyces pristinaespiralis]
21531	ENU05325	ANI61C1039	22-42	728-751	NAP		g1706694	601	238	3.00E-63	52	34	"lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene—lanosterol cyclase) (OSC) [Schizosaccharomyces pombe]" HUS1 protein [Schizosaccharomyces pombe]
21532	ENU05326	ANI61C5507	25-44	802-829	NAP		g3219811	312	77	2.00E-13	32	70	[AL031534] Chaperonin hsp78p [Schizosaccharomyces pombe]
21533	ENU05327	ANI61C8456	27-48	611-638	NAP		g3560150	2216	359	1.00E-98	65	34	Synapsins IA and IB []
21534	ENU05328	ANI61S1345			NAP		g135153	105	52	0.000004	26	32	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21535	ENU05329	ANI61C1768	70-89	721-740	NAP		g584806	1414	492	e-138	83	51	hypothetical 100.5 KD protein C1B9.04 in chromosome I [Schizosaccharomyces pombe]
21536	ENU05330	ANI61C5226	22-49	804-823	NAP		g1723540	910	61	3.00E-13	36	27	hypothetical 77.8 KD protein in MKRPS28-HXT7 intergenic region [Saccharomyces cerevisiae]
21537	ENU05331	ANI61C3227	22-47	732-755	NAP		g2501559	681	142	5.00E-61	45	38	(X14612) myb protein [Gallus gallus]
21538	ENU05332	ANI61C2826	67-87	651-672	NAP		g63628	107	40	0.000000	35	79	(U13644) F56D2.2 gene product [Caenorhabditis elegans]
21539	ENU05333	ANI61C991	1 46-70	280-299	NAP		g1945500	98	59	0.000000	30	25	(AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobacter aureus]
21540	ENU05334	ANI61C1082	22-41	577-603	NAP		g3249039	245	120	1.00E-26	36	53	

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21541	ENU05335	ANI61C1043:	22-45	803-822	NAP	g3687510	372	123	2.00E-27	58	65		(AL031788) ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]
21542	ENU05336	ANI61C4716:	22-41	313-332	NAP	g1084771	445	183	7.00E-46	70	77		ribosomal protein L18a.c13 - yeast (Saccharomyces cerevisiae)
21543	ENU05337	ANI61C2614:	39-62	724-749	NAP	g543806	1224	299	2.00E-80	58	40		[Saccharomyces cerevisiae] "glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) [Aspergillus oryzae]" (Z99163) WD repeat protein [Schizosaccharomyces pombe]
21544	ENU05338	ANI61C1067	36-55	802-829	NAP	g4884474	624	121	7.00E-49				[Schizosaccharomyces pombe]
21545	ENU05339	ANI61C7406:	41-62	645-664	NAP	g2076715	737	288	2.00E-78	67	46		(Y11322) SEC61 protein [Yarrowia lipolytica]
21546	ENU05340	ANI61C1013	1:2643..3799		NAP	g1834315	855	217	1.00E-55	52	67		(D78351) nuclease O [Aspergillus oryzae]
21547	ENU05341	ANI61S2200:	23-45	415-438	NAP	g3738162	502	180	6.00E-45	70	32		(AL031856) putative involvement in protein glycosylation in the golgi [Schizosaccharomyces pombe]
21548	ENU05342	ANI61C9766:	46-65	375-398	NAP	g3913082	99	53	0.000000	33	38		Aquaporin 9 [Homo sapiens]
21549	ENU05343	ANI61C8029:	45-72	265-284	NAP	g485111	168	73	6.00E-13	36	26		(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
21550	ENU05344	ANI61S1642:	22-49	327-348	NAP	g1335873	264	108	2.00E-23	50	24		(U46690) ATP-dependent RNA helicase [Mus musculus]
21551	ENU05345	ANI61C659:1	174-193	342-361	NAP	g4581500	133	64	4.00E-10	33	18		(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]
21552	ENU05346	ANI61C2064:	40-59	726-751	NAP	g458284	1502	269	1.00E-94	85	37		(U05811) serine/threonine protein kinase [Trichoderma reesei]
21553	ENU05347	ANI61C4060:			NAP	g3023651	435	172	3.00E-42	37	48		D-lactate dehydrogenase [Kluveromyces lactis]
21554	ENU05348	ANI61S4097:			NAP	g2499312	127	57	0.000000	36	22		NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (CI-51KD) [Aspergillus niger]

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21555	ENU05349	ANI61C2044: 488..893			NAP		g2851654	219	110	7.00E-24	46	22	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21556	ENU05350	ANI61C9912: 1396..2092	22-47	480-505	NAP		g1125833	569	167	3.00E-55	80	78	(U43283) Similar to ras-related protein; coded for by C. elegans cDNA CEESK32F; coded for by C. elegans cDNA yk82h5.3; coded for by C. elegans cDNA yk82h5.5; coded for by C. elegans cDNA yk168c1.3; coded for by C. elegans cDNA yk168c1.5 [Caecili
21557	ENU05351	ANI61C55:78	24-47	498-520	NAP		g4895135	87	78	4.00E-14			(AF127374) Mmcr [Streptomyces lavendulae]
21558	ENU05352	ANI61C8078: 450..4089	37-59	722-749	NAP		g3355628	1981	267	6.00E-71	48	17	(X91867) CPC3 protein [Neurospora crassa]
21559	ENU05353	ANI61C806:2 543..1	22-43	725-745	NAP		g3114719	1435	217	1.00E-67	50	16	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21560	ENU05354	ANI61C2673: 850..36	58-83	729-746	NAP		g547901	760	262	6.00E-78	64	70	"MAlate dehydrogenase, mitochondrial precursor [Saccharomyces cerevisiae]"
21561	ENU05355	ANI61C1129 4:1..562	103-122	516-535	NAP		g2497072	315	96	3.00E-32	47	18	hypothetical 103.0 KD protein in RAD10-PRS4 intergenic region [Saccharomyces cerevisiae]
21562	ENU05356	ANI61C1032 7:1..1791	108-127	727-748	NAP		g2673947	1501	272	2.00E-72	52	21	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21563	ENU05357	ANI61C949:5 42..1402	22-47	787-814	NAP		g1938424	293	94	3.00E-22	35	25	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
21564	ENU05358	ANI61C7361: 1583..2751	37-56	773-800	NAP		g1077257	282	111	8.00E-24	27	27	hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21565	ENU05359	ANI61C179:1 ..1794	22-44	755-780	NAP		g3288709	1767	377	e-104	63	19	(AB010442) PMR1 [Penicillium digitatum]
21566	ENU05360	ANI61C9217: 135..888	31-56	707-733	NAP		g3183391	118	78	7.00E-14	29	97	hypothetical 27.3 KD protein C9G1.08C in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21567	ENU05361	ANT61C1120	22-45	786-805	NAP		g3702641	498	124	9.00E-28	41	86	(AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]
21568	ENU05362	ANT61C1045	34-55	728-747	NAP		g2342601	1392	174	8.00E-43	32	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21569	ENU05363	ANT61C8576	23-41	802-829	NAP		g586858	223	81	1.00E-14	42	94	hypothetical 21.4 KD protein in DACA-SERS intergenic region [Bacillus subtilis]
21570	ENU05364	ANT61C258:1	46-65	773-792	NAP		g2132903	436	73	2.00E-12	24	33	probable membrane protein YOR165w - yeast [Saccharomyces cerevisiae]
21571	ENU05365	ANT61C1091			NAP		g2144323	357	143	1.00E-33	46	14	[Saccharomyces cerevisiae] xanthine dehydrogenase (EC 1.1.1.204) / xanthine oxidase (EC 1.1.3.22) - rat []
21572	ENU05366	ANT61S4059	183-208	527-554	NAP		g1020096	596	252	1.00E-66	76	41	(D49832) stearoyl-acyl carrier protein desaturase [Sesamum indicum]
21573	ENU05367	ANT61C1047	63-82	806-825	NAP		g2506150	325	101	5.00E-21	35	88	Versicolorin reductase (VER-1) [Aspergillus parasiticus]
21574	ENU05368	ANT61C7245	22-41	596-618	NAP		g2493389	343	159	2.00E-38	35	53	probable sterigmatocystin biosynthesis P450 MONOOxygenase STCF (cytochrome P450 60A2) [Emmericella nidulans]
21575	ENU05369	ANT61S3950			NAP		g1572721	143	40	0.022	27	18	(U70136) megakaryocyte stimulating factor: MSF [Homo sapiens]
21576	ENU05370	ANT61C5314	22-44	666-693	NAP		g2245026	104	78	6.00E-14	35	100	(Z97341) hypothetical protein [Arabidopsis thaliana]
21577	ENU05371	ANT61C4173	24-43	629-652	NAP		g2624405	163	98	6.00E-20	27	30	(X92655) gluconate [Schizosaccharomyces pombe]
21578	ENU05372	ANT61C1147	22-46	669-688	NAP		g731806	1647	347	6.00E-95	63	23	probable calcium-transporting ATPase 7 [Saccharomyces cerevisiae]
21579	ENU05373	ANT61C5508	2:1..2042		NAP		g2511761	1185	458	e-128	86	34	(AF023156) carnitine acetyl transferase FacC [Emmericella nidulans]
21580	ENU05374	ANT61C8155	104-123	352-371	NAP		g1073534	165	75	2.00E-15	38	36	iucB protein - Escherichia coli [Escherichia coli]
21581	ENU05375	ANT61S365:5	182-204	462-484	NAP		g131154	895	364	e-100	94	23	Photosystem I P700 chlorophyll A apoprotein A2 [Nicotiana tabacum]
21582	ENU05376	ANT61C4338	38-57	550-573	NAP		g2239236	674	255	3.00E-67	66	16	(Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]

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21583	ENU05377	ANI61C2934: 335..1201	27-46	748-768	NAP		g1345571	376	104	2.00E-40	47	25	(X80010) starch branching enzyme II [Pisum sativum]
21584	ENU05378	ANI61C403:1 ..2381	71-90	806-824	NAP		g2842700	1133	155	4.00E-56	41	15	hypothetical 192.5 KD protein C6G9.10C in chromosome I [Schizosaccharomyces pombe]
21585	ENU05379	ANI61C196:1 130..2491	22-44	764-790	NAP		g538067	809	227	7.00E-59	43	20	(M77661) putative pol polyprotein [Magnaporthe grisea]
21586	ENU05380	ANI61S822:6 60..160	215-234	414-433	NAP		g3913995	217	63	0.000000	39	19	ATP-dependent protease LA [Azospirillum brasilense]
21587	ENU05381	ANI61C2843: 533..1	72-91	409-428	NAP		g120609	238	93	9.00E-20			uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTase) [Saccharomyces cerevisiae]
21588	ENU05382	ANI61C9743: 2636..1864	26-45	731-752	NAP		g1730032	230	89	4.00E-17	32	99	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Escherichia coli]
21589	ENU05383	ANI61C1137: 1..333			NAP		g83727	544	218	1.00E-56	96	33	hypothetical nox3 protein - Emmericella nidulans mitochondrion (SGC3) [Emmericella nidulans]
21590	ENU05384	ANI61C3195: 68..609	40-59	468-487	NAP		g1168269	223	95	3.00E-22	38	53	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]" (AB010442) PMR1 [Penicillium digitatum]
21591	ENU05385	ANI61C966:6 8..566	37-62	390-417	NAP		g3288709	623	245	5.00E-66	78	11	probable aflatoxin biosynthesis P450 monooxygenase ORD1 (cytochrome P450 60A1) [Aspergillus parasiticus]
21592	ENU05386	ANI61C3723: 1163..494	162-182	621-648	NAP		g2493388	228	107	6.00E-27	39	49	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]" (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21593	ENU05387	ANI61C2144: 1..645	103-122	520-540	NAP		g1168269	189	103	1.00E-21	31	64	mitochondrial respiratory function protein homolog [Schizosaccharomyces pombe]
21594	ENU05388	ANI61S1049: 1..735			NAP		g3153821	127	50	0.00001	23	27	
21595	ENU05389	ANI61C6621: 621..1	26-45	497-520	NAP		g1709097	286	121	2.00E-29	37	50	

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21596	ENU05390	ANI61C5111:	108-127	654-673	NAP		g3560142	252	123	1.00E-27	36	29	(AL031534) Major facilitator superfamily protein
		885..1782											[Schizosaccharomyces pombe]
21597	ENU05391	ANI61C7295:	22-45	800-827	NAP		g3139137	259	98	2.00E-26	41	22	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
		928..1											[Schizosaccharomyces pombe]
21598	ENU05392	ANI61C5341:	22-49	766-787	NAP		g3395584	868	273	8.00E-73	52	24	(AL031179) importin beta subunit [Schizosaccharomyces pombe]
		1491..1											[Schizosaccharomyces pombe]
21599	ENU05393	ANI61C6532:	118-137	448-473	NAP		g2388906	396	183	6.00E-46	57	54	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
		1..494											[Schizosaccharomyces pombe]
21600	ENU05394	ANI61C986:1	113-139	476-503	NAP		g3023676	495	187	5.00E-49	48	31	probable translation initiation factor EIF-2B epsilon subunit (EIF-2B GDP-GTP exchange factor)
		..646											[Schizosaccharomyces pombe]
21601	ENU05395	ANI61C7272:	54-73	372-399	NAP		g1723230	305	123	6.00E-28	45	58	hypothetical 28.5 KD protein CID4.08 in chromosome I
		4101..4547											[Schizosaccharomyces pombe]
21602	ENU05396	ANI61C1104	107-129	609-628	NAP		g3978466	567	215	2.00E-55	51	31	(AF086822) dihydroxyacetone synthase [Candida boidinii]
		5:1..681											(U68040) polyketide synthase [Cochliobolus heterostrophus]
21603	ENU05397	ANI61C1017	137-156	722-749	NAP		g1546072	249	118	6.00E-26	34	10	AXL2 protein precursor (SRO4 protein) [Saccharomyces cerevisiae]
		3:859..1											(K03205) salivary proline-rich protein precursor [Homo sapiens]
21604	ENU05398	ANI61C6174:	39-57	555-574	NAP		g731878	197	105	3.00E-22	29	25	regulator Y protein GAL4 [Saccharomyces cerevisiae]
		1218..1848											(X89442) peptide synthetase [Metarhizium anisopliae]
21605	ENU05399	ANI61S1311:			NAP		g190504	97	45	0.0004			(AF132563) BcDNA.LD14392 [Drosophila melanogaster]
		1..713											Maltese permease MAL3T (maltose transport protein MAL3T) [Saccharomyces cerevisiae]
21606	ENU05400	ANI61C9864:	54-73	803-822	NAP		g1169823	368	33	3.1			(X05204) arom polypeptide [Emeticella nidulans]
		455..2549											putative mitochondrial carrier C17H9.08 [Schizosaccharomyces pombe]
21607	ENU05401	ANI61C1033	24-41	625-645	NAP		g2342601	2035	119	1.00E-42	43	5	
		0:1..4071											
21608	ENU05402	ANI61C9342:	36-55	703-723	NAP		g4689350	727	298	3.00E-80			
		2795..2015											
21609	ENU05403	ANI61C4212:	23-48	707-730	NAP		g585446	660	180	9.00E-45	33	45	
		1230..2470											
21610	ENU05404	ANI61C6072:	26-47	803-829	NAP		g3834343	1545	436	e-121	97	17	
		1..926											
21611	ENU05405	ANI61C3958:	126-149	287-306	NAP		g3219962	210	88	2.00E-17	46	33	
		1437..1101											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21612	ENU05406	ANI61C937:1	102-127	440-465	NAP		g4587971	772	277	2.00E-74	96	12	(AF082072) ABC transporter protein AtcC [Emmericella nidulans]
21613	ENU05407	ANI61C2980:586..1	56-77	527-546	NAP		g2462911	321	105	9.00E-32	42	28	(Z83832) UDP-glucose:sterol glucosyltransferase [Avena sativa]
21614	ENU05408	ANI61S3826:146-165	507-524		NAP		g2327063	174	45	0.0005	22	23	(AF001305) protease 1 [Pneumocystis carinii f. sp. carinii]
21615	ENU05409	ANI61C9451:41-61	625-649		NAP		g2076715	914	231	6.00E-91	76	51	(Y11322) SEC61 protein [Yarrowia lipolytica]
21616	ENU05410	ANI61C199:6			NAP		g539218	106	42	0.003	20	25	hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
21617	ENU05411	ANI61C1002:5:4341..3161	25-52	807-829	NAP		g1586814	736	205	3.00E-52	48	63	glycerol-3-phosphate dehydrogenase [Schizosaccharomyces pombe]
21618	ENU05412	ANI61C3264:1240..2489	22-45	766-783	NAP		g2414609	1146	354	4.00E-97	69	53	(Z99295) citrate lyase [Schizosaccharomyces pombe]
21619	ENU05413	ANI61C7483:1457..719	22-46	691-718	NAP		g584766	537	173	2.00E-42	66	99	ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]
21620	ENU05414	ANI61C9092:1..1170	54-73	765-782	NAP		g4581500	838	252	2.00E-66	50	47	(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]
21621	ENU05415	ANI61C3548:1816..1030			NAP		g126791	816	233	2.00E-73	88	42	MRNA maturase BII (COBA intron protein) []
21622	ENU05416	ANI61C2656:1..644	87-114	562-581	NAP		g731288	474	175	3.00E-43	43	27	hypothetical 87.5 KD protein in ACS1-GCV3 intergenic region [Saccharomyces cerevisiae]
21623	ENU05417	ANI61C1514:1..1308			NAP		g2493965	1869	244	e-108	84	20	xanthine dehydrogenase (purine hydroxylase J) [Emmericella nidulans]
21624	ENU05418	ANI61C305:2	22-44	723-749	NAP		g245997	1553	144	3.00E-49	45	20	(AF012898) protein phosphatase Ssd1 homolog [Candida albicans]
21625	ENU05419	ANI61C9125:1..431	22-44	378-397	NAP		g3646447	92	53	0.000001	35	69	"(AL031603) peroxisomal membrane protein pmp20p, Ahpc-TSA family protein [Schizosaccharomyces pombe]"
21626	ENU05420	ANI61C5598:513..1	100-118	462-481	NAP		g1805262	292	131	3.00E-30	49	7	"(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
21627	ENU05421	ANI61C2807:844..335	109-130	465-487	NAP		g4262222	299	105	2.00E-22	39	30	"(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]"
21628	ENU05422	ANI61C8964:6972..6519	108-127	375-394	NAP		g2493143	335	72	3.00E-23	74	66	vacuolar ATP synthase 16 KD proteolipid subunit [Candida tropicalis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21629	ENU05423	ANI61C9643: 1704..1	34-53	724-743	NAP		g1723575	515	83	2.00E-15			hypothetical protein C26F1.01 in chromosome I [Schizosaccharomyces pombe]
21630	ENU05424	ANI61C4970: 1460..125	22-46	795-822	NAP		g699196	560	141	8.00E-33	42	52	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
21631	ENU05425	ANI61C1099: 1:1..1013	22-49	766-785	NAP		g3114719	588	196	1.00E-49	48	15	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21632	ENU05426	ANI61C5574: 556..1	59-86	410-437	NAP		g3947855	244	67	2.00E-20	45	60	(AL034381) putative Golgi membrane protein [Schizosaccharomyces pombe]
21633	ENU05427	ANI61C9448: 4363..3345	22-48	806-829	NAP		g403179	367	114	3.00E-42	34	55	(L24441) kinesin light chain [Loligo pealii]
21634	ENU05428	ANI61S991:1..576			NAP		g3329623	165	57	0.000000	21	57	(AF078790) No definition line found [Caenorhabditis elegans]
21635	ENU05429	ANI61C9118: 1..1241	25-47	802-824	NAP		g3163927	1659	187	e-106	99	63	(AJ001157) hymA [Emmericella nidulans]
21636	ENU05430	ANI61C1327: 804..1520			NAP		g3850093	228	124	7.00E-28	30	47	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
21637	ENU05431	ANI61C9639: 9628..9095	122-141	489-513	NAP		g2137308	66	42	0.003	23	47	G protein beta subunit like - mouse [Mus musculus]
21638	ENU05432	ANI61C1236: 3252..1	36-60	714-736	NAP		g1805261	1628	259	1.00E-68	48	15	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21639	ENU05433	ANI61C1001: 1:314..1	79-98	275-294	NAP		g2612805	142	80	1.00E-14	37	21	(AL008883) glnA4 [Mycobacterium tuberculosis]
21640	ENU05434	ANI61C2961: 1431..2728	31-50	770-789	NAP		g2342601	645	152	4.00E-36	41	4	(X89442) peptide synthetase [Metarhizium anisopliae]
21641	ENU05435	ANI61C1258: 1..467	53-75	398-417	NAP		g732372	90	50	0.000000	37	38	hypothetical oxidoreductase in PTA-ROCC intergenic region [Bacillus subtilis]
21642	ENU05436	ANI61C2743: 1213..1800	22-49	542-567	NAP		g2707191	124	36	0.22	38	53	(U94186) glutamine rich protein similar to glutenins [Glomerella cingulata]
21643	ENU05437	ANI61C3684: 1985..2821	28-55	784-811	NAP		g4502229	435	122	7.00E-40	53	100	ADP-ribosylation factor-like 2 [Homo sapiens]
21644	ENU05438	ANI61C9235: 1..631	106-128	561-580	NAP		g549795	384	161	4.00E-39			GTP-binding protein YPT51/VP521 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21645	ENU05439	ANT61C6976:	23-45	638-657	NAP		g2706459	179	85	5.00E-16	26	75	(AL021046) hypothetical PHD finger domain protein [Schizosaccharomyces pombe]
21646	ENU05440	ANT61C8570:			NAP		g2408082	806	96	1.00E-27	37	28	(Z99167) putative helicase [Schizosaccharomyces pombe]
21647	ENU05441	ANT61C1109			NAP		g1709159	449	120	2.00E-49	42	39	putative methylenetetrahydrofolate reductase [Saccharomyces cerevisiae]
21648	ENU05442	ANT61C4289:	24-44	803-829	NAP		g238482	269	135	4.00E-31	36	73	"long chain alpha-hydroxy acid oxidase=FMN-dependent alpha-hydroxy acid-oxidizing enzyme [EC 1.1.3.15] [rats, kidney, Peptide, 352 aa]"
21649	ENU05443	ANT61C1038	27-49	722-749	NAP		g3123262	1765	341	e-115	73	33	DNA repair protein RHP54 [Schizosaccharomyces pombe]
21650	ENU05444	ANT61C5267:	222-241	503-530	NAP		g2266427	229	99	1.00E-21	43	67	(Y13917) ynfF [Bacillus subtilis]
21651	ENU05445	ANT61C1038	22-43	802-829	NAP		g3929362	648	92	4.00E-36	42	45	Pisatin demethylase (cytochrome P450 57A1) [Nectria haematococca mp VII] (Z69793) R03A10.3 [Caenorhabditis elegans]
21652	ENU05446	ANT61C7643:	22-45	760-779	NAP		g3878874	351	124	9.00E-28	34	49	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Emericella nidulans mitochondrion (SGC3) [] (AL023517) putative iron-sulfur binding oxidoreductase [Streptomyces coelicolor]
21653	ENU05447	ANT61S4583:			NAP		g101813	585	141	1.00E-33	91	99	26S protease regulatory subunit 4 homolog (MTS2 protein) [Schizosaccharomyces pombe]
21654	ENU05448	ANT61C1798:	120-141	260-279	NAP		g3130015	75	50	0.000005	27	19	(Z98560) hypothetical protein [Schizosaccharomyces pombe]
21655	ENU05449	ANT61C9805:	186-213	551-570	NAP		g547935	581	106	1.00E-47	72	41	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21656	ENU05450	ANT61C1029	72-91	717-736	NAP		g2330803	2374	353	1.00E-96	58	19	putative 60S ribosomal protein YEL050C [Saccharomyces cerevisiae]
21657	ENU05451	ANT61C617:	96-120	700-727	NAP		g1834342	1276	472	e-139	97	18	probable membrane protein YDL246c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21658	ENU05452	ANT61C1022	27-48	810-829	NAP		g418426	594	233	1.00E-60	54	59	
21659	ENU05453	ANT61S4056:			NAP		g2117435	101	64	5.00E-10	27	33	

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21660	ENU05454	ANI61C9713: 1..383	98-118	336-362	NAP		g2995374	273	120	6.00E-27	53	56	(AL022245) hypothetical 21.5 kd protein [Schizosaccharomyces pombe]
21661	ENU05455	ANI61C6683: 873..377	110-129	451-471	NAP		g1565203	151	92	2.00E-18	32	41	(D87894) chitinase [Rhizopus microsporus var. oligosporus]
21662	ENU05456	ANI61C1044 2:1202..1	28-48	686-710	NAP		g2132863	600	238	4.00E-62	45	38	probable membrane protein YOR001w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21663	ENU05457	ANI61C5918: 863..1	42-61	765-784	NAP		g416900	422	115	6.00E-25	42	46	probable aldehyde dehydrogenase [Pseudomonas sp.]
21664	ENU05458	ANI61S1481: 84..985			NAP		g1334398	166	32	6.9	29	75	(X15081) MURF2 protein (AA 1-348) [Crithidia fasciculata]
21665	ENU05459	ANI61C9981: 336..2698	42-62	724-749	NAP		g3023272	2834	458	e-128	76	28	alpha-glucosidase precursor (maltase) (AGL) [Aspergillus oryzae]
21666	ENU05460	ANI61C1118 3:742..1	31-50	616-641	NAP		g2308977	977	100	2.00E-52	99	11	(AB000125) chitin synthase [Emericella nidulans]
21667	ENU05461	ANI61C6359: 1003..1	23-50	803-829	NAP		g3021303	1362	359	e-127	100	10	(Y15996) acetyl-CoA carboxylase [Emericella nidulans]
21668	ENU05462	ANI61C540:1 100..1	104-123	722-741	NAP		g3947883	562	215	4.00E-55	44	55	(AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
21669	ENU05463	ANI61C1212: 8468..8970	53-76	463-482	NAP		g4505739	119	45	0.0003	26	100	prefoldin 1 [Homo sapiens]
21670	ENU05464	ANI61C739:6 90..1	33-54	626-650	NAP		g4210899	68	54	0.000001	22	48	(AF045609) OrfL [Sinorhizobium meliloti]
21671	ENU05465	ANI61C3278: 825..1	108-131	701-724	NAP		g3116113	454	212	3.00E-54	53	29	(AL023286) probable atp-dependent ma helicase [Schizosaccharomyces pombe]
21672	ENU05466	ANI61C2706: 1..385	65-84	317-343	NAP		g1168403	183	81	4.00E-15	41	15	regulatory protein ALCR []
21673	ENU05467	ANI61C1097 1:1..430	90-114	370-389	NAP		g731385	147	68	4.00E-11	35	46	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21674	ENU05468	ANI61C558:3 433..5023	26-46	803-829	NAP		g522302	959	143	8.00E-45	39	23	(L35053) endonuclease [Magnaporthe grisea]
21675	ENU05469	ANI61C2976: 1157..228	23-47	805-826	NAP		g3868931	342	125	9.00E-37	39	66	(AB014769) glutaminyl cyclase [Bothrops jararaca]
21676	ENU05470	ANI61C4309: 1..3926	48-67	762-781	NAP		g1654096	1237	78	4.00E-50	54	8	(Y09076) RAD3 [Schizosaccharomyces pombe]
21677	ENU05471	ANI61S1014: 335..931			NAP		g3037018	170	33	0.011	27	92	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21678	ENU05472	ANI6IS1690:			NAP		g786117	159	49	0.00003	17	52	(L41834) nuclear protein [Ensis minor]
21679	ENU05473	ANI6IC1127:	63-90	551-575	NAP		g3006175	448	191	3.00E-48	53	33	(AL022305) putative transcription factor [Schizosaccharomyces pombe]
21680	ENU05474	ANI6IC6111:	22-44	810-829	NAP		g117619	450	122	4.00E-27	34	41	Choline transport protein [Saccharomyces cerevisiae]
21681	ENU05475	ANI6IC3619:	41-60	616-635	NAP		g4033411	533	222	3.00E-57	44	27	putative importin beta-2 subunit (karyopherin beta-2 subunit) (importin 104) (transportin) (TRN) [Schizosaccharomyces pombe]
21682	ENU05476	ANI6IC4102:	112-131	321-343	NAP		g416963	402	171	2.00E-42			C-5 sterol desaturase [Saccharomyces cerevisiae]
21683	ENU05477	ANI6IC1696:	70-89	625-644	NAP		g2501730	328	92	5.00E-18	29	75	Peroxisome assembly protein PER8 (peroxin-10) [Pichia angusta]
21684	ENU05478	ANI6IC1763:	22-45	748-767	NAP		g4160581	644	227	2.00E-61	48	67	(AL035218) possible involvement in nuclear protein localisation [Schizosaccharomyces pombe]
21685	ENU05479	ANI6IC7954:	24-44	807-826	NAP		g2833327	329	100	2.00E-20	33	54	Hexokinase [Schistosoma mansoni]
21686	ENU05480	ANI6IC5158:	22-48	695-714	NAP		g140925	419	144	3.00E-37	37	99	hypothetical oxidoreductase in INLA 5'region (ORFA) [Listeria monocytogenes]
21687	ENU05481	ANI6IC3007:	23-46	714-741	NAP		g1916927	769	286	2.00E-76	55	48	(U87965) putative G-protein [Mus musculus]
21688	ENU05482	ANI6IC9656:	40-59	495-520	NAP		g2330829	307	123	8.00E-28	35	13	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
21689	ENU05483	ANI6IC4620:	183-203	528-548	NAP		g2780359	448	194	3.00E-49	49	34	(AB010110) ascorbate oxidase [Acremonium sp.]
21690	ENU05484	ANI6IC7917:	28-55	724-749	NAP		g1077412	376	136	3.00E-31	42	22	hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae)
21691	ENU05485	ANI6IC1002	38-56	764-784	NAP		g2492658	1339	111	6.00E-24	27	14	[Saccharomyces cerevisiae] putative stergmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
21692	ENU05486	ANI6IC3789:	221-240	738-764	NAP		g4481951	583	243	8.00E-64	41	11	(AL035637) putative alpha-glucan synthase [Schizosaccharomyces pombe]
21693	ENU05487	ANI6IC1946:	53-75	515-534	NAP		g113701	422	185	2.00E-46	46	38	Acetamidase [Emericella nidulans]

Table 1

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21694	ENU05488	AN161C2383: 22-45	438-457		NAP		g417567	136	84	8.00E-16			protein-tyrosine phosphatase 2 (PTPase 2) [Schizosaccharomyces pombe]
21695	ENU05489	AN161C8573: 22-47	798-825		NAP		g4836505	296	64	0.000000			(AF124929) putative deacetylcephalosporin C acetyltransferase [Streptomyces clavuligerus]
21696	ENU05490	AN161C1008 65-84	806-829		NAP		g559964	194	102	3.00E-21	40	74	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
21697	ENU05491	AN161C513:1 102-129	617-640		NAP		g4557525	590	208	2.00E-53	54	44	dihydrolipoamide dehydrogenase precursor [Homo sapiens]
21698	ENU05492	AN161C8488: 68-86	435-453		NAP		g1723495	168	61	0.000000	39	23	hypothetical 63.2 KD protein C1F3.09 in chromosome I [Schizosaccharomyces pombe]
21699	ENU05493	AN161C9883: 25-44	661-687		NAP		g2326833	704	200	9.00E-51	38	33	(Z73502) ORF YPL147w [Saccharomyces cerevisiae]
21700	ENU05494	AN161C1003: 23-49	802-829		NAP		g1653242	559	70	2.00E-11	28	53	(D90912) hypothetical protein [Synechocystis sp.]
21701	ENU05495	AN161C855:1 128-147	408-428		NAP		g1749490	138	82	4.00E-15	31	69	"(D89141) similar to Saccharomyces cerevisiae hypothetical 27.6KD protein in chromosome VII, SWISS-PROT Accession Number P46948 [Schizosaccharomyces pombe]"
21702	ENU05496	AN161C1018 22-48	365-392		NAP		g1437475	134	64	8.00E-10	30	38	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
21703	ENU05497	AN161C1003 51-70	515-534		NAP		g4049543	131	60	0.000000	33	39	(AL034564) putative protease; endopeptidase [Schizosaccharomyces pombe]
21704	ENU05498	AN161C1042 22-43	804-829		NAP		g2995339	199	91	8.00E-18	27	32	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
21705	ENU05499	AN161C1057 41-60	788-807		NAP		g113314	4339	538	e-152	99	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
21706	ENU05500	AN161C5776: 206-225	681-701		NAP		g4826880	94	62	0.000000			oxidase (cytochrome c) assembly 1-like [Homo sapiens]
21707	ENU05501	AN161C6356: 22-49	725-749		NAP		g3702200	717	252	2.00E-66	47	43	(AJ011686) methylenetetrahydrofolate reductase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21708	ENU05502	ANI61C4103: 987..1	42-61	795-814	NAP		g1346660	464	145	5.00E-34	37	58	Salicylate hydroxylase (salicylate 1-monoxygenase) [Pseudomonas putida]
21709	ENU05503	ANI61C1102: 1..483	25-46	390-413	NAP		g1333356	258	115	2.00E-25			DNA-directed RNA polymerase III largest subunit (C160) [Saccharomyces cerevisiae]
21710	ENU05504	ANI61C9104: 4840..5692	45-64	762-781	NAP		g1173383	328	163	1.00E-39	37	66	SCN1 protein [Schizosaccharomyces pombe]
21711	ENU05505	ANI61C1296: 1318..1	22-43	728-749	NAP		g4500377	415	143	6.00E-38	36	47	(AL035439) putative NADPH cytochrome reductase
21712	ENU05506	ANI61C6074: 1430..1			NAP		g1805262	2017	391	e-108	77	13	[Schizosaccharomyces pombe] "(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
21713	ENU05507	ANI61C9521: 1556..843	37-57	661-679	NAP		g2826168	235	106	2.00E-22	39	49	(AB010714) salicylate hydroxylase [Pseudomonas putida]
21714	ENU05508	ANI61C4432: 892..547	40-66	303-325	NAP		g1790870	191	90	7.00E-18	38	44	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
21715	ENU05509	ANI61C7537: 1247..2374	23-42	740-765	NAP		g67385	736	154	7.00E-52	42	52	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21716	ENU05510	ANI61C8019: 1..467	178-195	422-446	NAP		g113701	170	81	5.00E-15	28	28	Acetamidase [Emmericella nidulans]
21717	ENU05511	ANI61C3497: 1..606	61-80	388-413	NAP		g3122272	717	261	4.00E-69	70	37	Importin alpha subunit (karyopherin alpha subunit) (serine-rich RNA polymerase I suppressor protein) [Schizosaccharomyces pombe]
21718	ENU05512	ANI61C2554: 778..1	42-66	730-749	NAP		g2244898	254	132	3.00E-30	29	26	"(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]"
21719	ENU05513	ANI61C3764: 587..1	23-47	494-517	NAP		g730378	502	141	4.00E-48			Proteasome component C11 (macropain subunit C11) (proteinase YSCE subunit 11) (multicatalytic endopeptidase complex subunit C11) [Saccharomyces cerevisiae]
21720	ENU05514	ANI61C7285: 541..1312	23-42	729-751	NAP		g4105147	848	175	8.00E-69	68	100	"(AF043595) xyloglucanase precursor beta-1,4-glucanase precursor [Aspergillus aculeatus]"

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21721	ENU05515	ANI61C3973:	37-64	713-737	NAP			g730881	1645	210	1.00E-87	64	33	"threonyl-tRNA synthetase, cytoplasmic (threonine--tRNA ligase) (THRRS) [Saccharomyces cerevisiae]"
21722	ENU05516	ANI61C3026:	22-49	392-419	NAP			g1362793	168	84	8.00E-16	35	69	emopannil-binding protein - human [Homo sapiens]
21723	ENU05517	ANI61C4961:	121-140	799-824	NAP			g1666269	261	83	2.00E-29	40	75	(Z82021) cytochrome P450 [Agaricus bisporus]
21724	ENU05518	ANI61C7020:	23-42	762-780	NAP			g3219785	885	288	4.00E-77	58	65	putative cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine (thiol)-lyase) (CSASE) [Schizosaccharomyces pombe]
21725	ENU05519	ANI61S2922:	22-45	398-420	NAP			g1723436	610	221	2.00E-57	74	14	hypothetical 119.9 KD protein C56F8.03 in chromosome I [Schizosaccharomyces pombe]
21726	ENU05520	ANI61C7675:	146-168	506-525	NAP			g538605	828	265	8.00E-88	86	41	glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Emericella nidulans [Emericella nidulans]
21727	ENU05521	ANI61C8815:	117-136	570-589	NAP			g2894300	256	90	2.00E-17	43	36	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
21728	ENU05522	ANI61C1562:	22-49	727-747	NAP			g1834342	1513	512	e-144	96	18	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21729	ENU05523	ANI61C2594:	22-46	810-829	NAP			g401013	4308	384	e-120	73	21	DNA-directed RNA polymerase II 138 KD polypeptide (RNA polymerase II subunit 2) [Schizosaccharomyces pombe]
21730	ENU05524	ANI61C8067:	62-81	780-799	NAP			g2407176	1822	553	e-157	98	27	(AF016850) alpha-mannosidase [Emericella nidulans]
21731	ENU05525	ANI61S775:1.			NAP			g4240179	204	39	0.029	26	29	(AB020652) KIAA0845 protein [Homo sapiens]
21732	ENU05526	ANI61C3351:	22-43	468-493	NAP			g3982753	86	70	1.00E-11	32	37	(AF070937) gibberellin 3 beta-hydroxylase [Arabidopsis thaliana]
21733	ENU05527	ANI61C1027	57-77	482-509	NAP			g1770576	154	51	8.00E-14	31	54	(X95073) Translin associated protein X [Homo sapiens]
21734	ENU05528	ANI61C5396:	24-43	805-829	NAP			g462156	1450	172	2.00E-42			GTPase-activating protein [Schizosaccharomyces pombe]
21735	ENU05529	ANI61C1028	35-54	809-829	NAP			g2117970	341	71	1.00E-11			triacylglycerol lipase (EC 3.1.1.3) I-yeast (Geotrichum candidum) (strain CBS 178.71) []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21736	ENU05530	ANI61S302.1	41-60	438-457	NAP		g2245050	599	172	1.00E-63	72	6	(Z97342) resistance gene homolog [Arabidopsis thaliana]
21737	ENU05531	ANI61C667.4	31-50	487-507	NAP		g1906796	349	133	2.00E-32	44	70	(D85181) fungal sterol-C5-desaturase homolog [Homo sapiens]
21738	ENU05532	ANI61S1332	321..887		NAP		g4759100	115	45	0.0004			"splicing factor, arginine/serine-rich 11 [Homo sapiens]"
21739	ENU05533	ANI61C2473	48-67	658-677	NAP		g226788	501	178	6.00E-44	37	14	erythrocyte ankyrin [Homo sapiens]
21740	ENU05534	ANI61C3738	107-126	546-565	NAP		g2924771	126	95	6.00E-19	27	53	(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]
21741	ENU05535	ANI61C3590	32-51	427-448	NAP		g1749552	224	72	8.00E-28	33	35	"(D89172) similar to Saccharomyces cerevisiae transketolase 2(TK2), SWISS-PROT Accession Number P33315 [Schizosaccharomyces pombe]"
21742	ENU05536	ANI61C8544	25-44	804-828	NAP		g2791647	454	110	8.00E-35	33	47	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
21743	ENU05537	ANI61S3134	551..1		NAP		g4558826	242	106	2.00E-22	42	41	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]
21744	ENU05538	ANI61C4840	34-53	770-797	NAP		g3914984	432	181	5.00E-45	39	7	Ferrichrome siderophore peptide synthetase [Ustilago maydis]
21745	ENU05539	ANI61C1550	41-60	423-442	NAP		g4456808	130	52	0.000002	33	22	(A1236923) ifc3 protein [Shewanella frigidimarina]
21746	ENU05540	ANI61C9547	118-138	478-503	NAP		g3136025	165	104	4.00E-22	33	62	(AL023587) putative DNA repair protein [Schizosaccharomyces pombe]
21747	ENU05541	ANI61C5119	734..1		NAP		g2909514	88	47	8.00E-10	34	48	(AL021932) hypothetical protein Rv0439c [Mycobacterium tuberculosis]
21748	ENU05542	ANI61C6475	166-185	369-388	NAP		g121649	389	115	2.00E-42	52	14	GRR1 protein [Saccharomyces cerevisiae]
21749	ENU05543	ANI61C1044	39-58	803-822	NAP		g1708621	930	231	1.00E-67	57	23	serine/threonine-protein kinase PMK1 [Schizosaccharomyces pombe]
21750	ENU05544	ANI61C6941	62-81	804-829	NAP		g1171738	809	240	1.00E-62	48	52	nonsense-mediated mRNA decay protein 3 [Saccharomyces cerevisiae]
21751	ENU05545	ANI61C1198	83-109	692-719	NAP		g1652509	1338	520	e-147	96	72	(D90906) poly(3-hydroxyalkanoate) synthase [Synechocystis sp.]
21752	ENU05546	ANI61C3622	22-47	803-829	NAP		g538067	1959	143	1.00E-33	38	16	(M77661) putative pol polyprotein [Magnaporthe grisea]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21753	ENU05547	ANI6IC7101: 1816..452	38-57	802-829	NAP		g82865	231	99	4.00E-20	28	23	regulatory protein LAC9 - yeast (Kluyveromyces marxianus var. lactis)
21754	ENU05548	ANI6IC7111: 430..1	102-120	444-471	NAP		g731968	281	100	6.00E-21	47	43	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region [Saccharomyces cerevisiae]
21755	ENU05549	ANI6IS878:1..614	187-206	408-431	NAP		g2494125	468	172	1.00E-48	48	44	(AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb D70895). [Arabidopsis thaliana] (X89442) peptide synthetase [Metarhizium anisopliae] (AB009461) MUIS38 [Neurospora crassa]
21756	ENU05550	ANI6IC1047 2:1..1931	22-41	772-795	NAP		g2342601	1299	244	5.00E-64	45	5	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21757	ENU05551	ANI6IC4808: 1813..2678			NAP		g3219304	463	131	3.00E-36	58	26	(AB009461) MUIS38 [Neurospora crassa]
21758	ENU05552	ANI6IC3351: 420..1	102-121	437-456	NAP		g2408015	200	73	2.00E-12	36	42	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21759	ENU05553	ANI6IC1065 5:1469..1894	24-51	391-410	NAP		g1363742	442	182	2.00E-45	61	51	probable membrane protein YLR243w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21760	ENU05554	ANI6IS835:1..787			NAP		g3097062	168	72	4.00E-12	32	50	(Y17145) putative betaine transporter [Eubacterium acidaminophilum]
21761	ENU05555	ANI6IC3157: 1..418	111-130	370-397	NAP		g1172532	521	183	4.00E-46	72	39	Penicillolysin precursor (deuterolysin) [Penicillium citrinum]
21762	ENU05556	ANI6IC18:1..767	114-133	716-736	NAP		g2330791	188	83	5.00E-20	32	35	(Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]
21763	ENU05557	ANI6IC8494: 3514..3060	22-48	455-479	NAP		g1304227	167	91	5.00E-18	32	44	(D63781) Epoxide hydrolase [Glycine max]
21764	ENU05558	ANI6IC9184: 3881..3418	219-237	382-401	NAP		g129766	316	69	8.00E-19			methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid methyltransferase) [Saccharomyces cerevisiae]
21765	ENU05559	ANI6IC9126: 1..1738	22-44	765-789	NAP		g127736	1164	141	5.00E-33	28	18	Myosin-2 isoform [Saccharomyces cerevisiae]
21766	ENU05560	ANI6IC9707: 4373..1505	22-48	785-811	NAP		g3646452	569	93	2.00E-18	28	19	(AL031603) BTB domain and Ankaryin repeat containing protein. [Schizosaccharomyces pombe]
21767	ENU05561	ANI6IC6194: 1239..1	60-85	780-802	NAP		g1580818	1021	201	3.00E-98	71	34	(Z69254) alpha-galactosidase [Hypocrea jecorina]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21768	ENU05562	ANI61C9491: 22-43		570-594	NAP		g416922	381	100	9.00E-32	53	97	Deoxyuridine 5'-triphosphate nucleotidohydrolase (DUTPase) (DUTP pyrophosphatase) (P18) [Lycopersicon esculentum] (AL023534) hypothetical protein [Schizosaccharomyces pombe] (L11574) p68 RNA helicase [Schizosaccharomyces pombe] (AL023594) amino-acid permease [Schizosaccharomyces pombe]
21769	ENU05563	ANI61C1103: 118-143		508-527	NAP		g3130037	318	128	3.00E-29	45	45	
21770	ENU05564	ANI61C4837: 60-79		579-599	NAP		g173419	787	317	5.00E-86	70	38	
21771	ENU05565	ANI61C1966: 22-46		371-389	NAP		g3150139	181	61	2.00E-19	31	32	
21772	ENU05566	ANI61C5006: 22-45		782-801	NAP		g1078626	3748	328	e-122	97	17	bimD protein - Emericella nidulans [Emericella nidulans]
21773	ENU05567	ANI61C6675: 181-202		609-636	NAP		g1723187	397	116	4.00E-44	46	20	112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
21774	ENU05568	ANI61S2718: 1..561			NAP		g2967448	102	40	0.013	31	13	(AB008683) alpha2(I) collagen [Bos taurus]
21775	ENU05569	ANI61C4825: 76-95		728-747	NAP		g3978134	779	256	2.00E-67	52	26	(U65409) Sla2p [Yarrowia lipolytica]
21776	ENU05570	ANI61S4379: 1..1071			NAP		g1572721	254	50	0.00002	29	19	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21777	ENU05571	ANI61C7082: 22-41		805-829	NAP		g4490992	219	61	3.00E-11	31	55	(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
21778	ENU05572	ANI61C5323: 23-42		726-744	NAP		g117619	215	56	0.000000	32	38	Choline transport protein [Saccharomyces cerevisiae]
21779	ENU05573	ANI61C1707: 35-62		718-744	NAP		g29494820	518	134	1.00E-45	46	48	Rhamnogalacturonase B precursor (rhamnogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]
21780	ENU05574	ANI61C8098: 22-49		550-575	NAP		g1351596	221	98	7.00E-20	32	19	hypothetical 86.2 KD protein C4G8.04 in chromosome I [Schizosaccharomyces pombe]
21781	ENU05575	ANI61C1069 5:940..306			NAP		g1351689	297	85	1.00E-22	44	36	Potential CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PPSEP 1) [Schizosaccharomyces pombe]
21782	ENU05576	ANI61C1129 9:784..1565		720-739	NAP		g132845	598	137	1.00E-31	78	100	60S ribosomal protein L27A (L29) (CRP1) [Neurospora crassa]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21783	ENU05577	ANI61C6931: 1..396			NAP		g1877482	65	53	0.000000	32	39	(U89271) short-chain alcohol dehydrogenase [Tripsacum dactyloides]
21784	ENU05578	ANI61C7468: 1494..592	69-88	776-795	NAP		g2213907	1272	438	e-122	81	93	(AF004837) putative vacuolar protein sorting homolog [Aspergillus fumigatus]
21785	ENU05579	ANI61S4063: 1..645	90-109	528-548	NAP		g3929649	463	167	6.00E-41	84	36	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]
21786	ENU05580	ANI61C1014 0:1..515	102-121	468-494	NAP		g1806234	120	63	6.00E-14	31	61	(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
21787	ENU05581	ANI61C1014 8:1981..1	34-61	726-749	NAP		g4185560	3327	571	e-162	99	12	(AF112473) PyrABCN [Emeticella nidulans]
21788	ENU05582	ANI61C6750: 1851..2553	34-53	625-644	NAP		g4759160	252	69	5.00E-17			small nuclear ribonucleoprotein D3 polypeptide (18kD) [Homo sapiens]
21789	ENU05583	ANI61C4308: 1..641	117-136	584-603	NAP		g4262650	245	98	5.00E-26	38	31	(AF125969) contains similarity to GTP-binding proteins [Caenorhabditis elegans]
21790	ENU05584	ANI61C1086 1:1263..821	43-64	395-422	NAP		g3023956	101	69	2.00E-11	34	9	Vegetable incompatibility protein HET-E-1 [Podospora anserina]
21791	ENU05585	ANI61C9585: 637..1	22-48	502-521	NAP		g1175439	599	258	3.00E-68	57	22	hypothetical 107.1 KD protein C24H6.11C in chromosome I [Schizosaccharomyces pombe]
21792	ENU05586	ANI61C4157: 3992..3384	102-127	562-588	NAP		g1723926	248	130	1.00E-29	40	24	hypothetical 78.1 KD protein in TTP20-MRF1 intergenic region [Saccharomyces cerevisiae]
21793	ENU05587	ANI61C3304: 827..1	56-75	699-717	NAP		g729611	371	122	3.00E-27			Vanadate resistance protein GOG5/VRG4/VAN2 [Saccharomyces cerevisiae]
21794	ENU05588	ANI61C8348: 1658..2190	22-42	447-472	NAP		g3560147	263	122	2.00E-27	38	24	"(AL031534) ribosomal processing, ma binding, nucleolar protein [Schizosaccharomyces pombe]"
21795	ENU05589	ANI61C700:1 ..887	122-141	712-731	NAP		g1580818	1013	312	5.00E-90	64	37	(Z69254) alpha-galactosidase [Hypocrea jecorina]
21796	ENU05590	ANI61C6928: 775..1	25-52	680-707	NAP		g2342691	167	68	8.00E-14	29	33	(AC000106) F7G19.26 [Arabidopsis thaliana]
21797	ENU05591	ANI61C1019 2:1383..2024	27-46	563-582	NAP		g544013	143	64	7.00E-16	35	28	endochitinase precursor [Manduca sexta]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21798	ENU05592	ANI61C1575:	22-49	594-614	NAP		g3004863	530	214	4.00E-55	54	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
21799	ENU05593	535..1227 ANI61C9237:	64-83	806-825	NAP		g1723929	1819	261	6.00E-69	51	17	hypothetical 171.5 KD helicase in NUT1-ARQ2 intergenic region [Saccharomyces cerevisiae]
21800	ENU05594	936..1 ANI61C1582:	22-45	725-748	NAP		g2500542	247	105	4.00E-22	31	19	putative ATP-dependent RNA helicase YMR128W [Saccharomyces cerevisiae]
21801	ENU05595	278..1134 ANI61C7665:	69-88	761-780	NAP		g586486	508	178	4.00E-44	37	41	hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region [Saccharomyces cerevisiae]
21802	ENU05596	ANI61C2116:			NAP		g2105430	687	216	2.00E-55	48	24	(U97079) U5-116kD [Mus musculus]
21803	ENU05597	1..964 ANI61C3561:	95-114	609-630	NAP		g1437475	194	105	4.00E-22	38	57	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
21804	ENU05598	1230..568 ANI61C5947:			NAP		g2924313	552	120	1.00E-26	34	25	"(AJ002397) beta-1,3-exoglucanase [Trichoderma harzianum]"
21805	ENU05599	58..1380 ANI61C431:8	22-48	452-471	NAP		g4803936	138	80	1.00E-17			(AC006264) unknown protein [Arabidopsis thaliana]
21806	ENU05600	32..1303 ANI61C374:1	204-223	380-399	NAP		g2117310	70	39	0.032	22	63	(Z95620) hypothetical protein [Schizosaccharomyces pombe]
21807	ENU05601	..592 ANI61C6452:	27-54	805-829	NAP		g3810847	471	192	3.00E-48	37	41	(AL032684) zinc finger protein [Schizosaccharomyces pombe]
21808	ENU05602	22..1176 ANI61C9353:	72-90	496-518	NAP		g3851530	195	59	4.00E-17	41	32	(AF065435) nodulin [Glycine max]
21809	ENU05603	1..539 ANI61C32:1..	22-45	522-549	NAP		g3929312	145	51	0.000007	34	7	(AF100426) fimbriae-associated protein Fap1 [Streptococcus parasanguis]
21810	ENU05604	573 ANI61S133:1.			NAP		g2804455	274	79	3.00E-23	47	10	(AF043699) similar to a human orf (GB:DL3642) and human UV-damaged DNA binding factor (GB:U32986) in separate non-overlapping regions [Caenorhabditis elegans]
21811	ENU05605	73..1 ANI61S618:5	212-232	456-476	NAP		g136600	886	360	3.00E-99			transcriptional regulator Y protein TYRR [Escherichia coli]
21812	ENU05606	6..1023..1 ANI61C1008	70-89	727-746	NAP		g1708982	810	143	4.00E-62	53	54	Ammonium transporter MIEP3 [Saccharomyces cerevisiae]
21813	ENU05607	ANI61S222:1			NAP		g1708463	131	78	5.00E-14	28	37	IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21814	ENU05608	ANT61C6473: 22-46		727-749	NAP		g2408055	154	59	3.00E-11	28	35	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
21815	ENU05609	ANT61C9354: 898..1			NAP		g2565275	361	146	1.00E-34	68	81	(AF023611) Dim1p homolog [Homo sapiens]
21816	ENU05610	ANT61C5269: 37-58		712-730	NAP		g550452	766	154	1.00E-65	57	39	"(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]"
21817	ENU05611	ANT61C8323: 164-183		361-386	NAP		g1084969	612	190	2.00E-58	94	23	sulfate adenylyltransferase (EC 2.7.7.4) - Emericella nidulans [Emericella nidulans]
21818	ENU05612	ANT61C3094: 98-125		805-829	NAP		g1652620	459	96	1.00E-47	55	45	(D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.]
21819	ENU05613	ANT61C2132: 22-41		425-446	NAP		g3878950	252	80	2.00E-23	44	98	(Z32683) similar to RNA binding domain; cDNA EST EMBL:D74891 comes from this gene; cDNA EST EMBL:D75208 comes from this gene; cDNA EST EMBL:D72347 comes from this gene; cDNA EST EMBL:D75552 comes from this gene; cDNA EST EMBL:D... [] (AL049498) hypothetical rho1 gdp-gtp exchange protein
21820	ENU05614	ANT61C8419: 28-46		805-827	NAP		g4539278	553	81	2.00E-15			[Schizosaccharomyces pombe] hypothetical 51.7 KID protein in CTP1-SUL2 intergenic region
21821	ENU05615	ANT61S2455: 33-52		413-438	NAP		g586361	127	62	0.000000	30	32	[Saccharomyces cerevisiae] (L10328) o197 [Escherichia coli]
21822	ENU05616	ANT61S2364: 61-87		427-452	NAP		g290544	730	234	1.00E-74	98	72	(Z97208) hypothetical protein [Schizosaccharomyces pombe]
21823	ENU05617	ANT61C1143 22-47		803-829	NAP		g2239185	1187	253	1.00E-66	45	45	[Schizosaccharomyces pombe] proline-rich protein MP3 - mouse (fragment) []
21824	ENU05618	ANT61S4374: 1..547			NAP		g91210	117	61	0.000000	30	73	DNA-directed RNA polymerase II largest subunit (B220) [Saccharomyces cerevisiae]
21825	ENU05619	ANT61C6626: 22-48		780-807	NAP		g2507347	1984	48	0.00008	56	14	(AL031262) hypothetical protein [Schizosaccharomyces pombe]
21826	ENU05620	ANT61C7149: 28-50		770-790	NAP		g3417430	359	90	1.00E-17	31	30	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21827	ENU05621	AN161C2318:			NAP		g2267008	195	112	4.00E-24	32	10	(AF006827) adenylate cyclase [Magnaporthe grisea]
21828	ENU05622	1..1219 AN161C1143	88-108	368-390	NAP		g3978466	217	103	5.00E-22	42	19	(AF086822) dihydroxyacetone synthase [Candida boidinii]
21829	ENU05623	6:8708..8293 AN161C1455:	122-143	491-510	NAP		g3738169	289	92	3.00E-18	41	41	(AL031856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe]
21830	ENU05624	4657..5330 AN161C1069:	23-46	590-612	NAP		g2967835	661	214	1.00E-61	66	54	(AF052061) polygalacturonase [Ophiostoma novo-ulmi]
21831	ENU05625	3615..6275 AN161C4657:			NAP		g1703456	1367	231	3.00E-68	53	23	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21832	ENU05626	5:1472..2568 AN161C1004	51-71	641-660	NAP		g1352388	377	173	1.00E-42	38	32	"Lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC) [Rattus rattus]"
21833	ENU05627	1..422 AN161C1035:	118-138	381-400	NAP		g4150918	263	109	7.00E-24	51	55	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
21834	ENU05628	1119..1 AN161C9868:	29-49	805-824	NAP		g2133268	1616	457	e-128	91	32	DNA-binding protein amda - Emericella nidulans [Emericella nidulans]
21835	ENU05629	939..1 AN161C9030:	22-45	720-739	NAP		g2414578	251	68	2.00E-20	39	60	(Z99292) hypothetical protein [Schizosaccharomyces pombe]
21836	ENU05630	7:1..469 AN161C1122	116-142	423-448	NAP		g84160	98	64	8.00E-10	32	40	fragmin - slime mold (Physarum polycephalum) (fragments) []
21837	ENU05631	5:381..1235 AN161C1120	25-48	808-828	NAP		g2133293	814	154	8.00E-84	72	98	pectate lyase (EC 4.2.2.2) C - fungus (Fusarium solani) []
21838	ENU05632	1762..3768 AN161C5075:	22-49	720-745	NAP		g3738146	528	75	7.00E-13			"(AL031852) putative cleavage and polyadenylation specificity factor subunit, yeast pre-mRNA 3'-end processing factor CF II homolog [Schizosaccharomyces pombe]"
21839	ENU05633	1287..495 AN161C5115:	60-85	727-750	NAP		g4539609	279	101	9.00E-21	39	100	(AL049522) WD repeat protein [Schizosaccharomyces pombe]
21840	ENU05634	584..1 AN161C7762:	24-45	540-561	NAP		g2408044	695	287	5.00E-77	65	24	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
21841	ENU05635	368..710 AN161C6096:	202-223	454-479	NAP		g3242653	155	55	0.000000	45	26	(AB015510) FII-CMCase [Aspergillus aculeatus]

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21842	ENU05636	ANI61C3621:	22-45	419-440	NAP		g2664240	476	199	1.00E-50	59	47	(AL009227) electron transfer flavoprotein alpha-subunit precursor [Schizosaccharomyces pombe]
21843	ENU05637	ANI61C2544:	22-43	805-824	NAP		g3287941	210	101	5.00E-21	45	26	hypothetical 44.3 KD protein C25H2.15 in chromosome II [Schizosaccharomyces pombe]
21844	ENU05638	ANI61C6113:	44-71	806-826	NAP		g1723894	806	238	6.00E-67	56	40	hypothetical GTP-binding protein in SEH1-PRP20 intergenic region [Saccharomyces cerevisiae]
21845	ENU05639	ANI61C2481:	22-42	581-600	NAP		g1787798	482	206	2.00E-52	43	91	(AE000249) putative enzyme [Escherichia coli]
21846	ENU05640	ANI61C8019:	38-58	485-507	NAP		g4106657	466	189	2.00E-47	57	46	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]
21847	ENU05641	ANI61C8982:	22-42	762-780	NAP		g1346661	337	74	1.00E-12	47	10	NAM9 protein precursor [Saccharomyces cerevisiae]
21848	ENU05642	ANI61C1079	24-45	775-794	NAP		g3133101	832	215	1.00E-64	56	72	(AL023554) conserved hypothetical protein. [Schizosaccharomyces pombe]
21849	ENU05643	ANI61C1061	43-62	709-734	NAP		g2133034	385	151	7.00E-36	26	45	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (X96943)
21850	ENU05644	ANI61C1799:	40-67	464-489	NAP		g1524045	165	63	1.00E-12	39	37	Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] (L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
21851	ENU05645	ANI61S1588:			NAP		g340613	112	41	0.007	25	68	(Z99091) putative exocyst complex component [Schizosaccharomyces pombe]
21852	ENU05646	ANI61C1255:	22-45	297-321	NAP		g4867840	299	137	5.00E-32			hypothetical 29.7 KD protein in RPL1-CPDB intergenic region (F286) [Escherichia coli]
21853	ENU05647	ANI61C1043	119-136	453-479	NAP		g732284	99	52	0.000002	30	31	(AL049495) putative synaptobrevin-type protein transport protein [Schizosaccharomyces pombe]
21854	ENU05648	ANI61S2100:	81-100	388-405	NAP		g4539261	197	61	0.000000	42	66	

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21855	ENU05649	ANI61C5945: 1471..1055	221-240	373-396	NAP		g549725	90	50	5.00E-12			NADH-cytochrome B5 reductase precursor (P34/P32) [Saccharomyces cerevisiae]
21856	ENU05650	ANI61C1909: 1..546	71-92	504-525	NAP		g1827509	203	100	9.00E-21	33	24	(D83993) similar to pir: S52731 (23.4% identity in 273 aa overlap) [Schizosaccharomyces pombe]
21857	ENU05651	ANI61C1058 2:545..1	62-81	470-487	NAP		g2494052	138	57	0.000000	41	45	purine nucleoside phosphorylase (inosine phosphorylase) (PNP) [Bacillus stearothermophilus]
21858	ENU05652	ANI61C5888: 2738..1935	22-44	731-750	NAP		g3121767	72	49	0.00003	31	99	ARP2/3 complex 16 KD subunit (P16-ARC) [Homo sapiens]
21859	ENU05653	ANI61C7786: 1..843	222-244	795-822	NAP		g2131466	205	55	5.00E-10	30	35	hypothetical protein YDR398w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21860	ENU05654	ANI61S4503: 777..1			NAP		g2330699	356	104	2.00E-28	39	53	(Z98529) putative mna polymerase ii transcription factor b subunit [Schizosaccharomyces pombe]
21861	ENU05655	ANI61C4705: 1..1508	22-40	792-811	NAP		g2133259	2209	485	e-136	77	48	tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae]
21862	ENU05656	ANI61C1133: 6948..6145	22-47	756-783	NAP		g953179	189	85	4.00E-16	28	98	(Z37980) ORF14 [Escherichia coli]
21863	ENU05657	ANI61C1141: 1350..2351			NAP		g3411013	412	97	1.00E-37	46	27	(AF000232) protein mannosyltransferase 1 [Candida albicans]
21864	ENU05658	ANI61C1090 1:1..499	35-57	436-460	NAP		g1351919	184	103	9.00E-22	37	24	Copper amine oxidase precursor (MAOXI) [Arthrobacter sp.]
21865	ENU05659	ANI61S1834: 1..670			NAP		g4757882	344	167	8.00E-41			bystin-like [Homo sapiens]
21866	ENU05660	ANI61C6155: 3059..2512	107-130	504-527	NAP		g731763	318	109	8.00E-32	47	27	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region [Saccharomyces cerevisiae]
21867	ENU05661	ANI61C1098 4:966..1386	22-42	421-440	NAP		g134039	337	71	7.00E-16	64	100	Small nuclear ribonucleoprotein SM D1 (SNRNP core protein D1) (SM-D1) (SM-D autoantigen) [Mus musculus]
21868	ENU05662	ANI61C7744: 8689..8335	24-44	313-334	NAP		g2959371	315	95	2.00E-29	63	18	(AL022117) asparagine synthetase [Schizosaccharomyces pombe]
21869	ENU05663	ANI61C6500: 632..1	41-60	495-512	NAP		g1020413	120	57	8.00E-11	32	33	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]

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21870	ENU05664	ANI61C6591:	34-52	808-827	NAP		g2132842	532	237	6.00E-62	51	87	probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae)
		1145..2267											[Saccharomyces cerevisiae]
21871	ENU05665	ANI61C1112	117-136	670-697	NAP		g3859709	344	176	2.00E-43	37	44	(AL033497) nucleotide phosphodiesterase [Candida albicans]
		0:799..1											probable reverse transcriptase Mars1 (clone pCGC20) - fungus (Ascobolus immersus) (fragment) [Ascobolus immersus]
21872	ENU05666	ANI61C1213:	43-62	715-742	NAP		g2133333	215	50	9.00E-17	27	37	
		864..2097											
21873	ENU05667	ANI61C1105	50-69	755-781	NAP		g2293196	397	176	2.00E-43	34	65	(AF008220) YteT [Bacillus subtilis]
		7:851..1											
21874	ENU05668	ANI61C3631:			NAP		g2244802	208	101	5.00E-21	33	16	(Z97336) retrovirus-related polypeptide homolog [Arabidopsis thaliana]
		1..879											(D90914) hypothetical protein [Synechocystis sp.]
21875	ENU05669	ANI61C4225:	71-90	437-456	NAP		g1653493	403	153	2.00E-40	63	66	(X89442) peptide synthetase [Metarhizium anisopliae]
		2092..1609											hypothetical protein YOR021c - yeast (Saccharomyces cerevisiae)
21876	ENU05670	ANI61C8023:	40-66	738-765	NAP		g2342601	463	168	6.00E-41	33	5	[Saccharomyces cerevisiae]
		1..1115											mitochondrial carrier protein RIM2 [Saccharomyces cerevisiae]
21877	ENU05671	ANI61C6494:	22-44	787-813	NAP		g1078030	294	79	2.00E-30	42	94	tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae]
		2741..1905											"(AF038596) beta-1,3-glucanosyltransferase [Aspergillus fumigatus]"
21878	ENU05672	ANI61C246:7	23-44	723-750	NAP		g585856	415	164	8.00E-40	43	60	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
		71..1											(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21879	ENU05673	ANI61C6363:	23-42	718-737	NAP		g2133259	1584	467	e-131	78	48	Arginase [Emmericella nidulans]
		1281..1											
21880	ENU05674	ANI61C7430:	36-62	430-453	NAP		g2967691	453	108	5.00E-46	68	45	TOR2(DRR2) gene [Saccharomyces cerevisiae]
		3318..2845											(AF093142) aconitase [Aspergillus terreus]
21881	ENU05675	ANI61S1195:			NAP		g283032	192	64	0.000000	27	78	
		1..938								001			
21882	ENU05676	ANI61C8808:	22-48	809-829	NAP		g3925779	177	42	0.005	24	48	
		3399..4931											
21883	ENU05677	ANI61C9823:			NAP		g2492940	1531	200	e-127	95	77	
		2105..910											
21884	ENU05678	ANI61C8194:	24-48	779-801	NAP		g742559	1859	200	1.00E-50	41	10	
		1..2472											
21885	ENU05679	ANI61C3566:	48-67	805-829	NAP		g3661614	1985	242	2.00E-63	50	35	
		2989..526											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21886	ENU05680	ANT61C1218:	28-55	601-621	NAP		g1339938	428	185	2.00E-46	51	25	(D50430) glycerol-3-phosphate dehydrogenase [Mus musculus]
21887	ENU05681	1644..1003	27-46	244-261	NAP		g2500536	283	79	5.00E-26	50	20	probable ATP-dependent RNA helicase DBP9 [Saccharomyces cerevisiae]
21888	ENU05682	1..368	27-46	244-261	NAP		g1168351	198	49	0.000005	29	76	Alcohol dehydrogenase (ADH) [Bacillus stearothermophilus]
21889	ENU05683	3114..2036	61-80	792-811	NAP		g2947228	184	39	0.054	25	16	(AF031886) erythrocyte binding protein [Plasmodium yoelii yoelii]
21890	ENU05684	ANT61S1114:	22-41	804-824	NAP		g1730777	1772	367	e-109	72	26	hypothetical 119.3 KD protein in FPR1-TOM22 intergenic region [Saccharomyces cerevisiae]
21891	ENU05685	1477..1	102-125	335-361	NAP		g2132680	166	81	3.00E-15	40	3	probable membrane protein YLR087c - yeast [Saccharomyces cerevisiae]
21892	ENU05686	1..382	22-49	801-828	NAP		g4007758	666	139	2.00E-32	53	55	[Saccharomyces cerevisiae] (AL034433) conserved hypothetical protein [Schizosaccharomyces pombe] (Z95397) unknown
21893	ENU05687	2:484..2062	23-44	784-803	NAP		g2104465	627	87	2.00E-16			[Schizosaccharomyces pombe] hypothetical 24.6 KD protein in MCK1-RP55B intergenic region [Saccharomyces cerevisiae]
21894	ENU05688	1648..159	22-47	457-479	NAP		g1353100	176	91	4.00E-18	43	45	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Saccharomyces cerevisiae]
21895	ENU05689	ANT61C1031	27-46	450-477	NAP		g730430	239	116	1.00E-25	49	22	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21896	ENU05690	706..1089	22-41	772-799	NAP		g67385	673	114	4.00E-66	45	55	"dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glued) [Neurospora crassa]"
21897	ENU05691	68..1154	22-47	792-819	NAP		g2493479	1035	201	4.00E-51	36	21	(Y10542) homologous to 40kD subunit of RNA-polymerase I and III [Cricetus griseus]
21898	ENU05692	3:1..1399	22-49	768-787	NAP		g1914859	814	282	2.00E-75	56	75	putative stigmastocystin biosynthesis protein STCQ [Emmericella nidulans]
21899	ENU05693	2330..1180			NAP		g2498970	539	202	6.00E-52	78	54	(Y17332) proline-rich protein [Zea mays]
21900	ENU05694	ANT61C7771:			NAP		g4138732	194	55	0.000000	23	71	
		4940..5391			NAP								
		ANT61S4257:			NAP								
		1..892			NAP								

Genetic Information

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21901	ENU05695	ANI61C7923: 605..1	23-44	456-483	NAP		g1805251	184	61	0.000000	31	36	(U58946) transposase [Aspergillus awamori]
21902	ENU05696	ANI61C8749: 1..490	122-141	352-371	NAP		g3135990	365	157	4.00E-38	53	27	(AL023589) membrane transporter [Schizosaccharomyces pombe]
21903	ENU05697	ANI61C1122 4:8141..7555	35-62	537-564	NAP		g3925779	138	68	7.00E-11	32	27	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21904	ENU05698	ANI61C1033 9:1..929	23-42	786-813	NAP		g4583552	1171	327	e-103	74	75	"(AJ012316) arabinogalactan endo-1,4-beta-galactosidase [Aspergillus tubingensis]"
21905	ENU05699	ANI61C7064: 2540..1	22-43	720-743	NAP		g113314	4318	575	e-163	98	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emicella nidulans]
21906	ENU05700	ANI61C9189: 1466..994	75-98	426-449	NAP		g1174433	146	78	4.00E-14	42	40	Signal recognition particle 19 KD protein homolog [Yarrowia lipolytica]
21907	ENU05701	ANI61C3701: 1333..1834	27-46	446-465	NAP		g3219956	168	44	0.0008	45	98	hypothetical protein C57A7.01 in chromosome I [Schizosaccharomyces pombe]
21908	ENU05702	ANI61C1058 8:1..587	36-63	531-556	NAP		g4160397	299	134	5.00E-31	39	53	(AL035210) halotolerance protein [Schizosaccharomyces pombe]
21909	ENU05703	ANI61C7089: 1104..733	22-42	320-347	NAP		g2501094	96	52	0.000001	24	48	Syntaxin 6 [Rattus norvegicus]
21910	ENU05704	ANI61C908:1 778..2087	22-42	363-382	NAP		g1085674	414	135	2.00E-31	75	79	blasticidin S deaminase - Aspergillus terreus [Aspergillus terreus]
21911	ENU05705	ANI61C1584: 4315..4806	92-111	391-413	NAP		g730406	106	46	0.0001	36	84	Profilin []
21912	ENU05706	ANI61C5748: 1..512	46-65	448-467	NAP		g3293344	150	77	7.00E-14	29	16	(AF059614) transportin; TRN [Xenopus laevis]
21913	ENU05707	ANI61C8295: 1..1117	22-48	775-802	NAP		g2342601	436	92	8.00E-30	31	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21914	ENU05708	ANI61C9805: 2499..885	24-45	805-829	NAP		g4512702	567	121	7.00E-27	30	41	(AC006569) hypothetical protein [Arabidopsis thaliana]
21915	ENU05709	ANI61C8160: 1976..3983			NAP		g3885836	414	69	8.00E-19	30	34	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
21916	ENU05710	ANI61C1615: 734..1516	74-93	660-679	NAP		g4499837	276	88	2.00E-27	30	57	(AJ011963) dimethyl-allyl-trypphan-synthase [Claviceps purpurea]
21917	ENU05711	ANI61C6187: 1366..1	35-54	722-749	NAP		g585965	1184	371	e-102	67	37	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]

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21918	ENU05712	ANI6IC8757: 1724..1329	121-140	332-351	NAP		g3560215	203	77	5.00E-14	36	28	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]" (AL035229) possible RanBP7-importin-beta-Cse1p superfamily [Schizosaccharomyces pombe] (X96767) U1 snRNP-specific protein C [Mus musculus]
21919	ENU05713	ANI6IC1104: 1..1964	24-43	802-821	NAP		g4176546	284	50	0.00003			
21920	ENU05714	ANI6IC2656: 2041..2589			NAP		g1360017	117	70	1.00E-11	45	62	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
21921	ENU05715	ANI6IS3099: 1..507			NAP		g82698	220	36	0.14	36	49	aminomethyltransferase precursor (glycine cleavage system T protein) [Saccharomyces cerevisiae]
21922	ENU05716	ANI6IC8555: 1..331	42-66	284-310	NAP		g1707880	154	84	3.00E-16			"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]"
21923	ENU05717	ANI6IS1431: 1..746			NAP		g2246532	170	46	0.0002	21	22	hypothetical 138.8 KD protein C11D3.14C in chromosome I [Schizosaccharomyces pombe]
21924	ENU05718	ANI6IC3881: 801..1	96-115	681-698	NAP		g1351710	415	203	2.00E-51	43	18	proline-rich protein - mouse (fragment) [Mus musculus]
21925	ENU05719	ANI6IS2549: 73..645			NAP		g91206	110	60	0.000000	29	96	[X81635) RAD26 [Saccharomyces cerevisiae]
21926	ENU05720	ANI6IC4525: 662..1	102-127	605-631	NAP		g550429	592	233	9.00E-61	53	20	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
21927	ENU05721	ANI6IC5834: 446..2035	64-83	785-804	NAP		g731689	1635	491	e-138	61	7	(AF112473) PyrABCN [Emmericella nidulans]
21928	ENU05722	ANI6IC117: 1..1174	23-45	722-749	NAP		g4185560	1852	534	e-151	97	12	beta-galactosidase (lactase) [Arthrobacter sp.]
21929	ENU05723	ANI6IC9675: 2354..1	24-43	786-813	NAP		g3913155	1105	101	5.00E-21	30	22	(AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe]
21930	ENU05724	ANI6IC4143: 1..818	86-111	693-712	NAP		g3650382	253	115	5.00E-25	30	26	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]
21931	ENU05725	ANI6IC1116: 3:21..1728	22-43	807-829	NAP		g3184098	1329	173	1.00E-85	64	50	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
21932	ENU05726	ANI6IC4422: 1470..2350	26-45	720-739	NAP		g3150262	167	58	2.00E-14	31	65	[Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21933	ENU05727	ANI61C2800:	94-113	420-445	NAP		g4539248	339	132	2.00E-30	48	41	(AL049489) conserved hypothetical TBC domain-containing protein [Schizosaccharomyces pombe]
21934	ENU05728	ANI61C8872:	22-43	760-780	NAP		g2909783	511	187	1.00E-46	33	17	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]
21935	ENU05729	ANI61C1089	33-54	728-747	NAP		g3850091	199	73	1.00E-15	30	46	(AL033383) putative aminotransferase [Schizosaccharomyces pombe]
21936	ENU05730	ANI61C283:5	22-44	460-479	NAP		g2494072	256	127	4.00E-29	42	32	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Agaricus bisporus]
21937	ENU05731	ANI61C9677:	202-223	804-829	NAP		g1352666	963	333	7.00E-98	82	83	"serine/threonine protein phosphatase PP2A-beta, catalytic subunit [Sus scrofa]"
21938	ENU05732	ANI61C9325:	22-43	729-749	NAP		g1345625	423	61	5.00E-14			Biotin--protein ligase (biotin apo-protein ligase) (biotin-- [Saccharomyces cerevisiae]
21939	ENU05733	ANI61C7546:	47-66	784-807	NAP		g3929399	1088	185	1.00E-67	46	51	proline-specific permease (proline transport protein) [Emmericella nidulans]
21940	ENU05734	ANI61C9605:	27-46	723-742	NAP		g729007	358	56	3.00E-14	43	49	CAJ1 protein [Saccharomyces cerevisiae]
21941	ENU05735	ANI61C601:6	63-84	294-314	NAP		g284071	175	83	7.00E-16	41	56	DTMP kinase (EC 2.7.4.9) - human [Homo sapiens]
21942	ENU05736	ANI61S645:1	39-62	287-314	NAP		g2988417	43	46	0.0002	39	43	(U97573) peptidyl-prolyl cis-trans isomerase [Treponema pallidum]
21943	ENU05737	ANI61C678:8	27-46	729-747	NAP		g3914273	448	96	1.00E-34	49	65	Pectate lyase precursor [Emmericella nidulans]
21944	ENU05738	ANI61C8413:	30-49	797-816	NAP		g125348	1078	76	3.00E-19	33	31	KEX1 protease precursor [Kluyveromyces lactis]
21945	ENU05739	ANI61C2004:	54-73	740-759	NAP		g3088571	1869	485	e-136	86	47	(AF059523) heat shock protein 60 [Paracoccidoides brasiliensis]
21946	ENU05740	ANI61S2337:			NAP		g4325349	302	86	1.00E-24	52	43	(AF128394) contains similarity to Petunia PTTA' (GB:AF009516)
21947	ENU05741	ANI61C5790:	104-121	361-381	NAP		g4210461	260	87	8.00E-17	49	20	[Arabidopsis thaliana]
21948	ENU05742	ANI61C4064:	204-227	788-807	NAP		g2342601	301	116	2.00E-32	35	4	(Neurospora crassa) [X89442] peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21949	ENU05743	ANI61C8506: 1137..1	22-44	720-746	NAP		g3136057	427	153	1.00E-36	38	58	(AL023592) actin-like protein [Schizosaccharomyces pombe]
21950	ENU05744	ANI61C7482: 915..1	22-47	752-771	NAP		g2388975	336	67	2.00E-25	44	69	(Z98980) phosphotyrosyl phosphatase activator [Schizosaccharomyces pombe]
21951	ENU05745	ANI61S2702: 1..589			NAP		g3157413	113	44	0.0008	26	25	(AJ001386) catalase [Claviceps purpurea]
21952	ENU05746	ANI61C1084: 2:460..1			NAP		g731385	112	46	0.0002	33	49	hypotheical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21953	ENU05747	ANI61C1087: 2:1270..2819	22-45	806-825	NAP		g4176751	2421	443	e-130	92	43	(AF052391) heat shock protein 70 [Trichophyton rubrum]
21954	ENU05748	ANI61C5200: 1338..2380	22-42	780-799	NAP		g2388905	459	188	5.00E-47	48	59	(Z98974) hypotheical protein [Schizosaccharomyces pombe]
21955	ENU05749	ANI61C21:96 5..1	37-56	728-749	NAP		g2132242	1203	379	e-104	81	56	hypotheical protein YPL235w - yeast (Saccharomyces cerevisiae)
21956	ENU05750	ANI61C7402: 1..1593	22-44	720-740	NAP		g83711	2184	314	e-135	94	34	[Saccharomyces cerevisiae] "nitrite reductase (NADH) (EC 1.6.6.4), short form - Emericella nidulans ["]
21957	ENU05751	ANI61C7966: 3747..3004	25-44	700-723	NAP		g2133240	196	50	8.00E-11	34	100	immunoreactive protein - Coccidioides immitis [Coccidioides immitis] (AL035065) putative urea active transporter [Schizosaccharomyces pombe]
21958	ENU05752	ANI61C8144: 449..2530	22-48	715-734	NAP		g4106690	946	104	6.00E-48	42	36	exonuclease II (exo II) (P140) [Schizosaccharomyces pombe]
21959	ENU05753	ANI61C9575: 4706..8327	22-41	749-769	NAP		g729456	2757	227	7.00E-59	44	21	(AL023592) ma binding protein [Schizosaccharomyces pombe]
21960	ENU05754	ANI61C7591: 1015..1722	22-43	666-687	NAP		g3136047	385	169	1.00E-41	44	53	[Schizosaccharomyces pombe]
21961	ENU05755	ANI61C1370: 533..4			NAP		g1363749	151	89	2.00E-17	38	35	probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae)
21962	ENU05756	ANI61C7297: 576..1016	22-44	375-402	NAP		g3402004	273	94	6.00E-19	58	78	[Saccharomyces cerevisiae]
21963	ENU05757	ANI61C543:1 ..1874	34-61	628-651	NAP		g3913210	1707	324	e-117	73	29	Mbp1 From Saccharomyces Cerevisiae
21964	ENU05758	ANI61C811:1 ..1042	22-43	756-781	NAP		g3417424	410	180	1.00E-44	38	10	putative ATP-dependent RNA helicase CDC28 [Schizosaccharomyces pombe]
21965	ENU05759	ANI61C1079: 5:2047..3775	28-48	806-828	NAP		g626178	834	204	6.00E-52	42	28	(AL031261) putative transport protein [Schizosaccharomyces pombe]
													[HIR1 protein - yeast (Saccharomyces cerevisiae)] [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
21966	ENU05760	ANI61C9078: 22-45	4178..1	668-694	NAP		g2492604	2285	157	9.00E-38	37	15	multidrug resistance protein CDR2 [Candida albicans]
21967	ENU05761	ANI61C1585: 42-68	1..491	448-470	NAP		g2144467	267	120	6.00E-27	43	22	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae) []
21968	ENU05762	ANI61C1208: 22-44	6485..8096	810-829	NAP		g2894293	295	101	7.00E-21	24	54	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
21969	ENU05763	ANI61C7167: 41-64	2698..3037	424-444	NAP		g3861442	255	83	1.00E-15	50	41	(AL033505) hypothetical protein SC1E6.19c [Streptomyces coelicolor] (Z99126) putative dna helicases.
21970	ENU05764	ANI61C3924: 22-46	920..1	719-738	NAP		g2656007	782	183	1.00E-77	50	44	[Schizosaccharomyces pombe] mitochondrial carrier protein RIM2
21971	ENU05765	ANI61C4789: 118-137	1..431	307-326	NAP		g585856	211	96	2.00E-19	40	32	[Saccharomyces cerevisiae] (AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21972	ENU05766	ANI61C1039: 35-54	8:2329..550	803-829	NAP		g3925779	282	55	4.00E-10	23	45	RAS-related protein RAB2BV [Beta vulgaris]
21973	ENU05767	ANI61S3461: 28-53	1..322	272-298	NAP		g3024528	435	176	5.00E-44	80	50	"phosphate cytidyltransferase 2, ethanolamine [Homo sapiens]"
21974	ENU05768	ANI61C4749: 22-42	2526..4013	780-801	NAP		g4505651	524	54	8.00E-12	36	59	putative glucosyltransferase C17C9.07 [Schizosaccharomyces pombe]
21975	ENU05769	ANI61C1954: 710..1	1785..1260		NAP		g1723566	534	196	3.00E-56	52	43	(Z82019) sepin [Agaricus bisporus]
21976	ENU05770	ANI61C4887: 105-123	1785..1260	396-415	NAP		g2244629	415	120	6.00E-32	58	94	putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit [Emmericella nidulans]
21977	ENU05771	ANI61C1913: 31-50	2849..1	806-829	NAP		g2492657	4813	558	e-158	98	18	Glucose Oxidase (E.C.1.1.3.4) []
21978	ENU05772	ANI61S1288: 47-70	1..553	350-369	NAP		g442927	133	54	0.000000	33	28	(AL049498) activator of Hsp70 and Hsp90 chaperones [Schizosaccharomyces pombe]
21979	ENU05773	ANI61C7281: 28-46	1246..1	716-735	NAP		g4539286	849	213	9.00E-55	44	47	probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21980	ENU05774	ANI61C243: 23-50	559..4334	692-712	NAP		g2132889	228	163	1.00E-39	32	22	"ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) [Homo sapiens]"
21981	ENU05775	ANI61C7816: 46-65	1..546	498-525	NAP		g4502887	198	94	9.00E-19	40	28	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21982	ENU05776	ANI61C525:7	22-47	799-818	NAP		g1077042	3207	122	9.00E-54	61	14	cadmium resistance protein YCF1 - yeast (Saccharomyces cerevisiae)
		159..2357											[Saccharomyces cerevisiae]
21983	ENU05777	ANI61C1705:	22-45	802-829	NAP		g586361	733	153	2.00E-36	45	54	hypothetical 51.7 KD protein in CTP1-SUL2 intergenic region [Saccharomyces cerevisiae]
		5289..6343											[Saccharomyces cerevisiae]
21984	ENU05778	ANI61S4513:	35-57	317-334	NAP		g136232	115	68	6.00E-11	30	18	"potassium transport protein, low-affinity [Saccharomyc cerevisiae]" (M20319) aminotriazole resistance protein [Saccharomyc cerevisiae]
		377..75											[Saccharomyc cerevisiae]
21985	ENU05779	ANI61C1142	48-67	784-803	NAP		g171124	411	101	7.00E-21	25	48	hypothetical protein YLR063w - yeast (Saccharomyc cerevisiae)
		7:3870..2510											[Saccharomyc cerevisiae]
21986	ENU05780	ANI61C9782:	49-70	446-465	NAP		g2131764	128	73	9.00E-13	33	40	hypothetical protein YLR063w - yeast (Saccharomyc cerevisiae)
		505..1											[Saccharomyc cerevisiae]
21987	ENU05781	ANI61C5615:			NAP		g3021303	2839	531	e-150	95	12	(Y15996) acetyl-CoA carboxylase [Emeticella nidulans]
		1694..1											(AL031261) putative transport protein [Schizosaccharomyc pombe]
21988	ENU05782	ANI61C8296:	24-43	804-828	NAP		g3417424	791	39	0.000000			hypothetical 88.2 KD protein C2F7.18C in chromosome I []
		2054..49											phosphoribosylformylglycinamide synthase (FGAM synthase) (formylglycinamide ribotide amidotransferase) (FGARAT) [Saccharomyc cerevisiae]
21989	ENU05783	ANI61C8795:	22-47	807-826	NAP		g1175379	428	151	7.00E-36	30	36	(Z95395) putative taf; transcription factor TFHD complex component [Schizosaccharomyc pombe]
		1067..1											probable calcium-transporting ATPase 8 [Saccharomyc cerevisiae]
21990	ENU05784	ANI61C3558:			NAP		g1709924	491	214	5.00E-55	50	15	(AL049587) putative transcriptional regulator [Streptomyc coelicolor]
		1569..916											"sodium channel" alpha subunit [human, skeletal muscle, Peptide, 1836 aa]
21991	ENU05785	ANI61C4915:	39-58	711-731	NAP		g2104421	1647	139	2.00E-32	34	23	hypothetical 25.6 KD protein in SMI1-PHO81 intergenic region [Saccharomyc cerevisiae]
		2886..1											(AJ224922) ATP citrate lyase [Sordaria macrospora]
21992	ENU05786	ANI61C2010:	29-50	720-744	NAP		g2493011	732	254	8.00E-67	47	17	
		1..1196											
21993	ENU05787	ANI61C6994:	27-49	563-590	NAP		g4584493	174	101	4.00E-21	35	58	
		783..1393											
21994	ENU05788	ANI61S1378:	41-59	219-239	NAP		g243989	474	192	5.00E-49	90	5	
		1..327											
21995	ENU05789	ANI61C3854:	30-57	808-829	NAP		g1723752	242	91	2.00E-23	35	99	
		068..4993											
21996	ENU05790	ANI61C4905:			NAP		g4107343	436	175	1.00E-43	62	23	
		1..545											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21997	ENU05791	ANI61C3311:	103-124	388-407	NAP		g4680709	322	97	3.00E-32			(AF132969) CGI-35 protein [Homo sapiens]
21998	ENU05792	ANI61C7708:	22-43	802-821	NAP		g3005587	326	33	2.3	30	33	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
21999	ENU05793	ANI61C8066:	41-60	715-742	NAP		g1710663	1183	111	5.00E-69	58	22	putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) [Schizosaccharomyces pombe]
22000	ENU05794	ANI61C8202:	34-53	724-743	NAP		g553118	646	132	2.00E-54	38	53	(M27081) alkane hydroxylating cytochrome P-450 [Candida maltosa]
22001	ENU05795	ANI61C1091	43-62	780-799	NAP		g3024986	265	142	3.00E-33			hypothetical zinc-type alcohol dehydrogenase-like protein in AHPF-RNK intergenic region [Escherichia coli]
22002	ENU05796	ANI61C3211:	22-43	714-733	NAP		g3183035	1559	159	1.00E-41	41	27	importin beta-1 subunit (karyopherin beta-1 subunit) (importin 95) [Schizosaccharomyces pombe]
22003	ENU05797	ANI61C1633:	22-46	442-463	NAP		g1706221	211	62	3.00E-17	43	100	cytochrome B5 [Saccharomyces cerevisiae]
22004	ENU05798	ANI61C8674:	102-125	263-290	NAP		g409547	127	66	8.00E-11	33	19	(L07492) sugar transport protein [Saccharomyces cerevisiae]
22005	ENU05799	ANI61C1106	67-94	500-527	NAP		g2131422	184	83	2.00E-15	34	38	hypothetical protein YDR306c - yeast [Saccharomyces cerevisiae]
22006	ENU05800	ANI61C5670:			NAP		g83726	714	280	4.00E-75	97	42	[Saccharomyces cerevisiae] hypothetical nox2 protein - Emericella nidulans mitochondrion (SGC3)
22007	ENU05801	ANI61C7760:	29-56	306-331	NAP		g631806	233	104	3.00E-22	41	26	[Emericella nidulans] "beta2-chimerin, cerebellar - rat (fragment) []"
22008	ENU05802	ANI61C6462:	29-54	804-824	NAP		g1805251	924	159	6.00E-60	44	50	(U58946) transposase [Aspergillus awamori]
22009	ENU05803	ANI61C7280:	43-62	793-820	NAP		g2956768	400	122	4.00E-27	37	71	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22010	ENU05804	ANI61C4923:	39-60	804-823	NAP		g2507441	1041	135	4.00E-80	63	53	"T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta) [Saccharomyces cerevisiae]"
22011	ENU05805	ANI61C2862:	105-124	580-602	NAP		g4158188	147	74	1.00E-12	37	49	(AL035206) putative alcohol dehydrogenase [Streptomyces coelicolor]

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22012	ENU05806	ANI61C1129	119-146	443-465	NAP		g2408082	398	169	8.00E-42	52	17	(Z99167) putative helicase [Schizosaccharomyces pombe]
22013	ENU05807	ANI61C9103	32-50	776-802	NAP		g2673955	1266	357	6.00E-98	87	32	(U62935) multidrug resistance protein 2 [Aspergillus fumigatus]
22014	ENU05808	ANI61C6282	112-135	711-738	NAP		g731262	220	125	4.00E-28	24	23	vacuolar protein sorting-associated protein VPS8 [Saccharomyces cerevisiae]
22015	ENU05809	ANI61C6738	57-76	810-829	NAP		g731597	300	94	2.00E-18	31	70	hypothetical 36.1 KD protein in YLF2-PRPS4 intergenic region [Saccharomyces cerevisiae]
22016	ENU05810	ANI61C1129	23-47	788-808	NAP		g1352980	778	300	1.00E-85	64	24	ATP-dependent RNA helicase DOB1 (MRNA transport regulator MTR4) [Saccharomyces cerevisiae]
22017	ENU05811	ANI61C850	7 22-46	601-626	NAP		g1706480	212	87	8.00E-18	34	19	DNA ligase I (polydeoxyribonucleotide synthase (ATP)) [Xenopus laevis]
22018	ENU05812	ANI61C3634	22-45	804-823	NAP		g1546072	1105	147	8.00E-35	32	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22019	ENU05813	ANI61C5125	22-47	770-797	NAP		g731899	947	280	6.00E-75	49	18	putative membrane glycoprotein in SDL 1 5'region precursor [Saccharomyces cerevisiae]
22020	ENU05814	ANI61C5245	31-58	604-631	NAP		g3738163	347	94	1.00E-18	38	99	(AL031856) putative DNA J domain containing protein [Schizosaccharomyces pombe]
22021	ENU05815	ANI61S1152	118-145	505-524	NAP		g2498506	271	85	3.00E-25	42	26	proline-rich protein LAS17 [Saccharomyces cerevisiae]
22022	ENU05816	ANI61C1643	78-97	720-740	NAP		g1261823	684	229	1.00E-59	48	25	(L77234) glycine rich protein [Neurospora crassa]
22023	ENU05817	ANI61S3304	52-71	285-312	NAP		g4097158	162	94	6.00E-19	37	7	(U46488) Nrps [Proteus mirabilis]
22024	ENU05818	ANI61C8526			NAP		g3004634	798	113	6.00E-53	59	81	(U96385) GATA transcription factor [Penicillium chrysogenum]
22025	ENU05819	ANI61C4111	27-46	807-826	NAP		g1076802	134	38	0.12			extensin-like protein - maize [Zea mays]
22026	ENU05820	ANI61C3323	32-59	603-622	NAP		g401335	526	114	1.00E-42	77	99	vacuolar ATP synthase 16 KD proteolipid subunit [Neurospora crassa]
22027	ENU05821	ANI61C1225	190-211	528-548	NAP		g131768	217	87	1.00E-16	41	31	quinate permease (quinate transporter) [Emeticella nidulans]

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22028	ENU05822	ANI61C9283:	107-126	444-463	NAP		g871830	113	39	0.017	35	60	(D30747) mini-collagen [Acropora done]
22029	ENU05823	ANI61C2431:	77-96	719-737	NAP		g3319315	977	290	7.00E-78	54	33	(AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
22030	ENU05824	ANI61C1512:	26-53	796-819	NAP		g3929395	2040	328	4.00E-89	67	32	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit) [Neurospora crassa]
22031	ENU05825	ANI61C5551:	22-48	785-809	NAP		g2120666	724	241	6.00E-63	42	48	"2,4-chlorocatechol 1,2-dioxygenase (EC 1.13.11.-) ttdB - Pseudomonas putida [Pseudomonas putida]" (AL022071) hypothetical protein [Schizosaccharomyces pombe]
22032	ENU05826	ANI61S2863:	36-55	436-454	NAP		g2950458	228	88	3.00E-17	29	19	(AF019254) DNA polymerase epsilon homolog [Emicella nidulans]
22033	ENU05827	ANI61C5475:	22-46	792-812	NAP		g4102990	9834	578	e-164	98	12	(AJ223459) Pm α protein [Emicella nidulans]
22034	ENU05828	ANI61C4262:	22-47	806-828	NAP		g2808662	854	122	3.00E-27	30	33	"glucan (1,4- α -), branching enzyme I (glycogen branching enzyme) [Homo sapiens]" (U07187) Mlh1p [Saccharomyces cerevisiae]
22035	ENU05829	ANI61C2219:	42-65	613-638	NAP		g4557619	1082	161	1.00E-87	66	35	protein kinase (EC 2.7.1.37) - fission yeast (Schizosaccharomyces pombe) [Schizosaccharomyces pombe]
22036	ENU05830	ANI61C8552:			NAP		g460627	92	53	0.000000	31	15	hypothetical 143.7 KD protein C11D3.15 in chromosome I [Schizosaccharomyces pombe]
22037	ENU05831	ANI61C1129	112-136	548-567	NAP		g2130466	719	290	7.00E-78	62	51	hypothetical 89.4 KD TRP-ASP repeats containing protein in PMT6-PCT1 intergenic region [Saccharomyces cerevisiae]
22038	ENU05832	ANI61C4402:	27-48	622-649	NAP		g1351711	1351	311	4.00E-88	66	18	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]
22039	ENU05833	ANI61C1064	22-41	671-695	NAP		g1176045	1101	286	2.00E-76	50	35	(AF027687) beta glucosidase homolog [Cochliobolus heterotrophus]
22040	ENU05834	ANI61C1036	77-96	564-590	NAP		g4539186	228	102	7.00E-23	45	51	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emicella nidulans]
22041	ENU05835	ANI61C9204:	59-78	805-829	NAP		g2598192	900	375	e-103	67	30	
22042	ENU05836	ANI61C5575:			NAP		g1705828	123	63	0.000000	32	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22043	ENU05837	ANI61C1100: 5121..4463	22-49	616-638	NAP		g3695005	256	115	3.00E-25	37	49	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]
22044	ENU05838	ANI61S37:44 6..1	72-91	391-414	NAP		g1881271	210	78	4.00E-14	35	73	"(AB001488) function unknown, similar product in H. influenzae and synecocystis. [Bacillus subtilis]"
22045	ENU05839	ANI61C1145 1:441..1	102-124	455-479	NAP		g4760360	115	76	1.00E-13			"(AL035213) predicted using hexExon; L3291.5, Hypothetical protein, len: 300 aa [Leishmania major]"
22046	ENU05840	ANI61S2374: 1..339	66-86	257-276	NAP		g78837	517	205	9.00E-53	95	38	rimK protein - Escherichia coli [Escherichia coli]
22047	ENU05841	ANI61C7587: 2400..2047	33-55	294-313	NAP		g729611	286	126	5.00E-29			Vanadate resistance protein GOG5/VRG4/VAN2 [Saccharomyces cerevisiae]
22048	ENU05842	ANI61C8467: 1..411	189-208	367-388	NAP		g3059184	147	79	1.00E-14	33	40	(D88014) homologous to HpcE (HHDD isomerase) protein of E. coli [Rhodococcus erythropolis]
22049	ENU05843	ANI61C5479: 1309..2279	28-49	802-829	NAP		g114878	379	147	8.00E-35	37	83	carboxyvinyl-carboxyphosphonate phosphorylmutase (carboxyphosphonoenolpyruvate phosphonmutase) (CPEP phosphonmutase) [Streptomyces hygroscopicus]
22050	ENU05844	ANI61C1078 6:1..423	102-124	354-373	NAP		g4249409	111	63	4.00E-13	33	29	(AC006072) putative sugar transporter [Arabidopsis thaliana]
22051	ENU05845	ANI61C4441: 1..966	22-48	633-659	NAP		g1351645	869	324	6.00E-88	55	52	hypothetical amino-acid permease C8A4.11 [Schizosaccharomyces pombe]
22052	ENU05846	ANI61C1134 6:1472..493	32-51	774-793	NAP		g4583351	380	185	4.00E-46	41	47	(AF114167) lysosomal peptidain insensitive protease [Canis familiaris]
22053	ENU05847	ANI61C2920: 387..1499	37-56	790-809	NAP		g1723578	381	102	1.00E-38	36	78	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
22054	ENU05848	ANI61C7166: 267..653	50-69	442-461	NAP		g3136036	128	82	2.00E-15	40	48	(AL023590) Glutathione S-transferase [Schizosaccharomyces pombe]
22055	ENU05849	ANI61C2437: 2082..3715	25-52	725-751	NAP		g728771	639	101	5.00E-42	52	23	Alanine/arginine aminopeptidase [Saccharomyces cerevisiae]
22056	ENU05850	ANI61C6823: 576..1	53-73	530-549	NAP		g2226425	124	71	6.00E-12	25	10	(Z97204) hypothetical protein [Schizosaccharomyces pombe]

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22057	ENU05851	ANI61C2391: 1406..2123	24-43	634-654	NAP	g3800835	205	67	2.00E-10	38	4	(AF079138) type I polyketide synthase PlkAII [Streptomyces venezuelae]
22058	ENU05852	ANI61S1602: 316..1	49-76	439-466	NAP	g2909465	110	56	0.000000	34	38	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]
22059	ENU05853	ANI61C7205: 1..473	49-71	414-434	NAP	g1588283	463	205	2.00E-52	61	12	MSH6 gene [Saccharomyces cerevisiae]
22060	ENU05854	ANI61C4233: 71..904	101-126	791-813	NAP	g600810	228	90	2.00E-17	39	99	(Z46921) unknown [Saccharomyces cerevisiae]
22061	ENU05855	ANI61C918:2 37..1076	54-73	770-789	NAP	g731502	351	153	1.00E-36	32	25	importin beta-4 subunit (karyopherin beta-4 subunit) (ran binding protein YRB4) [Saccharomyces cerevisiae]
22062	ENU05856	ANI61C8801: 1..566	165-182	469-488	NAP	g130582	196	97	1.00E-19	35	12	Retrovirus-related pol polyprotein from transposon TNT 1-94 [Nicotiana tabacum]
22063	ENU05857	ANI61C3205: 1997..1	23-44	649-668	NAP	g3288709	1601	291	6.00E-78	52	19	(AB010442) PMR1 [Penicillium digitatum]
22064	ENU05858	ANI61C4172: 1..921	89-108	681-700	NAP	g3413518	506	231	5.00E-60	41	16	(AB010810) phospholipase D [Candida albicans]
22065	ENU05859	ANI61C3591: 1109..2671	29-48	793-811	NAP	g3116147	329	64	7.00E-17	30	47	(AL023290) amino acid permease [Schizosaccharomyces pombe]
22066	ENU05860	ANI61C5426: 653..1	43-63	522-549	NAP	g1731075	306	178	4.00E-44	43	53	probable NADH-dependent flavin oxidoreductase YQJM [Bacillus subtilis]
22067	ENU05861	ANI61C1073: 7..1064..2403	22-48	778-796	NAP	g3393022	397	176	2.00E-43	38	38	(AL031174) hypothetical protein [Schizosaccharomyces pombe]
22068	ENU05862	ANI61C7940: 1..685	127-145	642-664	NAP	g2498701	94	71	1.00E-11	26	46	sterigmatocystin 7-O-methyltransferase precursor [Aspergillus flavus]
22069	ENU05863	ANI61C3966: 918..16	24-46	760-781	NAP	g4539255	359	129	3.00E-29			(AL049495) hypothetical protein [Schizosaccharomyces pombe]
22070	ENU05864	ANI61S4253: 1..822			NAP	g3153821	160	47	0.0001	23	30	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22071	ENU05865	ANI61C9594: 1..503			NAP	g3282229	293	78	3.00E-14			(U68722) BcLHH [Botryotinia fuckeliana]
22072	ENU05866	ANI61C8675: 5936..6350	92-111	368-387	NAP	g1749656	105	73	2.00E-12	35	38	(D89224) similar to Saccharomyces cerevisiae ORF YCR028 [Schizosaccharomyces pombe]

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22073	ENU05867	ANI6IC4988:	36-58	483-510	NAP		g1351666	316	119	4.00E-27	50	30	putative ATP-dependent RNA helicase C1F7.02C [Schizosaccharomyces pombe]
22074	ENU05868	ANI6IC5515:	115-134	391-410	NAP		g2501339	327	148	2.00E-35	44	24	Copper amine oxidase 1 [Aspergillus niger]
22075	ENU05869	ANI6IC7746:	22-49	615-635	NAP		g2133285	298	129	3.00E-29			tryptophan dimethylallyltransferase (EC 2.5.1.34) - ergot fungus [Claviceps purpurea]
22076	ENU05870	ANI6IC1105:			NAP		g135140	570	219	9.00E-63	54	22	"Leucyl"-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) [Neurospora crassa]
22077	ENU05871	ANI6IC6132:			NAP		g1730744	352	136	1.00E-31	56	45	hypothetical 33.5 KD protein in MKS1-MSK1 intergenic region [Saccharomyces cerevisiae]
22078	ENU05872	ANI6IC1070:	42-61	806-828	NAP		g998355	455	71	2.00E-22	31	31	(U35661) colony 1 [Ophiostoma ulmi]
22079	ENU05873	ANI6IC2660:	25-44	709-736	NAP		g2145937	415	57	7.00E-17	33	12	polyketide synthase pksE - Mycobacterium leprae [Mycobacterium leprae]
22080	ENU05874	ANI6IS2794:	113-139	459-486	NAP		g3327882	453	205	1.00E-52	54	43	(AB016221) SSL1 [Schizosaccharomyces pombe]
22081	ENU05875	ANI6IC8962:	31-58	754-773	NAP		g1407655	179	46	0.0003			(U58884) SH3P7 [Mus musculus]
22082	ENU05876	ANI6IC8475:	28-47	793-812	NAP		g4107343	1137	243	e-111	91	36	(AJ224922) ATP citrate lyase [Sordaria macrospora]
22083	ENU05877	ANI6IC5331:	117-134	425-444	NAP		g1723448	339	124	9.00E-31	46	28	hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]
22084	ENU05878	ANI6IS1813:			NAP		g2635194	425	173	9.00E-43	47	99	(Z99117) similar to hypothetical proteins [Bacillus subtilis]
22085	ENU05879	ANI6IS6176:	216-235	527-546	NAP		g4091929	422	185	2.00E-46	47	50	"(AF069752) C5,6 desaturase [Candida albicans]"
22086	ENU05880	ANI6IS564:	51..1		NAP		g2635812	276	125	1.00E-28	46	70	(Z99120) similar to hypothetical proteins [Bacillus subtilis]
22087	ENU05881	ANI6IC5372:	22-48	790-817	NAP		g2342601	820	242	3.00E-63	48	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22088	ENU05882	ANI6IC4407:	26-45	584-606	NAP		g118239	131	42	0.000000	31	71	Dihydrodipicolinate synthase (DHDPs) [Corynebacterium glutamicum]

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22089	ENU05883	ANT61C4408: 1363..1	22-44	633-652	NAP		g3116018	679	134	1.00E-46	44	53	(Y13067) vanillin: NAD+ oxidoreductase [Pseudomonas fluorescens]
22090	ENU05884	ANT61C1974: 1..699	133-152	494-517	NAP		g83673	183	96	3.00E-19	36	34	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22091	ENU05885	ANT61C409: 879..1	29-48	761-780	NAP		g114971	1192	181	6.00E-45	37	33	beta-glucosidase precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucosylhydrolase) [Kluyveromyces marxianus]
22092	ENU05886	ANT61C9938: 927..454	183-204	430-453	NAP		g3947883	172	68	3.00E-11	31	31	(AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
22093	ENU05887	ANT61C1941: 1..1874	22-43	792-819	NAP		g3915963	1019	192	2.00E-48	45	14	ATP-dependent bile acid permease [Saccharomyces cerevisiae]
22094	ENU05888	ANT61C9360: 882..1542	23-47	522-545	NAP		g2765195	214	101	7.00E-21	33	6	(Y12527) HMMWP1 protein [Yersinia enterocolitica]
22095	ENU05889	ANT61C7355: 925..159	22-43	727-746	NAP		g2132992	120	104	9.00E-22	34	21	probable membrane protein YPL183c - yeast (Saccharomyces cerevisiae)
22096	ENU05890	ANT61C7856: 1..541	24-43	485-504	NAP		g3080368	162	91	6.00E-18	34	24	[Saccharomyces cerevisiae] (AL022580) putative protein [Arabidopsis thaliana]
22097	ENU05891	ANT61S1700: 1..605	36-63	387-413	NAP		g2894215	104	71	6.00E-12	29	38	(AL021841) amB [Mycobacterium tuberculosis]
22098	ENU05892	ANT61C2695: 1..616	58-83	404-425	NAP		g4505499	213	119	1.00E-26	40	18	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) [Homo sapiens]
22099	ENU05893	ANT61C2136: 5058..4203	115-134	805-829	NAP		g266448	648	252	3.00E-66			long-chain-fatty-acid--COA ligase 1 (long-chain acyl-CoA synthetase 1) (fatty acid activator 1) [Saccharomyces cerevisiae]
22100	ENU05894	ANT61C1060: 5:839..1	153-176	654-679	NAP		g2499125	458	196	2.00E-49	37	8	vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22101	ENU05895	ANT61C7807: 1308..332	22-46	804-829	NAP		g3220205	166	55	0.000000			(AF0544613) peroxin [Yarrowia lipolytica]
22102	ENU05896	ANT61C3104: 1..1521	61-80	807-826	NAP		g4007757	1872	368	e-126	72	51	(AL034433) glucose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22103	ENU05897	ANI6IC6457: 22-47		801-826	NAP		g2052244	324	92	3.00E-18	37	52	[Schizosaccharomyces pombe] [] (Y12561) Cdc1 protein
22104	ENU05898	314..1526 ANI6IC477:1 24-45		535-560	NAP		g3879684	151	85	4.00E-16	36	49	[Schizosaccharomyces pombe] [] (Z74042) predicted using GeneFinder. Similarity to Haemophilus 3-oxoacyl-(acyl-carrier protein) reductase (SW:FABG_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis elegans] (AB010274) fatty acid synthetase [Schizosaccharomyces pombe]
22105	ENU05899	ANI6IC9467: 22-42		796-819	NAP		g4115480	1564	122	2.00E-43	42	12	[Schizosaccharomyces pombe] cell division-associated protein B1MB []
22106	ENU05900	3514..72 ANI6IC9162: 27-49		434-456	NAP		g416716	917	254	3.00E-67	92	10	(AF080217) acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme [Sinorhizobium meliloti] (D90912) hypothetical protein [Synechocystis sp.]
22107	ENU05901	1823..2453 ANI6IC1100 50-69		795-814	NAP		g3769519	982	209	2.00E-53	45	41	(AL031741) putative membrane transporter [Schizosaccharomyces pombe]
22108	ENU05902	4252..5353 ANI6IC4407: 34-54		707-730	NAP		g1653242	390	91	1.00E-23	32	58	(L10127) ORF17 [Molluscum contagiosum virus type 1]
22109	ENU05903	684..1 ANI6IC1871: 22-49		640-660	NAP		g3650370	299	116	1.00E-25	37	41	(AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe]
22110	ENU05904	2:1..1341 ANI6IC1015 37-54		764-790	NAP		g462768	85	41	0.008			(AL023706) hypothetical protein [Schizosaccharomyces pombe]
22111	ENU05905	607..2155 ANI6IC9626: 22-48		802-829	NAP		g3650405	960	216	2.00E-55	49	53	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
22112	ENU05906	3953..1900 ANI6IC9067: 26-49		806-825	NAP		g4574121	402	100	2.00E-20	36	27	putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22113	ENU05907	4685..3207 ANI6IC7016: 25-48		806-825	NAP		g2257494	737	122	4.00E-27	45	41	(AF082072) ABC transporter protein AtrC [Emmericella nidulans]
22114	ENU05908	1..1423 ANI6IC7570: 24-50		803-822	NAP		g3169091	1112	199	4.00E-81	59	46	
22115	ENU05909	1..791 ANI6IS1726: 2707..3778		803-829	NAP		g1572721	130	45	0.0008	25	18	
22116	ENU05910	ANI6IC6647: 22-41		803-829	NAP		g3219964	455	158	4.00E-38	46	87	
22117	ENU05911	2584..1 ANI6IC7639: 22-49		807-829	NAP		g4587971	3918	501	e-141	99	20	

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22118	ENU05912	ANT6IC2128: 22-41		725-746	NAP		g1709029	1120	295	2.00E-79	56	27	MIC1 protein [Saccharomyces cerevisiae]
22119	ENU05913	ANT6IC1267: 22-42		786-805	NAP		g2133039	685	218	4.00E-56	45	17	probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)
22120	ENU05914	ANT6IS4277: 69-88		527-547	NAP		g4733981	345	57	4.00E-18			[Saccharomyces cerevisiae] (AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]
22121	ENU05915	ANT6IS4437: 204-225		414-436	NAP		g2414610	170	53	4.00E-13	43	48	"(Z99295) oxidoreductase, possible sorbitol utilization
22122	ENU05916	ANT6IC7381: 34-61		686-713	NAP		g1666269	430	90	6.00E-36	40	97	[Schizosaccharomyces pombe] (Z82021) cytochrome P450 [Agaricus bisporus]
22123	ENU05917	ANT6IC2718: 50-76		457-479	NAP		g229530	193	75	5.00E-20	43	97	cytochrome b2 1-103 [Saccharomycetales]
22124	ENU05918	ANT6IS3976: 136..520			NAP		g547782	162	73	1.00E-12	36	47	"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3))I [Plasmid NTP16]"
22125	ENU05919	ANT6IC775:2 24-51		682-709	NAP		g1730771	602	172	3.00E-42	55	25	hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region [Saccharomyces cerevisiae]
22126	ENU05920	ANT6IC2389: 72-93		375-401	NAP		g1351972	666	153	7.00E-37	95	16	Nitrogen regulatory protein area [Emeticella nidulans]
22127	ENU05921	ANT6IC1098 91-110		738-756	NAP		g3914054	447	131	5.00E-30	32	35	MUTS protein homolog 1 [Schizosaccharomyces pombe]
22128	ENU05922	ANT6IC3268: 22-44		802-829	NAP		g2132229	149	47	0.0002	31	94	hypothetical protein YPL199c - yeast (Saccharomyces cerevisiae)
22129	ENU05923	ANT6IC1371: 112-133		640-667	NAP		g3702646	135	72	5.00E-12	26	38	[Saccharomyces cerevisiae] (AL031825) putative membrane transport protein
22130	ENU05924	ANT6IC6060: 22-47		597-624	NAP		g4495124	436	174	5.00E-43	43	62	[Schizosaccharomyces pombe] (AL035675) WD repeat protein; human U5 SNRNP-specific-like
22131	ENU05925	ANT6IC679:2 22-45		721-748	NAP		g2131263	2782	396	e-109	66	13	[Schizosaccharomyces pombe] GLT1 protein - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]

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22132	ENU05926	AN161C1134:	52-71	781-800	NAP		g2132124	1978	445	e-124	75	25	hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22133	ENU05927	AN161C2187:	24-47	680-702	NAP		g2144167	351	70	7.00E-26	32	34	beta-glucosidase (EC 3.2.1.21) - yeast (Candida molischiana) [Pichia capsulata]
22134	ENU05928	AN161C7216:	22-48	793-815	NAP		g4033486	238	56	6.00E-20	33	51	putative tartarate transporter [Agrobacterium vitis]
22135	ENU05929	AN161C247:1	29-48	797-816	NAP		g3133104	154	61	0.000000	34	74	(AL023554) conserved hypothetical protein [Schizosaccharomyces pombe]
22136	ENU05930	AN161C8055:	22-47	765-784	NAP		g117298	1073	194	9.00E-49			cytochrome P450(BM-3) / NADPH-cytochrome P450 reductase [Bacillus megaterium]
22137	ENU05931	AN161C8057:	91-110	417-444	NAP		g586797	112	61	0.000000	26	28	hypothetical 59.1 KD protein ZK637.1 in chromosome III []
22138	ENU05932	AN161S1712:	22-41	395-420	NAP		g114971	415	173	5.00E-43	53	17	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]
22139	ENU05933	AN161C7085:	26-45	803-829	NAP		g1352079	1500	357	e-126	77	32	beta-glucosidase 1 precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Aspergillus aculeatus]
22140	ENU05934	AN161S2736:			NAP		g786117	236	48	0.0001	19	55	(L41834) nuclear protein [Ensis minor]
22141	ENU05935	AN161C323:3	22-49	808-829	NAP		g2956768	907	242	3.00E-63	47	67	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22142	ENU05936	AN161S1621:	67-85	320-344	NAP		g3925755	110	62	0.000000	30	21	(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor
22143	ENU05937	AN161C978:8	22-48	718-737	NAP		g2132846	275	113	2.00E-24	31	48	[Schizosaccharomyces pombe] probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22144	ENU05938	AN161C1138	26-48	442-461	NAP		g731462	179	94	9.00E-19	40	22	hypothetical 74.0 KD protein in CA11-HOM3 intergenic region [Saccharomyces cerevisiae]

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22145	ENU05939	ANI61C1146	22-45	714-732	NAP		g3810838	429	88	7.00E-17	37	38	"(AL032684) putative DNA polymerase epsilon, subunit b [Schizosaccharomyces pombe]"
22146	ENU05940	ANI61C1098	26-45	721-743	NAP		g3451448	195	80	3.00E-14	35	80	(AL031350) putative dehydrogenase [Streptomyces coelicolor]
22147	ENU05941	ANI61C1053	22-43	710-734	NAP		g3914984	1047	72	4.00E-12	22	7	Ferriochrome siderophore peptide synthetase [Ustilago maydis]
22148	ENU05942	ANI61C9561: 1:3372..1	32-51	758-785	NAP		g2342601	674	128	6.00E-43	39	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22149	ENU05943	ANI61C2459: 288..1649	22-49	788-812	NAP		g101795	1373	406	e-112	98	51	nitrate transport protein crmA - Emericella nidulans []
22150	ENU05944	ANI61C1143	24-46	735-756	NAP		g3869276	296	138	4.00E-32	33	97	(AF053764) NADP-dependent mannitol dehydrogenase [Agaricus bisporus]
22151	ENU05945	ANI61S973:1..511			NAP		g631954	402	145	2.00E-34	53	18	chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans [Emericella nidulans]
22152	ENU05946	ANI61C8446: 608..1	34-53	480-506	NAP		g3850084	308	105	2.00E-29	44	52	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
22153	ENU05947	ANI61C6254: 1232..2582	58-77	768-787	NAP		g2501339	541	161	2.00E-47	49	37	Copper amine oxidase 1 [Aspergillus niger]
22154	ENU05948	ANI61C3968: 789..1	22-42	712-739	NAP		g470731	1194	269	e-126	97	60	(L31778) alkaline protease [Aspergillus nidulans]
22155	ENU05949	ANI61S75:52	215-232	463-482	NAP		g3915105	430	189	9.00E-48	55	31	threonine dehydratase precursor (threonine deaminase) [Arxula adenivorans]
22156	ENU05950	ANI61C6610: 702..1	30-50	577-601	NAP		g2559008	345	131	1.00E-32	57	30	"(AF026291) chaparotin containing t-complex polypeptide 1, delta subunit; CCT-delta [Homo sapiens]"
22157	ENU05951	ANI61S3152: 590..107	122-146	437-463	NAP		g1546698	456	111	3.00E-24	93	34	(X98808) peroxidase ATP3a [Arabidopsis thaliana]
22158	ENU05952	ANI61C9158: 1..560	22-43	446-464	NAP		g1708464	689	171	2.00E-62	73	31	"putative dihydroxy-acid dehydratase precursor (DAD) (2,3-dihydroxy acid hydrolyase) [Schizosaccharomyces pombe]"
22159	ENU05953	ANI61C5582: 1..745	103-128	683-706	NAP		g1351078	107	76	3.00E-13	25	26	High-affinity glucose transporter SNF3 [Saccharomyces cerevisiae]
22160	ENU05954	ANI61S2588: 580..188	205-232	343-370	NAP		g128192	514	209	8.00E-54	82	15	Nitrate reductase (NADPH) (NR) [Emericella nidulans]

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22161	ENU05955	ANT61S4224: 997..549			NAP		g3329623	130	30	8.7	28	44	(AF078790) No definition line found [Caenorhabditis elegans]
22162	ENU05956	ANT61C6104: 1..1195	22-49	810-829	NAP		g2499716	755	217	8.00E-56	46	59	"exopolygalacturonase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
22163	ENU05957	ANT61C4643: 1007..1	72-89	777-796	NAP		g1346380	1126	383	e-105	81	30	Kinesin heavy chain []
22164	ENU05958	ANT61C9251: 2690..2369	23-45	408-434	NAP		g3130014	63	61	0.000000	29	40	(AL023517) putative lipoprotein [Streptomyces coelicolor]
22165	ENU05959	ANT61C1307: 317..1363	25-44	808-829	NAP		g114275	698	223	1.00E-57	46	80	L-Asparaginase precursor (L-asparagine amidohydrolase) [Erwinia chrysanthemi]
22166	ENU05960	ANT61S4270: 610..1			NAP		g3738194	192	59	0.000000	41	26	(AL031854) hypothetical protein [Schizosaccharomyces pombe]
22167	ENU05961	ANT61C1126: 71..477	24-43	394-421	NAP		g464369	108	64	5.00E-10	32	18	Phenol 2-monooxygenase (phenol hydroxylase) [Trichosporon cutaneum]
22168	ENU05962	ANT61C1110: 0:8975..10390	46-65	723-744	NAP		g3650376	720	216	1.00E-55	44	30	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
22169	ENU05963	ANT61C2411: 2469..1213	22-41	803-829	NAP		g3395556	724	146	1.00E-63	58	70	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
22170	ENU05964	ANT61C2118: 1698..2569	51-70	763-780	NAP		g2388904	528	173	8.00E-55	51	39	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
22171	ENU05965	ANT61C3180: 242..753	23-42	436-455	NAP		g3036901	89	55	0.000000	28	55	(AJ222715) DapA [Sinorhizobium meliloti]
22172	ENU05966	ANT61C1061: 5:1250..1	94-113	732-749	NAP		g461623	522	155	4.00E-37	38	25	beta-galactosidase precursor (lactase) [Aspergillus niger]
22173	ENU05967	ANT61C5650: 327..1072	56-78	702-725	NAP		g227874	482	98	1.00E-41	50	28	Extracellular beta glucosidase [Trichoderma reesei]
22174	ENU05968	ANT61C8513: 724..1	65-86	658-677	NAP		g1498245	324	151	6.00E-36	38	29	"(X99960) putative, YGL139w [Saccharomyces cerevisiae]"
22175	ENU05969	ANT61C3470: 262..1249	22-49	806-829	NAP		g217326	396	82	3.00E-32	40	42	(D13332) Ca2+/calmodulin-dependent protein kinase II [Drosophila sp.]
22176	ENU05970	ANT61C4698: 1522..1924	92-119	375-398	NAP		g3913326	173	88	3.00E-17	31	31	Cytochrome P450 52A9 (CYP11A9) (alkane-inducible P450-ALK5-A) [Candida maltosa]

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22177	ENU05971	ANI61C7088:	108-127	719-738	NAP		g2407970	666	209	2.00E-53	63	38	(Y14750) TOM70 [Podospora anserina]
22178	ENU05972	ANI61C8560:	60-87	519-546	NAP		g640053	144	50	2.00E-12	41	35	(U19714) 3-phosphoserine aminotransferase [Saccharomyces cerevisiae]
22179	ENU05973	ANI61C8579:	22-47	793-820	NAP		g4586928	449	155	5.00E-37	39	5	(AB017641) polyketide synthase [Micromonospora griseorubida]
22180	ENU05974	ANI61C1021	22-48	710-732	NAP		g3087842	624	152	8.00E-53	48	55	(Y08841) core protein II [Neurospora crassa]
22181	ENU05975	ANI61S557:1.	5:1152..1		NAP		g2213913	92	53	8.00E-10	21	9	(AF004884) neuronal calcium channel alpha 1A subunit isoform A-1 [Homo sapiens]
22182	ENU05976	ANI61C9522:	22-43	646-669	NAP		g4104764	293	119	2.00E-26	40	54	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
22183	ENU05977	ANI61S3702:	1062..1831		NAP		g125462	90	38	0.046			"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3)I) [Cloning vector pHIND2.2]"
22184	ENU05978	ANI61C7393:	22-41	568-595	NAP		g113701	332	128	5.00E-33	48	36	Acetamidase [Emericella nidulans]
22185	ENU05979	ANI61C4935:	40-59	499-521	NAP		g4803681	131	73	2.00E-12			(AL049819) putative AraC-family transcriptional regulator [Streptomyces coelicolor]
22186	ENU05980	ANI61C5316:	47-65	533-552	NAP		g4008543	98	61	0.000000	29	62	(AL034492) putative deacetylase [Streptomyces coelicolor]
22187	ENU05981	ANI61C1030	22-45	633-660	NAP		g1708808	550	213	2.00E-59	47	79	Lactoylglutathione lyase (methylglyoxalase) (aldoketomutase) (glyoxalase I) (GLX I) (ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Saccharomyces cerevisiae]
22188	ENU05982	ANI61C1103	102-127	453-479	NAP		g3860373	466	171	4.00E-42	57	47	(AJ012668) tomatinase [Fusarium oxysporum f. sp. lycopersici]
22189	ENU05983	ANI61C2278:	39-66	721-748	NAP		g2275095	185	109	2.00E-23	26	24	(X86179) phosphoprotein [Schizosaccharomyces pombe]
22190	ENU05984	ANI61S2170:	30-49	334-361	NAP		g3183329	297	126	6.00E-29	53	26	Hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]

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22191	ENU05985	ANI61C2482:	102-125	653-680	NAP		g3850151	437	115	4.00E-44	58	70	(AL033396) rehydrin-like protein [Candida albicans]
22192	ENU05986	ANI61C1048	43-70	807-829	NAP		g1805251	1078	131	4.00E-43	41	50	(U58946) transposase [Aspergillus awamori]
22193	ENU05987	ANI61C1147:	22-45	705-730	NAP		g1749410	711	183	5.00E-59	59	41	"(D89101) similar to Saccharomyces cerevisiae Asparagine synthetase(glutamine-hydrolyzing)2, SWISS-PROT Accession Number P49090 [Schizosaccharomyces pombe]"
22194	ENU05988	ANI61C2507:	144-171	796-818	NAP		g2896707	511	138	4.00E-51	52	90	(AL021897) echA8 [Mycobacterium tuberculosis]
22195	ENU05989	ANI61S3763:	33-52	385-410	NAP		g4263063	213	98	7.00E-20	34	28	(AC005142) hypothetical protein [Arabidopsis thaliana]
22196	ENU05990	ANI61S1588:			NAP		g2500356	357	157	6.00E-38	54	69	60S ribosomal protein L10 (QM protein homolog) (SPQM)
22197	ENU05991	ANI61C1133	105-125	379-398	NAP		g1749480	179	82	3.00E-15	43	26	[Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]"
22198	ENU05992	ANI61C4764:	22-46	723-744	NAP		g1711623	1646	372	e-102	67	29	"alanyl-tRNA synthetase, cytoplasmic (alanine-tRNA ligase) (ALARS) [Saccharomyces cerevisiae]"
22199	ENU05993	ANI61C8670:	35-54	793-815	NAP		g2956768	384	80	3.00E-14	27	61	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22200	ENU05994	ANI61C1074	53-78	261-288	NAP		g3850084	134	54	0.000000	36	30	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
22201	ENU05995	ANI61C487:6	114-136	474-493	NAP		g731294	247	79	3.00E-14	37	43	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region [Saccharomyces cerevisiae]
22202	ENU05996	ANI61C9976:	23-50	809-828	NAP		g3549899	332	78	6.00E-14			(Y15013) copalyl diphosphate synthase [Gibberella fujikuroi]
22203	ENU05997	ANI61C7223:	23-49	794-813	NAP		g1171890	885	261	3.00E-71			"pyruvate dehydrogenase E1 component, beta subunit precursor (PDHE1-B) [Schizosaccharomyces pombe]"

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22204	ENU05998	ANI61C553.2	27-46	342-361	NAP		g3378446	112	48	0.00005	30	63	(AF079317) 4-hydroxy-2-oxovalerate aldolase [Sphingomonas aromaticivorans]
22205	ENU05999	ANI61S2740.1..354			NAP		g4218005	122	39	0.014	31	16	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22206	ENU06000	ANI61C9901.3907..4488			NAP		g2131340	358	127	8.00E-29	47	61	hypothetical protein YDL119c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22207	ENU06001	ANI61C9014.275..627	105-128	453-474	NAP		g1077357	232	99	4.00E-23	42	31	probable membrane protein YLR359w - yeast (Saccharomyces cerevisiae)
22208	ENU06002	ANI61C3570.331..1656	71-90	802-829	NAP		g4894182	652	183	2.00E-45			[Saccharomyces cerevisiae] (AJ24251) 12-oxophytodiencate reductase [Lycopersicon esculentum]
22209	ENU06003	ANI61C7889.1..837	49-70	788-807	NAP		g730115	395	158	4.00E-38	38	35	Nitrate reductase [Synechococcus sp.]
22210	ENU06004	ANI61C9695.892..1	37-56	717-744	NAP		g4507007	267	128	6.00E-29	31	37	Calcium binding mitochondrial carrier superfamily member Aralar [Homo sapiens]
22211	ENU06005	ANI61C1230.4470..1314	22-45	805-829	NAP		g1166378	1020	101	5.00E-21			"(L76169) reverse transcriptase, RnaseH [Glomerella cingulata]"
22212	ENU06006	ANI61C2256.1842..633	22-43	777-796	NAP		g140965	346	173	1.00E-42	40	48	Probable serine/threonine-protein kinase YKL116C [Saccharomyces cerevisiae]
22213	ENU06007	ANI61S1491.1..981			NAP		g119714	466	36	0.38	41	43	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) [Nicotiana tabacum]
22214	ENU06008	ANI61C4969.1048..17	22-41	711-730	NAP		g119791	181	80	2.00E-14	35	63	3-oxoacyl- [Cuphea lanceolata]
22215	ENU06009	ANI61C1471.1005..1	38-61	712-738	NAP		g4176721	683	196	1.00E-49	52	46	(AF038568) negative regulator Moel [Schizosaccharomyces pombe]
22216	ENU06010	ANI61C9067.114..1174	22-46	804-824	NAP		g2290999	409	163	2.00E-43	42	85	(AF006000) unknown [Bordetella pertussis]
22217	ENU06011	ANI61C1087.5:1444..2508	25-52	798-819	NAP		g1465804	295	143	1.00E-33	32	77	(U64852) W01A11.2 gene product [Caenorhabditis elegans]
22218	ENU06012	ANI61C5251.672..1	23-45	625-651	NAP		g113626	612	185	9.00E-56			fructose-bisphosphate aldolase [Saccharomyces cerevisiae]
22219	ENU06013	ANI61C1972.1260..386	202-221	802-822	NAP		g416875	353	116	6.00E-30	35	41	Allantoin permease (allantoin transport protein) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22220	ENU06014	ANT6IC1013			NAP		g2500936	447	196	2.00E-49	40	36	High-affinity glucose transporter RGT2 [Saccharomyces cerevisiae]
22221	ENU06015	4:1072..1 ANT6IC4401: 38-57 2373..1660		672-693	NAP		g549689	352	129	9.00E-32	51	99	Hypothetical 19.7 KD protein in LHS1-NUP100 intergenic region [Saccharomyces cerevisiae]
22222	ENU06016	ANT6IC6292: 22-45 1017..226		745-765	NAP		g3015626	1262	227	e-119	98	68	(AF041976) nitrogen metabolite repression regulator NmrA [Emmericella nidulans]
22223	ENU06017	ANT6IC2265: 72-91 1012..1		623-645	NAP		g4758416	489	201	5.00E-51			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
22224	ENU06018	ANT6IC1241: 42-61 1..3733		764-783	NAP		g1078633	5787	123	2.00E-69	97	21	myosin I myoA - Emmericella nidulans [Emmericella nidulans]
22225	ENU06019	ANT6IC8228: 23-42 1182..1		716-734	NAP		g2293233	152	76	3.00E-13	26	49	(AF008220) YtcJ [Bacillus subtilis]
22226	ENU06020	ANT6IC9644: 40-59 2543..1		725-749	NAP		g1546072	1051	144	9.00E-34	38	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22227	ENU06021	ANT6IC1915: 22-47 2189..2885		642-667	NAP		g462683	320	137	7.00E-32			putative N-acetylglucosamine-6-phosphate deacetylase (GLCNAC 6-P deacetylase) [Caenorhabditis elegans]
22228	ENU06022	ANT6IS4147: 62-81 1..360		310-329	NAP		g2633827	408	165	1.00E-40	63	65	(Z99111) similar to formylmethionine deformylase [Bacillus subtilis]
22229	ENU06023	ANT6IS2660: 399..1			NAP		g4249564	206	61	0.000000	48	30	(AB003111) actin [Hunnicola grisea var. thermoideal]
22230	ENU06024	ANT6IC8071: 27-46 516..1		447-474	NAP		g3560266	248	63	6.00E-20	44	72	(AL031535) putative n-terminal acetyltransferase complex su bunit [Schizosaccharomyces pombe]
22231	ENU06025	ANT6IS4267: 399..892			NAP		g730888	138	50	0.00001	31	85	Octapeptide-repeat protein T2 [Mus musculus]
22232	ENU06026	ANT6IC1090: 197-223 1..464		417-443	NAP		g585965	230	104	5.00E-22	37	19	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]
22233	ENU06027	ANT6IC4878: 634..1			NAP		g3202046	117	80	2.00E-14	30	9	(AF069525) 190 kDa ankyrin isoform; AnkG190 [Rattus norvegicus]
22234	ENU06028	ANT6IC6400: 39-58 1..496		433-460	NAP		g3819717	165	52	1.00E-13	31	42	(AJ012408) citrate synthase [Anabaena PCC7120]
22235	ENU06029	ANT6IC532:6 105..6538			NAP		g3023956	178	80	5.00E-15	34	11	Vegetable incompatibility protein HET-E-1 [Podospora anserina]
22236	ENU06030	ANT6IC3032: 84-103 885..1		720-738	NAP		g1834342	800	292	2.00E-79	54	19	(Z68905) ATP-binding cassette multidrug transporter [Emmericella nidulans]

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22237	ENU06031	ANI61C1134	104-131	483-510	NAP		g1711561	177	67	5.00E-17	47	18	Sugar transporter STL1 [Saccharomyces cerevisiae]
22238	ENU06032	5:1958..1415 ANI61C4015:	24-51	341-365	NAP		g1255425	86	46	0.0001	21	42	(U53154) No definition line found [Caenorhabditis elegans]
22239	ENU06033	507..1 ANI61C8048:	43-62	804-829	NAP		g3184558	290	82	4.00E-15	31	77	(AF052290) unknown [Synecococcus PCC7002]
22240	ENU06034	2217..3278 ANI61S3246:			NAP		g4204304	259	129	2.00E-29	42	24	(AC003027) lc prt. seq No definition line found [Arabidopsis thaliana]
22241	ENU06035	169..616 ANI61C1043	22-45	774-801	NAP		g1743374	143	69	5.00E-19	28	36	(Y10034) 1-aminocyclopropane-1-carboxylic acid oxidase [Rumex palustris]
22242	ENU06036	4:2564...3682 ANI61C1041	22-41	808-827	NAP		g3738182	1083	287	5.00E-77	63	47	"(AL031854) probable t-complex protein 1, theta subunit [Schizosaccharomyces pombe]"
22243	ENU06037	1:6403..7672 ANI61S1333:			NAP		g3153821	140	45	0.0006	22	21	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22244	ENU06038	1..588 ANI61C6363:	24-43	809-828	NAP		g1890776	157	68	9.00E-11			(U88574) syringomycin biosynthesis enzyme [Pseudomonas syringae pv. syringae]
22245	ENU06039	3584..2480 ANI61C6186:	23-50	802-829	NAP		g418150	726	157	7.00E-38			GABA-specific permease (GABA-specific transport protein) [Saccharomyces cerevisiae]
22246	ENU06040	1283..1 ANI61C5013:	193-220	784-808	NAP		g731276	967	314	6.00E-91	71	65	hypothetical 40.7 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
22247	ENU06041	1202..1 ANI61C5574:	53-72	371-394	NAP		g115943	334	103	4.00E-30	41	58	cytochrome C heme lyase (CCHL) (holocytochrome-C synthase) [Neurospora crassa]
22248	ENU06042	4289..4900 ANI61C9267:	56-82	455-474	NAP		g1890290	51	42	0.003	25	17	(U89999) Ski2 [Xenopus laevis]
22249	ENU06043	2297..2780 ANI61S2314:	65-84	392-411	NAP		g3891714	155	84	9.00E-16	32	38	Gal6 (Yeast Bleomycin Hydrolase) Mutant C73a []
22250	ENU06044	1..614 ANI61C7278:	29-48	444-463	NAP		g267125	511	154	1.00E-46	98	99	"Thioredoxin [Aspergillus nidulans, Peptide, 109 aa]"
22251	ENU06045	3793..4190 ANI61C3823:	22-41	650-675	NAP		g1171671	688	166	1.00E-71	74	100	hypothetical calcium-binding protein C18B11.04 in chromosome I [Schizosaccharomyces pombe]

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22252	ENU06046	ANI61C9568:	37-56	639-658	NAP		g399112	1005	242	4.00E-76	48	27	beta-galactosidase (lactase) [Kluveromyces lactis]
22253	ENU06047	ANI61C1019	1..1387		NAP		g1166378	376	72	4.00E-12	34	23	"(U76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
22254	ENU06048	ANI61C431:4	203-222	491-510	NAP		g2388991	206	69	2.00E-11	35	64	(Z98980) hypothetical protein [Schizosaccharomyces pombe]
22255	ENU06049	ANI61C4184:	22-45	723-741	NAP		g3850071	405	170	1.00E-41	37	54	(AL033385) cadmium resistance protein [Schizosaccharomyces pombe]
22256	ENU06050	ANI61C7503:	37-56	617-634	NAP		g1170811	2349	302	2.00E-81	53	25	putative mitochondrial ATP-dependent protease precursor
22257	ENU06051	ANI61C3397:	29-48	780-807	NAP		g4512354	202	71	1.00E-11			[Schizosaccharomyces pombe] (AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
22258	ENU06052	ANI61C3251:	39-58	804-824	NAP		g3738153	237	69	5.00E-23	39	25	(AL031852) putative cleavage and polyadenylation specificity factor [Schizosaccharomyces pombe]
22259	ENU06053	ANI61C9170:	22-47	806-829	NAP		g2225983	414	34	1			(Z97193) hypothetical protein Rv1877 [Mycobacterium tuberculosis]
22260	ENU06054	ANI61C2103:	111-130	456-480	NAP		g2370466	374	165	2.00E-40	46	3	(Z98951) hypothetical protein [Schizosaccharomyces pombe]
22261	ENU06055	ANI61C5199:	102-129	418-437	NAP		g2493134	299	50	4.00E-13	48	58	vacuolar ATP synthase subunit E (V-ATPase E subunit) (V-ATPase 26 KD subunit) [Neurospora crassa]
22262	ENU06056	ANI61C3111:	102-123	660-686	NAP		g1710848	428	138	3.00E-45	45	21	SIT4-associating protein SAP190 [Saccharomyces cerevisiae]
22263	ENU06057	ANI61C466:9	22-49	797-816	NAP		g4106672	57	37	0.16			(AL035064) hypothetical protein [Schizosaccharomyces pombe]
22264	ENU06058	ANI61C5033:	22-46	724-749	NAP		g3560147	522	117	1.00E-40	35	41	"(AL031534) ribosomal processing, ma binding, nucleolar protein [Schizosaccharomyces pombe]"
22265	ENU06059	ANI61S4450:	26-51	338-359	NAP		g1805251	275	79	2.00E-14	39	28	(U58946) transposase [Aspergillus awamori]
22266	ENU06060	ANI61C3498:	98-119	591-613	NAP		g3242651	554	187	2.00E-58	59	20	(AB015509) beta-mannosidase [Aspergillus aculeatus]
22267	ENU06061	ANI61C7525:	36-63	542-569	NAP		g2182006	76	56	0.000000	32	49	(Z96072) hypothetical protein Rv2715 [Mycobacterium tuberculosis]
22268	ENU06062	ANI61C6205:	66-85	794-813	NAP		g730569	888	238	4.00E-91	73	92	60S ribosomal protein YL6 (L5) (RP8) [Saccharomyces cerevisiae]

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22269	ENU06063	ANI61C9151: 27-48	27-48	703-727	NAP		g2497499	482	125	8.00E-54	52	100	Guanylate kinase (GMP kinase) [Mus musculus]
22270	ENU06064	2755..3502											
22271	ENU06065	ANI61C1564: 50-69	50-69	711-730	NAP		g1730729	441	79	4.00E-27	30	39	hypothetical 74.8 KD protein in ALG11-YTP3 intergenic region [Saccharomyces cerevisiae]
22272	ENU06066	1200..1											
22273	ENU06067	ANI61C7241: 27-46	27-46	722-748	NAP		g3006142	339	116	2.00E-25	36	43	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
22274	ENU06068	ANI61C498: 7 207-226	207-226	360-379	NAP		g1526987	117	66	3.00E-13	36	52	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]
22275	ENU06069	072..6630											
22276	ENU06070	ANI61C4158: 22-49	22-49	799-818	NAP		g1764018	622	108	2.00E-43	44	66	(Z83760) COS41.8 [Ciona intestinalis]
22277	ENU06071	2015..756											
22278	ENU06072	ANI61C7648: 22-48	22-48	373-398	NAP		g4886445	209	34	0.59			(AL050269) hypothetical protein [Homo sapiens]
22279	ENU06073	710..1253											
22280	ENU06074	ANI61C3744: 56-78	56-78	803-829	NAP		g118498	1074	252	3.00E-66	45	55	aldehyde dehydrogenase (ALDDH) [Emeticella nidulans]
22281	ENU06075	3348..4992											(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
22282	ENU06076	ANI61C4669: 111-130	111-130	736-758	NAP		g3114719	1141	336	1.00E-91	64	18	(U61842) cutinase negative acting protein [Fusarium solani f. sp. pisi]
22283	ENU06077	1..983											(Z82080) cDNA EST EMBL:D66071 comes from this gene; cDNA EST yk274a10.3 comes from this gene; cDNA EST yk289f12.3 comes from this gene; cDNA EST yk289f12.5 comes from this gene; cDNA EST yk274a10.5 comes from this gene; cDNA ES... []
22284	ENU06078	ANI61C867.1 40-60	40-60	808-829	NAP		g1438951	581	115	4.00E-25	46	51	hypothetical 23.1 KD protein in DMSC-PFLA intergenic region [Escherichia coli]
22285	ENU06079	6:537..1											(AL022244) hypothetical protein [Schizosaccharomyces pombe]
22286	ENU06080	ANI61C2627: 31-50	31-50	724-743	NAP		g2995341	190	66	4.00E-10	25	46	Clathrin heavy chain [Bos taurus]
22287	ENU06081	1104..1											
22288	ENU06082	ANI61C1049					g1705915	2051	309	2.00E-83	51	16	(AL023534) putative methionine aminopeptidase I [Schizosaccharomyces pombe]
22289	ENU06083	5:3803..6305											
22290	ENU06084	ANI61C1002: 23-42	23-42	604-631	NAP		g3130036	389	125	4.00E-28	50	49	
22291	ENU06085	732..1											

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22283	ENU06077	ANT61C3365:	23-49	721-740	NAP		g2290770	668	78	5.00E-37	45	21	(AF002163) delta-adapin [Homo sapiens]
22284	ENU06078	ANT61C3696:	113-132	561-581	NAP		g3874563	276	115	1.00E-32			(Z81042) similar to Yeast hypothetical protein YYY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... [] (X58824) cdc21 protein [Schizosaccharomyces pombe]
22285	ENU06079	ANT61C6044:	203-222	701-720	NAP		g4165293	583	245	2.00E-64	59	22	[Schizosaccharomyces pombe] putative ATP-dependent RNA helicase YDL031W [Saccharomyces cerevisiae]
22286	ENU06080	ANT61C3840:	102-119	599-618	NAP		g2500535	206	97	1.00E-19	37	20	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
22287	ENU06081	ANT61C1933:	64-84	472-499	NAP		g3850093	135	76	1.00E-13	28	33	(AF032988) spindle assembly checkpoint protein SLDB [Emmericella nidulans]
22288	ENU06082	ANT61C6667:			NAP		g3136096	1016	406	e-112	83	69	(AF043332) plasma membrane H(+)-ATPase [Emmericella nidulans] "(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]" (AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe]
22289	ENU06083	ANT61C130:1	197-215	624-648	NAP		g4206286	702	239	2.00E-62	63	24	(AL023780) ABC transporter [Schizosaccharomyces pombe]
22290	ENU06084	ANT61C1055	22-46	773-792	NAP		g1805261	8541	284	e-121	95	14	(AF112473) PyrABCN [Emmericella nidulans]
22291	ENU06085	ANT61C3890:	32-52	623-646	NAP		g4056558	104	85	8.00E-16	30	28	ubiquinone biosynthesis monooxygenase COQ6 [Saccharomyces cerevisiae]
22292	ENU06086	ANT61C6567:	51-78	603-630	NAP		g3184109	673	259	2.00E-71	81	28	(AF094507) B-type cyclin [Candida albicans]
22293	ENU06087	ANT61C6142:	35-54	790-809	NAP		g4185560	2042	460	e-147	99	12	(X99021) putative helicase [Schizosaccharomyces pombe]
22294	ENU06088	ANT61C4368:	119-138	802-827	NAP		g1723766	415	158	5.00E-38	40	57	
22295	ENU06089	ANT61C1060	22-46	718-738	NAP		g3929290	727	190	1.00E-69	54	51	
22296	ENU06090	ANT61C8408:	57-76	711-730	NAP		g1597721	1958	110	1.00E-23	36	18	

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22297	ENU06091	ANI61C1987:	30-57	477-504	NAP		g1813523	124	45	0.0005	28	28	(U67763) PbTRAP [Plasmodium berghei]
22298	ENU06092	ANI61C9063:	22-42	800-827	NAP		g2266911	600	156	3.00E-46	39	78	(AE001274) L4171.5 [Leishmania major]
22299	ENU06093	ANI61C9187:	29-50	522-544	NAP		g1346405	303	88	4.00E-30	39	28	Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase) (laccase I) [Emericella nidulans]
22300	ENU06094	ANI61C1765:	22-45	779-801	NAP		g543923	692	203	9.00E-61			Calnexin homolog precursor [Schizosaccharomyces pombe]
22301	ENU06095	ANI61C6158:	22-42	803-826	NAP		g2330690	184	69	3.00E-11	31	18	(Z98529) putative cytoskeleton assembly control protein
22302	ENU06096	ANI61C8249:	22-49	621-646	NAP		g193271	752	213	2.00E-65	61	62	[Schizosaccharomyces pombe] (M59288) ferrochelatase [Mus musculus]
22303	ENU06097	ANI61C9171:	58-76	797-816	NAP		g1706692	1173	189	3.00E-58	50	50	C-24(28) sterol reductase [Saccharomyces cerevisiae]
22304	ENU06098	ANI61C8836:	24-45	784-803	NAP		g3929395	1129	195	1.00E-85	61	31	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit) [Neurospora crassa]
22305	ENU06099	ANI61C3681:			NAP		g2492863	2264	409	e-124	98	58	Ornithine aminotransferase (ornithine--oxo-acid aminotransferase) [Emericella nidulans]
22306	ENU06100	ANI61C9107:	39-58	777-796	NAP		g1027486	805	73	3.00E-25	36	43	(D49538) dihydrogeodin oxidase [Aspergillus terreus]
22307	ENU06101	ANI61C5317:	114-133	281-300	NAP		g461830	176	86	1.00E-16	39	29	carboxypeptidase S1 [Penicillium janthinellum]
22308	ENU06102	ANI61C7469:	115-142	725-744	NAP		g461830	436	113	2.00E-24	35	52	carboxypeptidase S1 [Penicillium janthinellum]
22309	ENU06103	ANI61C8631:	22-49	799-826	NAP		g4468731	698	146	9.00E-44	46	50	(AL035592) hypothetical protein [Schizosaccharomyces pombe]
22310	ENU06104	ANI61C8596:	22-41	773-793	NAP		g1169885	1408	289	2.00E-77	51	26	putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein) [Schizosaccharomyces pombe]
22311	ENU06105	ANI61C2944:	212-231	500-524	NAP		g2494820	321	111	1.00E-25	52	28	Rhamnogalacturonase B precursor (rhamnogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]

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22312	ENU06106	ANI61C6952:	99-118	652-673	NAP		g3549877	116	67	1.00E-10	32	37	(Y15902) nitrogen metabolite repression-(nmr)-responsible protein [Gibberella fujikuroi]
22313	ENU06107	ANI61C8294:	22-46	611-630	NAP		g131618	1083	259	1.00E-86			phosphoribosylamine--glycine ligase (GARS) (glycinamide RIBOnucleotide synthetase) (phosphoribosylglycinamide synthetase) / phosphoribosylformylglycinamide cyclo-ligase (AIRS) (phosphoribosyl-aminimidazole synthetase) ... [Schizosaccharomyces pombe]
22314	ENU06108	ANI61C8529:	26-45	517-536	NAP		g3022956	369	166	8.00E-41	45	13	Vegetable incompatibility protein HET-E-1 [Podospira anserina]
22315	ENU06109	ANI61C3904:	35-54	714-735	NAP		g1352399	370	146	2.00E-34			"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase) [Cochliobolus carbonum]" (Z99759) ma binding protein [Schizosaccharomyces pombe]
22316	ENU06110	ANI61C6018	40-59	586-605	NAP		g2467274	466	127	6.00E-36	66	100	[Schizosaccharomyces pombe] (Z68905) ATP-binding cassette multidrug transporter [Emeticella nidulans]
22317	ENU06111	ANI61C1057	24-45	774-797	NAP		g1834342	1828	232	3.00E-60	70	15	(AL035548) meul4. ring zinc finger [Schizosaccharomyces pombe] (D88802) ydhJ [Bacillus subtilis]
22318	ENU06112	ANI61C4884:	64-91	451-478	NAP		g4456818	183	112	1.00E-24	27	47	"tyrosyl-TRNA synthetase, cytoplasmic (tyrosyl--TRNA ligase) (TYRRS) [Saccharomyces cerevisiae]"
22319	ENU06113	ANI61C4660:	52-78	444-464	NAP		g1945094	317	126	1.00E-28	42	51	hypothetical 41.8 KD protein (ORFM) [Schizosaccharomyces pombe]
22320	ENU06114	ANI61C3441	22-49	786-805	NAP		g549037	845	103	4.00E-42	44	63	hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae]
22321	ENU06115	ANI61C7626:	22-48	595-617	NAP		g2828499	226	117	8.00E-26	28	64	[Emeticella nidulans]
22322	ENU06116	ANI61C2105:	22-41	656-675	NAP		g731857	267	118	4.00E-26	37	26	(AF098669) pantothenate kinase [Emeticella nidulans]
22323	ENU06117	ANI61C3464	106-123	623-642	NAP		g4191500	1045	199	2.00E-50	97	49	(Z99759) hypothetical protein [Schizosaccharomyces pombe]
22324	ENU06118	ANI61S4392:			NAP		g2467272	701	275	3.00E-73	61	31	[Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22325	ENU06119	ANI61C1002	102-121	499-526	NAP		g585377	550	220	2.00E-57	51	39	probable mannosyltransferase KTR4 [Saccharomyces cerevisiae]
22326	ENU06120	ANI61C9979:	82-101	394-418	NAP		g280164	63	62	0.000000	22	43	probable dehydrogenase (EC 1.-.-.-) - Vibrio cholerae [Vibrio cholerae]
22327	ENU06121	ANI61C1079	22-46	766-789	NAP		g135100	1254	276	8.00E-84			"aspartyl-TRNA synthetase, cytoplasmic (aspartate--TRNA ligase) (ASPRS) [Saccharomyces cerevisiae]"
22328	ENU06122	ANI61C9357:	30-57	810-829	NAP		g1176581	1120	300	7.00E-81	53	31	hypothetical 101.7 KD protein in EGT2-KRE1 intergenic region [Saccharomyces cerevisiae]
22329	ENU06123	ANI61S3452:	59-86	462-489	NAP		g807674	327	99	4.00E-24	45	21	(M23385) pol protein [Simian sarcoma virus]
22330	ENU06124	ANI61C1040	115-134	777-796	NAP		g3183028	370	159	2.00E-38	35	77	probable histidinol-phosphatase [Schizosaccharomyces pombe]
22331	ENU06125	ANI61C5831:	57-84	262-289	NAP		g3220154	235	107	3.00E-23	47	28	(AF022789) ubiquitin hydrolyzing enzyme I [Homo sapiens]
22332	ENU06126	ANI61C6438:	102-129	620-642	NAP		g1709240	518	175	4.00E-43	48	31	cell division control protein NDA4 []
22333	ENU06127	ANI61C8710:	57-77	802-829	NAP		g2132227	364	96	2.00E-31	42	76	hypothetical protein YPL196w - yeast (Saccharomyces cerevisiae)
22334	ENU06128	ANI61C3623:	211-238	448-467	NAP		g1169590	164	89	3.00E-17	37	43	Malonyl (COA-acyl) carrier protein transacylase (MCT) [Haemophilus influenzae Rd]
22335	ENU06129	ANI61C4966:	22-49	657-684	NAP		g83673	503	78	1.00E-34	37	45	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22336	ENU06130	ANI61C6896:	43-62	652-671	NAP		g2226418	178	75	5.00E-13	34	53	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
22337	ENU06131	ANI61C3102:	115-137	514-533	NAP		g4481949	581	226	1.00E-58	67	51	(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe]
22338	ENU06132	ANI61C7249:	22-42	810-829	NAP		g731481	500	114	1.00E-24	44	42	hypothetical 58.0 KD peptidase in PTP3-IL-V1 intergenic region [Saccharomyces cerevisiae]
22339	ENU06133	ANI61C651:1	23-43	730-755	NAP		g4507711	119	49	0.00003	36	62	tetratricopeptide repeat domain 1 [Homo sapiens]
22340	ENU06134	ANI61C9781:	95-116	403-422	NAP		g3702642	285	97	8.00E-20	52	36	(AL031825) ma binding protein - putative pre mma splicing factor [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22341	ENU06135	ANI61C1861:	22-43	802-829	NAP		g1762781	1324	129	3.00E-29	44	27	(U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana]
22342	ENU06136	ANI61S2460:			NAP		g913016	107	79	2.00E-14	27	12	(S76267) Sng2 homolog=bfr1 [Schizosaccharomyces pombe]
22343	ENU06137	ANI61C6319:	34-53	806-825	NAP		g4539662	252	74	8.00E-22	31	27	(AF061282) polypotein [Sorghum bicolor]
22344	ENU06138	ANI61C9871:	22-41	790-810	NAP		g141051	419	81	6.00E-32	43	53	hypothetical protein in MMSB 3'region (ORF1) [Pseudomonas aeruginosa]
22345	ENU06139	ANI61C591:	33-52	644-662	NAP		g497653	70	38	0.058	19	11	(U09782) myosin heavy chain [Argopecten irradians]
22346	ENU06140	ANI61C4843:	86-109	514-538	NAP		g1488255	96	75	3.00E-13	26	32	(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
22347	ENU06141	ANI61S2985:			NAP		g186396	135	38	0.058	33	15	(M94131) mucin [Homo sapiens]
22348	ENU06142	ANI61C8111:	42-61	631-648	NAP		g2494820	1626	125	1.00E-55	85	36	Rhannogalacturonase B precursor (rhannogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]
22349	ENU06143	ANI61C1024:	24-51	806-829	NAP		g1723685	925	180	4.00E-62	56	78	hypothetical 38.3 KD protein in RPL16B-PDC6 intergenic region [Saccharomyces cerevisiae]
22350	ENU06144	ANI61S3184:			NAP		g539218	149	41	0.003	25	26	hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
22351	ENU06145	ANI61C2805:	68-87	465-484	NAP		g2131533	167	83	5.00E-16	32	29	hypothetical protein YDR501w - yeast (Saccharomyces cerevisiae) []
22352	ENU06146	ANI61C8818:	69-88	440-459	NAP		g2492821	330	143	6.00E-34	48	100	[Saccharomyces cerevisiae] Augmenter of liver regeneration (HERV1 protein) [Homo sapiens]
22353	ENU06147	ANI61C2583:	118-137	645-663	NAP		g4033486	270	122	2.00E-27	30	58	putative tartarate transporter [Agrobacterium vitis]
22354	ENU06148	ANI61C1112:	69-88	765-784	NAP		g2492491	971	167	5.00E-84	86	87	14-3-3 protein homolog (TH1433) [Trichoderma harzianum]
22355	ENU06149	ANI61C4678:	67-86	576-596	NAP		g2511761	938	215	4.00E-97	97	23	(AF023156) carnitine acetyl transferase FacC [Emmericella nidulans]
22356	ENU06150	ANI61C3182:	27-54	805-829	NAP		g549722	199	51	1.00E-20			DNA-directed RNA polymerase III 25 KD polypeptide (C25) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22357	ENU06151	ANT61C7398: 108..485	78-97	445-464	NAP		g3417421	266	126	8.00E-29	52	40	(AL031261) forkhead nuclear signalling domain protein
22358	ENU06152	ANT61C476:4 55..1	92-119	330-354	NAP		g4377374	113	43	0.000000	26	35	[Schizosaccharomyces pombe] (AE001684) Adenosylmethionine-8-Amino-7-Oxononanoate
22359	ENU06153	ANT61C4149: 592..1281	25-44	581-601	NAP		g2497670	43	49	0.00003	39	15	Aminotransferase [Chlamydia pneumoniae]
22360	ENU06154	ANT61C9601: 6926..7975	30-54	620-644	NAP		g2494036	218	60	7.00E-13			Homeobox protein LIM-1 [Danio rerio]
22361	ENU06155	ANT61C8113: 1170..2314	25-47	657-684	NAP		g729467	564	206	1.00E-52	42	48	D-amino acid oxidase (DAMOX) (DAO) (DAAO) [Trigonopsis variabilis]
22362	ENU06156	ANT61C4412: 5991..4552	59-86	807-829	NAP		g529564	532	115	4.00E-32	36	65	purine-cytosine permease (PCP) (cytosine/purine transport protein) [Saccharomyces cerevisiae]
22363	ENU06157	ANT61C3596: 572..1	102-124	490-515	NAP		g1703372	126	83	1.00E-15	27	35	"(L35343) 2,3-butanediol dehydrogenase [Pseudomonas putida]" Probable sterol O-acyltransferase (sterol-ester synthase)
22364	ENU06158	ANT61C1165: 1873..10	22-49	786-811	NAP		g1346405	736	181	5.00E-45	34	46	[Schizosaccharomyces pombe] Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase) (laccase I) [Emeticella nidulans]
22365	ENU06159	ANT61C508:2 561..3516	22-47	806-829	NAP		g2497175	396	92	4.00E-32	39	92	hypothetical 31.1 KD protein in SIP18-SPT21 intergenic region [Saccharomyces cerevisiae]
22366	ENU06160	ANT61C6718: 1..527	110-129	477-496	NAP		g1020413	84	55	0.000000	30	22	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
22367	ENU06161	ANT61C1080 2:818..1	24-43	684-703	NAP		g1723910	818	321	4.00E-87	66	33	Pre-mRNA splicing factor RNA helicase PRP43 (helicase JA1) [Saccharomyces cerevisiae]
22368	ENU06162	ANT61C9004: 1..550	95-114	423-442	NAP		g18343322	347	92	1.00E-29	45	52	(D50661) RNA polymerase II subunit 3 [Schizosaccharomyces pombe]
22369	ENU06163	ANT61C4804: 1622..1	22-49	725-749	NAP		g4102636	2457	555	e-159	99	43	(AF014812) G1/S regulator [Emeticella nidulans]
22370	ENU06164	ANT61C9461: 1625..2292	38-57	576-603	NAP		g586919	198	80	1.00E-14	37	71	YSA1 protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22371	ENU06165	ANT61C5506:	27-46	791-816	NAP		g1723769	261	134	6.00E-31	28	51	putative transporter YGR260W [Saccharomyces cerevisiae]
22372	ENU06166	ANT61C8552:	23-46	803-829	NAP		g2132019	392	70	2.00E-11			hypothetical protein YOL141w - yeast [Saccharomyces cerevisiae]
22373	ENU06167	ANT61C5975:	67-90	554-572	NAP		g3649751	421	174	5.00E-43	44	54	[Saccharomyces cerevisiae] (Z15137) esterase A [Streptomyces chrysomallus]
22374	ENU06168	ANT61C103:1	70-89	562-582	NAP		g2414601	250	63	3.00E-21	51	20	(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
22375	ENU06169	ANT61C5302:	46-66	802-829	NAP		g465480	283	145	3.00E-34			Dolichyl-diphosphooligosaccharide--protein glycosyltransferase beta subunit precursor [Oligosaccharyl transferase beta subunit] [Saccharomyces cerevisiae]
22376	ENU06170	ANT61C1132:	25-44	776-796	NAP		g3136056	1918	85	8.00E-16	32	22	(AL023592) RanBP7/importin-beta/Cse1p superfamily protein [Schizosaccharomyces pombe]
22377	ENU06171	ANT61C3382:	22-44	711-733	NAP		g4584836	913	273	3.00E-99	67	37	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
22378	ENU06172	ANT61C2441:	39-58	595-614	NAP		g1723485	403	182	2.00E-45	44	54	hypothetical 47.3 KD protein C17G8.13C in chromosome I [Schizosaccharomyces pombe]
22379	ENU06173	ANT61C9052:	122-142	344-363	NAP		g3581896	89	40	0.000007	34	18	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
22380	ENU06174	ANT61C3578:	109-128	300-319	NAP		g3282044	367	159	6.00E-39	66	8	(Y13967) alpha-aminoacidipate reductase large subunit [Penicillium chrysogenum]
22381	ENU06175	ANT61C9636:	103-121	521-540	NAP		g454894	354	148	1.00E-43	45	47	(Z29988) Mnt1 protein [Saccharomyces cerevisiae]
22382	ENU06176	ANT61C1147	60-79	805-827	NAP		g2414593	781	186	2.00E-46	42	52	(Z99258) molybdopterin biosynthesis [Schizosaccharomyces pombe]
22383	ENU06177	ANT61C1183:	36-55	449-476	NAP		g1723514	180	83	9.00E-16	31	100	hypothetical 16.7 KD protein C1F12.10C in chromosome I [Schizosaccharomyces pombe]
22384	ENU06178	ANT61C7662:	22-44	628-649	NAP		g1168807	485	207	5.00E-53	55	32	probable protein-tyrosine phosphatase CDC14 [Saccharomyces cerevisiae]
22385	ENU06179	ANT61C6688:	33-60	500-525	NAP		g476389	55	42	0.003	19	9	"myosin heavy chain-B, neuronal - chicken [Gallus gallus]"

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22386	ENU06180	ANI61C8735: 24-50	513-532	NAP		g2224699	197	102	2.00E-21	33	23		(AB002377) KIAA0379 [Homo sapiens]
22387	ENU06181	ANI61C9465: 47-66	776-795	NAP		g3785995	2130	204	6.00E-52	53	18		(AC005499) unknown protein [Arabidopsis thaliana]
22388	ENU06182	ANI61C6501: 93-115	606-625	NAP		g3915154	142	63	1.00E-10	32	42		trichodiene oxygenase (cytochrome P450 58) [Fusarium sporotrichoides]
22389	ENU06183	ANI61C8122: 1..553		NAP		g462024	312	91	4.00E-27	42	47		delta(24)-sterol C-methyltransferase [Saccharomyces cerevisiae]
22390	ENU06184	ANI61C6703: 206-229	539-561	NAP		g3695005	350	159	2.00E-38	54	47		(AF038586) pyruvate dehydrogenase kinase isoform 2, PDK2 [Zea mays]
22391	ENU06185	ANI61C4945: 50-73	396-420	NAP		g3282095	199	93	1.00E-18	37	48		(AJ007446) hypothetical protein [Thermotoga neapolitana]
22392	ENU06186	ANI61S920:1..784		NAP		g3005587	180	58	0.000000	21	31		(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
22393	ENU06187	ANI61C8511: 64-83	409-429	NAP		g1935000	587	190	5.00E-60	80	75		(Y12314) GTPase [Schizosaccharomyces pombe]
22394	ENU06188	ANI61C7695: 74-93	727-749	NAP		g2094861	234	118	5.00E-26	25	13		(Z95334) rT123.15 protein. [Schizosaccharomyces pombe]
22395	ENU06189	ANI61C7316: 22-47	732-759	NAP		g1666124	417	170	1.00E-41	32	100		(Z82098) hypothetical protein Rv3536c [Mycobacterium tuberculosis]
22396	ENU06190	ANI61C2480: 46-65	781-800	NAP		g1098357	1116	161	4.00E-75	66	43		shk1 gene [Schizosaccharomyces pombe]
22397	ENU06191	ANI61C1054 36-54	804-829	NAP		g1764155	1012	236	1.00E-61	46	46		(U16782) chlorophenol monooxygenase [Ralstonia eutropha]
22398	ENU06192	ANI61S1352: 1..677		NAP		g3153821	118	47	0.0001	24	21		(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22399	ENU06193	ANI61C5463: 102-126	539-560	NAP		g4107315	225	116	1.00E-25	42	20		(AL035075) conserved hypothetical protein [Schizosaccharomyces pombe]
22400	ENU06194	ANI61C1114 2:1..1798		NAP		g1834340	1288	93	2.00E-42	59	15		(Z68904) ATP-binding cassette multidrug transporter [Emmericella nidulans]
22401	ENU06195	ANI61C5207: 37-56	799-818	NAP		g1730102	781	294	6.00E-79	53	84		D-lactate dehydrogenase (D-LDH) [Escherichia coli]
22402	ENU06196	ANI61C7617: 23-44	714-735	NAP		g423973	536	227	7.00E-59	52	36		phenol 2-monooxygenase (EC 1.14.13.7) - jelly fungus (Trichosporon beigii) []

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22403	ENU06197	ANI61C3223:	102-125	514-536	NAP		g2554598	85	62	0.000000	29	31	(AB000508) poly(3-hydroxybutyrate) depolymerase precursor [Comamonas testosteroni]
22404	ENU06198	ANI61C6564:			NAP		g1351598	408	157	1.00E-37	40	44	hypothetical 59.6 KD protein C4G8.07C in chromosome I [Schizosaccharomyces pombe]
22405	ENU06199	ANI61S826:1.766			NAP		g134769	518	173	1.00E-46	50	59	Stage IV sporulation protein B [Bacillus subtilis]
22406	ENU06200	ANI61C7078:			NAP		g2245428	598	173	5.00E-43	94	15	(U91968) topoisomerase I [Emericella nidulans]
22407	ENU06201	ANI61C8669:			NAP		g4007795	354	90	3.00E-23			(AL034463) putative nuclear envelope pore membrane protein [Schizosaccharomyces pombe]
22408	ENU06202	ANI61C2274:	100-127	300-327	NAP		g115943	281	128	2.00E-29	51	32	cytochrome C heme lyase (CCHL) (holocytochrome-C synthase) [Neurospora crassa]
22409	ENU06203	ANI61S42:41	48-69	277-303	NAP		g466053	164	95	3.00E-19	38	23	hypothetical 68.7 KD protein ZK757.1 in chromosome III [Caenorhabditis elegans]
22410	ENU06204	ANI61C1077	49-76	807-826	NAP		g1352619	879	146	5.00E-50	73	40	Dihydrodiploamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex precursor (E2) [Saccharomyces cerevisiae]
22411	ENU06205	ANI61C3628:	72-91	661-680	NAP		g231717	1359	259	1.00E-86	75	36	Minichromosome maintenance protein 5 (cell division control protein 46) [Saccharomyces cerevisiae]
22412	ENU06206	ANI61C2430:	102-127	430-457	NAP		g3261632	375	152	1.00E-36	45	30	(Z79700) accD2 [Mycobacterium tuberculosis]
22413	ENU06207	ANI61C5576:	49-73	809-829	NAP		g3560142	633	109	2.00E-35	34	45	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
22414	ENU06208	ANI61C8479:			NAP		g347455	187	45	0.0003	39	93	(L22030) hydroxyproline-rich glycoprotein [Glycine max]
22415	ENU06209	ANI61C7459:	22-42	528-547	NAP		g4033735	286	156	1.00E-37	50	13	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]
22416	ENU06210	ANI61C1134	46-73	807-829	NAP		g1175452	332	107	1.00E-22	30	25	hypothetical 85.7 KD protein C13G6.03 in chromosome I [Schizosaccharomyces pombe]

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22417	ENU06211	ANI6IS1223:			NAP		g854065	401	49	0.00001	50	26	(X83413) U88 [Human herpesvirus 6]
22418	ENU06212	ANI6IS3220:	1..340		NAP		g1352438	195	91	5.00E-18	36	38	eukaryotic initiation factor 4A-like protein CIF5.10
22419	ENU06213	ANI6IC9889:	102-124	366-385	NAP		g112947	150	84	4.00E-16	38	28	[Schizosaccharomyces pombe] AAC-rich MRNA clone AAC3 protein [Dictyostelium discoideum]
22420	ENU06214	ANI6IC8653:	1..409		NAP		g4758510	735	195	4.00E-49			H beta 58 homolog [Homo sapiens]
22421	ENU06215	ANI6IC1095	22-48	509-536	NAP		g131782	524	132	1.00E-52	63	13	DNA repair protein RAD50 (153 KD protein) [Saccharomyces cerevisiae]
22422	ENU06216	ANI6IC8033:	22-47	806-829	NAP		g485111	405	159	8.00E-45	42	58	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
22423	ENU06217	ANI6IC9123:	46-65	773-800	NAP		g2493389	136	66	3.00E-10	23	55	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) [Emmericella nidulans]
22424	ENU06218	ANI6IC6123:	22-49	565-585	NAP		g91209	108	43	0.003	38	58	proline-rich protein MP2 - mouse (fragment) []
22425	ENU06219	ANI6IC6470:	22-46	801-828	NAP		g1791305	2018	420	e-143	98	65	(U83489) septin B [Emmericella nidulans]
22426	ENU06220	ANI6IS4337:	36-56	433-452	NAP		g3873862	182	89	2.00E-17	35	30	(Z35595) similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes from this gene; cDNA EST yk455e10.5 comes from this gene; cDNA EST yk286h10.3 comes from this gene; cDNA EST yk286h10.5 comes from this gene [Caenorhabditis ... []
22427	ENU06221	ANI6IS3166:	52-77	481-499	NAP		g3819099	300	127	6.00E-29	51	20	(AJ009825) copper amine oxidase [Cicer arietinum]
22428	ENU06222	ANI6IC1129	37-56	728-749	NAP		g2499576	1347	176	3.00E-89	85	21	protein kinase C-like [Aspergillus niger]
22429	ENU06223	ANI6IC293:1	3..1130..1		NAP		g1353167	126	61	0.000000	31	37	hypothetical 30.6 KD protein F52C9.4 in chromosome III [Caenorhabditis elegans]

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22430	ENU06224	ANI61C1386: 526..1	42-61	445-464	NAP		g1077342	200	66	1.00E-14	37	54	probable membrane protein YLR284c - yeast (Saccharomyces cerevisiae)
22431	ENU06225	ANI61C1975: 2764..1	23-42	661-685	NAP		g2342601	1548	166	2.00E-40	36	5	[Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]
22432	ENU06226	ANI61C4494: 772..1419	54-73	524-546	NAP		g3184512	524	150	8.00E-53	73	77	(U79756) GTPase cRac1B [Gallus gallus]
22433	ENU06227	ANI61C3323: 5084..4724	62-89	313-340	NAP		g585175	314	138	2.00E-32	57	33	guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [Neurospora crassa]
22434	ENU06228	ANI61C5753: 1..504	202-228	457-482	NAP		g4226107	372	110	7.00E-32	50	27	(AF125451) contains similarity to the NIFR3/SMM1 family [Caenorhabditis elegans]
22435	ENU06229	ANI61S2462: 1..570	24-46	345-372	NAP		g4104056	359	140	6.00E-33	40	38	(AF031194) S276 [Triticum aestivum]
22436	ENU06230	ANI61C2477: 1677..3344	22-44	799-826	NAP		g120965	2511	473	e-135	99	53	4-aminobutyrate aminotransferase (gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) [Emmericella nidulans]
22437	ENU06231	ANI61S1069: 331..740			NAP		g732387	196	77	3.00E-16			hypothetical LACA/RPIB family protein in SPOIIR-GLYC intergenic region [Bacillus subtilis]
22438	ENU06232	ANI61S769:1..859			NAP		g4584539	612			49	36	(AL049608) extensin-like protein [Arabidopsis thaliana]
22439	ENU06233	ANI61C6152: 1..682	51-69	601-620	NAP		g2493725	869	211	1.00E-84	96	39	"Citrate synthase, mitochondrial precursor [Emmericella nidulans]"
22440	ENU06234	ANI61C6829: 1799..286	22-43	801-828	NAP		g1730706	583	99	5.00E-20	29	55	hypothetical 49.9 KD protein in SPOI-SIS1 intergenic region [Saccharomyces cerevisiae]
22441	ENU06235	ANI61C4535: 2861..1	22-47	782-800	NAP		g1166378	958	114	7.00E-25	32	23	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
22442	ENU06236	ANI61C2280: 1536..1	24-51	768-795	NAP		g4490654	1064	162	2.00E-72	48	44	"(Z98762) SPAC4A8.16c, putative nuclear transport protein, len:639aa, similar eg. to YMR309C, NIP1_YEAST, P32497, nuclear transport protein nipl, (812aa), fasta scores, op t:926, E0:0, (34.3% identity in 581 aa overlap), ide... []"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22443	ENU06237	ANI61C1032	34-53	561-587	NAP		g1723482	236	125	3.00E-28	37	67	DMA1 protein [Schizosaccharomyces pombe]
22444	ENU06238	ANI61C1064	188-207	624-650	NAP		g1077386	337	82	8.00E-30	40	40	hypothetical protein YLR345w - yeast [Saccharomyces cerevisiae]
22445	ENU06239	ANI61C5085	23-42	716-742	NAP		g730753	1745	249	1.00E-65			[Saccharomyces cerevisiae] chromosome segregation protein SMC2 (DA-BOX protein SMC2) [Saccharomyces cerevisiae]
22446	ENU06240	ANI61C1135	22-48	776-801	NAP		g731834	596	159	2.00E-38	43	60	hypothetical 41.9 KD protein in SDS3-THS1 intergenic region [Saccharomyces cerevisiae]
22447	ENU06241	ANI61C3285	117-136	446-465	NAP		g2623295	174	82	2.00E-16	39	42	[Saccharomyces cerevisiae] (AC002409) hypothetical protein [Arabidopsis thaliana]
22448	ENU06242	ANI61S1082			NAP		g1169440	904	309	7.00E-87	81	5	"dynein heavy chain, cytosolic (DYHC) [Emeticella nidulans]"
22449	ENU06243	ANI61C9181	27-54	728-747	NAP		g2132141	286	80	4.00E-28	43	99	hypothetical protein YOR367w - yeast [Saccharomyces cerevisiae]
22450	ENU06244	ANI61C6586	24-45	723-746	NAP		g2499125	810	150	1.00E-35	28	9	[Saccharomyces cerevisiae] vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22451	ENU06245	ANI61C1112	32-51	458-481	NAP		g2879853	248	78	1.00E-20	45	36	(AL021815) arginase family protein [Schizosaccharomyces pombe]
22452	ENU06246	ANI61C2339	64-83	301-328	NAP		g1351629	109	90	1.00E-17			hypothetical 18.5 KD protein C12G12.05C in chromosome I [Schizosaccharomyces pombe]
22453	ENU06247	ANI61C4662	109-128	251-278	NAP		g984373	313	134	2.00E-31	65	27	[Schizosaccharomyces pombe] (U32375) tartrate dehydrogenase [Agrobacterium vitis]
22454	ENU06248	ANI61S1794			NAP		g3810866	78	36	0.00006	42	39	(AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
22455	ENU06249	ANI61C9545	100-119	625-644	NAP		g4927212	125	37	0.15			[AF134304] Scar2 [Homo sapiens]
22456	ENU06250	ANI61C9449	25-42	803-823	NAP		g128853	1179	273	4.00E-87	70	62	NADH-ubiquinone oxidoreductase 40 KD subunit precursor (complex I-40KD) (CI-40KD) [Neurospora crassa]
22457	ENU06251	ANI61C1021	22-44	740-767	NAP		g731434	253	126	2.00E-28	37	97	hypothetical 25.1 KD protein in PMID0-PAC2 intergenic region [Saccharomyces cerevisiae]

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22458	ENU06252	ANI61C8628:	102-124	610-637	NAP		g3256848	187	98	8.00E-20	41	78	(AP000002) 219aa long hypothetical protein [Pyrococcus horikoshii]
22459	ENU06253	ANI61C4897:	22-47	636-654	NAP		g1729996	127	62	8.00E-12	32	63	TOXD protein [Cochliobolus carbonum]
22460	ENU06254	ANI61C306:1	22-46	786-810	NAP		g2114323	287	35	0.73	26	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]
22461	ENU06255	ANI61C5208:	31-50	715-738	NAP		g2132688	1499	279	1.00E-74	47	5	probable membrane protein YLR106c - yeast (Saccharomyces cerevisiae)
22462	ENU06256	ANI61C1077	23-42	716-735	NAP		g1945493	1327	109	3.00E-36	44	25	[Saccharomyces cerevisiae] "(U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk35b9.3; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ... ["]
22463	ENU06257	ANI61C8566:	33-60	760-783	NAP		g3393020	965	348	5.00E-95	70	47	(AL031174) t-complex protein 1 gamma subunit homolog [Schizosaccharomyces pombe]
22464	ENU06258	ANI61C9752:	32-59	804-827	NAP		g1182038	583	153	2.00E-36	37	15	(Z69368) unknown [Schizosaccharomyces pombe]
22465	ENU06259	ANI61C7363:	22-46	710-737	NAP		g2501011	986	224	6.00E-58	43	27	Isoleucyl--TRNA synthetase (isoleucine--TRNA ligase) (ILERS) [Synecocystis sp.]
22466	ENU06260	ANI61C1027	22-44	608-630	NAP		g2131201	420	155	3.00E-37	42	55	"Ca2+/H+-exchanging protein, vacuolar - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]"
22467	ENU06261	ANI61S4372:			NAP		g581280	444	168	5.00E-42	82	85	(V00618) unidentified reading frame [Escherichia coli]
22468	ENU06262	ANI61C3636:	22-47	717-744	NAP		g4914370	131	66	1.00E-20			(AC007584) putative polypeptide [Arabidopsis thaliana]
22469	ENU06263	ANI61C5734:	51-78	696-716	NAP		g1870209	430	59	2.00E-18	34	50	(AC000133) ORF [Emeticella nidulans]
22470	ENU06264	ANI61C7800:	23-42	714-733	NAP		g2133034	228	95	3.00E-24	31	38	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]

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22471	ENU06265	ANI6IC2511:			NAP		g1351666	1401	129	6.00E-75	66	42	putative ATP-dependent RNA helicase C1F7.02C [Schizosaccharomyces pombe]
22472	ENU06266	ANI6IC6518:	22-49	756-782	NAP		g2440082	235	75	9.00E-23	33	31	(Y14849) putative glucose sensor [Kluveromyces fragilis]
22473	ENU06267	ANI6IC5564:	39-59	763-782	NAP		g1346390	334	149	2.00E-35	32	31	serine/threonine-protein kinase CLA4 [Saccharomyces cerevisiae]
22474	ENU06268	ANI6IC6853:	120-139	496-515	NAP		g1710791	354	118	2.00E-26	48	42	probable mitochondrial 40S ribosomal protein S5 [Schizosaccharomyces pombe]
22475	ENU06269	ANI6IC9440:	50-75	295-314	NAP		g416685	145	61	0.000000	36	36	ATP11 protein precursor [Saccharomyces cerevisiae]
22476	ENU06270	ANI6IC2599:	52-71	512-531	NAP		g3913432	740	214	5.00E-69	78	25	putative pre-mRNA splicing factor ATP-dependent RNA helicase SPBC16H5.10C [Schizosaccharomyces pombe]
22477	ENU06271	ANI6IC2216:	102-122	751-777	NAP		g1706440	247	71	1.00E-24	38	39	Spore wall maturation protein DTT1 [Saccharomyces cerevisiae]
22478	ENU06272	ANI6IC6865:	22-49	804-827	NAP		g3150262	468	150	2.00E-35	35	80	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
22479	ENU06273	ANI6IC1185:	22-47	805-824	NAP		g133356	3156	160	6.00E-75			DNA-directed RNA polymerase III largeST subunit (C160) [Saccharomyces cerevisiae]
22480	ENU06274	ANI6IC4836:	62-81	727-749	NAP		g279978	87	80	3.00E-14	24	46	benzoylformate decarboxylase (EC 4.1.1.7) - Pseudomonas putida []
22481	ENU06275	ANI6IC3148:	22-42	731-750	NAP		g416574	1638	550	e-156	94	75	probable formate dehydrogenase (NAD-dependent formate dehydrogenase) (FDH) [Emmericella nidulans]
22482	ENU06276	ANI6IC5449:	22-48	490-517	NAP		g1546072	131	66	2.00E-10	37	5	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22483	ENU06277	ANI6IC8576:	72-91	541-560	NAP		g1705652	369	99	2.00E-34	56	100	20 KD nuclear CAP binding protein (NCBP) (CBP20) [Xenopus laevis]
22484	ENU06278	ANI6IC1081:	22-46	763-782	NAP		g1546072	1253	117	8.00E-26	33	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22485	ENU06279	ANI6IC1043:	112-131	726-749	NAP		g1169440	9561	541	e-153	99	6	"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"

Database Information

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22486	ENU06280	ANI61C1146:	102-129	636-656	NAP		g1362615	405	204	6.00E-52	43	22	iswi protein - fruit fly (<i>Drosophila melanogaster</i>) [<i>Drosophila melanogaster</i>]
22487	ENU06281	ANI61C9941:	107-127	350-371	NAP		g106185	174	83	1.00E-15	42	53	GTP-binding protein Rab2 - human [<i>Homo sapiens</i>]
22488	ENU06282	ANI61C1081:	30-48	606-625	NAP		g1934645	174	92	3.00E-18	37	97	(U93876) hypothetical protein YrdC [<i>Bacillus subtilis</i>]
22489	ENU06283	ANI61C6360:	115-136	809-828	NAP		g1790870	380	87	2.00E-29	42	97	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [<i>Comamonas testosteroni</i>]
22490	ENU06284	ANI61C711:	56-78	373-394	NAP		g2493915	184	90	9.00E-18	41	60	cutinase precursor [<i>Botryotinia fuckeliana</i>]
22491	ENU06285	ANI61S3073:			NAP		g2950476	134	46	0.00009	38	51	(AL022070) vesicle transport v-snare protein [<i>Schizosaccharomyces pombe</i>]
22492	ENU06286	ANI61C2684:	114-133	467-487	NAP		g4506123	243	65	4.00E-21	39	44	pre-mRNA splicing factor similar to S. cerevisiae Prp18 [<i>Homo sapiens</i>]
22493	ENU06287	ANI61C4085:	22-49	809-828	NAP		g2649154	275	123	1.00E-27	31	98	(AE001006) membrane protein [<i>Archaeoglobus fulgidus</i>]
22494	ENU06288	ANI61C861:	22-41	711-730	NAP		g130155	853	162	4.00E-81	56	41	Deoxyribodipyrimidine photolyase (DNA photolyase) (photoreactivating enzyme) [<i>Neurospora crassa</i>]
22495	ENU06289	ANI61C2490:	27-53	807-829	NAP		g3322837	324	51	3.00E-14	31	41	(AE001229) T. pallidum predicted coding region TP0544 [<i>Treponema pallidum</i>]
22496	ENU06290	ANI61C6643:	50-69	802-821	NAP		g2648180	292	98	6.00E-20	34	66	(AE000943) conserved hypothetical protein [<i>Archaeoglobus fulgidus</i>]
22497	ENU06291	ANI61C7691:	22-48	686-708	NAP		g136642	433	131	6.00E-30			Ubiquitin-conjugating enzyme E2-34 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (cell division control protein 34) [<i>Saccharomyces cerevisiae</i>]
22498	ENU06292	ANI61C6883:	92-111	262-281	NAP		g984373	391	141	2.00E-33	72	31	(U32375) tartrate dehydrogenase [<i>Agrobacterium vitis</i>]
22499	ENU06293	ANI61C4294:	33-52	747-766	NAP		g228477	191			35	50	ECLF2 upstream ORF [saimirine herpesvirus 1]
22500	ENU06294	ANI61C7396:			NAP		g2117306	452	74	1.00E-14	35	39	(Z95620) dna-(apurinic or apyrimidinic site) lyase [<i>Schizosaccharomyces pombe</i>]

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22501	ENU06295	ANI61C9984: 1..520	126-145	308-330	NAP		g683698	138	74	3.00E-15	29	40	(Z48229) orf1 [Saccharomyces cerevisiae]
22502	ENU06296	ANI61C316:5 439..3993	46-65	804-829	NAP		g4499843	327	44	0.001			(AJ011965) oxidoreductase [Claviceps purpurea]
22503	ENU06297	ANI61C5121: 1..523	23-50	453-473	NAP		g3891484	142	37	0.0002	35	34	"Chain B, Co-Crystal Structure Of Protein Farnesyltransferase Complexed With A Farnesyl Diphosphate Substrate ["]
22504	ENU06298	ANI61C8634: 6707..2925	22-45	796-816	NAP		g538067	2311	123	1.00E-27	33	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
22505	ENU06299	ANI61C3333: 1033..1	22-49	705-732	NAP		g3004863	538	113	3.00E-57	50	30	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
22506	ENU06300	ANI61C5808: 237..1337	22-46	725-747	NAP		g2209087	897	345	2.00E-94	62	41	(AF000309) putative serine/threonine kinase [Colletotrichum lindemuthianum]
22507	ENU06301	ANI61C343:6 77..1	49-76	558-584	NAP		g3914984	143	80	2.00E-14	31	5	Ferrichrome siderophore peptide synthetase [Ustilago maydis]
22508	ENU06302	ANI61C1742: 3814..3210	72-93	553-577	NAP		g1652017	201	95	3.00E-19	32	65	(D90901) hypothetical protein [Synechocystis sp.]
22509	ENU06303	ANI61C4320: 1455..2587	22-46	805-829	NAP		g1723435	1087	350	6.00E-96	55	18	hypothetical 170.7 KD protein C56F8.02 in chromosome I [Schizosaccharomyces pombe]
22510	ENU06304	ANI61C6618: 88..850	49-68	677-699	NAP		g3080522	309	153	1.00E-36	39	36	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
22511	ENU06305	ANI61C4435: 20..619	48-69	516-542	NAP		g3913154	319	145	3.00E-34	39	19	beta-galactosidase (lactase) [Enterobacter cloacae]
22512	ENU06306	ANI61C8171: 253..1609	23-46	804-828	NAP		g2506360	276	108	5.00E-23	33	34	NPL1 protein (SEC63 protein) [Saccharomyces cerevisiae]
22513	ENU06307	ANI61C1086 0:1..554	122-141	500-519	NAP		g729747	411	155	3.00E-37	48	45	Flavohemoprotein (haemoglobin-like protein) (flavohemoglobin) [Ralstonia eutropha]
22514	ENU06308	ANI61C2206: 1..744	222-242	699-719	NAP		g171565	221	113	1.00E-24	35	56	(KO1609) gal10 [Saccharomyces carlsbergensis]
22515	ENU06309	ANI61C1729: 1119..1	35-54	730-749	NAP		g1703456	496	128	6.00E-29	43	21	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]
22516	ENU06310	ANI61C9369: 2700..1288	22-43	802-820	NAP		g1351635	462	73	4.00E-23	40	70	hypothetical 35.8 KD protein C12G12.12 in chromosome I [Schizosaccharomyces pombe]

Sequence Submission

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22517	ENU06311	ANI61C8401: 355..1384	36-55	774-797	NAP		g585255	756	277	7.00E-74	56	49	Histidine biosynthesis bifunctional amidotransferase / cyclase
22518	ENU06312	ANI61S14:62			NAP		g3114719	542	183	8.00E-57	62	13	[Saccharomyces cerevisiae] (Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
22519	ENU06313	ANI61C6428: 122-141	691-714		NAP		g1345625	322	153	4.00E-46			Biotin--protein ligase (biotin apo-protein ligase) (biotin--[Saccharomyces cerevisiae])
22520	ENU06314	ANI61C8003: 1200..1			NAP		g140464	594	99	5.00E-20	38	22	hypothetical 107.9 KD protein in POL4-SRD1 intergenic region [Saccharomyces cerevisiae]
22521	ENU06315	ANI61C1:108			NAP		g1777375	198	92	1.00E-18	46	11	(D78573) aspartate kinase-homoserine dehydrogenase [Oryza sativa]
22522	ENU06316	ANI61C8875: 24-43	809-829		NAP		g2340046	813	334	4.00E-91	51	39	(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]
22523	ENU06317	ANI61C796:1 850..1	22-42	709-731	NAP		g406769	921	229	2.00E-59	47	31	(X70694) trehalose-6-phosphate phosphatase [Saccharomyces cerevisiae]
22524	ENU06318	ANI61C8121: 994..1	22-47	723-740	NAP		g3121873	483	192	3.00E-48	50	32	Coronin-like protein [Saccharomyces cerevisiae]
22525	ENU06319	ANI61S4368: 1..670			NAP		g3687478	213	104	6.00E-22	34	39	(AL031786) putative delta-1-pyrroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe]
22526	ENU06320	ANI61C7484: 3606..4566	22-42	809-829	NAP		g3879532	213	86	3.00E-16	35	81	(Z49130) cDNA EST EMBL:D74028 comes from this gene; cDNA EST EMBL:D71354 comes from this gene; cDNA EST EMBL:D76320 comes from this gene; cDNA EST yk486c7.3 comes from this gene; cDNA EST yk486c7.5 comes from this gene; cDNA ES... []
22527	ENU06321	ANI61C1043 1:2329..410	23-50	803-829	NAP		g3560207	234	58	0.000000			(AL031536) fnx1p. [Schizosaccharomyces pombe]
22528	ENU06322	ANI61C4967: 756..1	22-48	625-644	NAP		g1389841	559	186	1.00E-58	55	33	(U59303) glucosylase precursor [Aspergillus awamori]
22529	ENU06323	ANI61C1205: 513..1	109-128	391-417	NAP		g2956751	205	105	2.00E-22	31	45	(AL022105) hypothetical protein [Schizosaccharomyces pombe]

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22530	ENU06324	ANI61C9687: 856..1	69-91	787-808	NAP		g1169870	365	185	3.00E-46	45	56	GCD14 protein [Saccharomyces cerevisiae]
22531	ENU06325	ANI61C8614: 2243..1	23-48	728-748	NAP		g4557481	325	97	2.00E-23	34	14	Canalicular multispecific organic anion transporter [Homo sapiens] (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]
22532	ENU06326	ANI61C7926: 3645..5762	34-53	808-829	NAP		g932	188	42	0.006			Hypothetical 141.1 KD protein in MET2-SEC2 intergenic region [Saccharomyces cerevisiae]
22533	ENU06327	ANI61C1343: 1..958	22-48	755-782	NAP		g1730639	299	136	2.00E-31	31	21	3-phosphatase B precursor (myo-inositol-hexaphosphate 3-phosphohydrolyase B) (3 phytase B) (myo-inositol hexakisphosphate phosphohydrolyase B) [Emericella nidulans]
22534	ENU06328	ANI61C1109: 6:561..884	51-70	361-380	NAP		g3914342	175	93	1.00E-18	51	17	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (X94769) choline dehydrogenase [Rattus rattus]
22535	ENU06329	ANI61C8939: 1157..39	22-47	803-829	NAP		g2132443	340	64	0.000000	30	76	hypothetical 72.8 KD protein in AGAI-MTR intergenic region (O678) [Escherichia coli]
22536	ENU06330	ANI61C1065: 7:6536..6055	23-42	413-437	NAP		g1154950	153	96	2.00E-19	34	37	"Ankyrin, brain variant 2 (ankyrin B) (ankyrin, nonerythroid) ["] (AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]
22537	ENU06331	ANI61S3435: 1..574	38-65	496-518	NAP		g1176816	899	176	1.00E-81	95	28	(U13049) pectate lyase C [Fusarium solani f. sp. pisi]
22538	ENU06332	ANI61C5381: 833..1	33-60	709-728	NAP		g231551	262	83	2.00E-28	31	14	hypothetical 20.1 KD protein in RTF1-CSE1 intergenic region [Saccharomyces cerevisiae]
22539	ENU06333	ANI61C6837: 476..1	118-136	454-479	NAP		g4007790	151	73	2.00E-13	39	25	putative ATP-dependent RNA helicase C31A2.07C [Schizosaccharomyces pombe]
22540	ENU06334	ANI61C993:8			NAP		g595570	151	82	2.00E-15	41	54	beta-glucosidase precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucosylhydrolase) [Kluyveromyces marxianus]
22541	ENU06335	ANI61C4542: 1163..562	23-42	515-534	NAP		g1723978	212	64	1.00E-19			
22542	ENU06336	ANI61C8821: 1679..2718	45-64	747-766	NAP		g1175401	940	371	e-102	66	33	
22543	ENU06337	ANI61C7550: 1..352			NAP		g114971	185	85	2.00E-16	40	13	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22544	ENU06338	ANI61C1577: 1.638	102-126	583-602	NAP	g1169546	177	67	7.00E-13	35	82	82	putative ER lumen protein retaining receptor C28H8.4 [Caenorhabditis elegans]
22545	ENU06339	ANI61C7523: 3198..2768	65-84	378-397	NAP	g2136261	77	62	0.000000	25	31	31	tetracycline transporter-like protein - human [Homo sapiens]
22546	ENU06340	ANI61S4287: 259..582	22-48	446-467	NAP	g3941500	153	66	2.00E-10	36	57	57	(AF062904) putative transcription factor [Arabidopsis thaliana]
22547	ENU06341	ANI61C1023 5:2077..2560	22-45	375-399	NAP	g4539247	196	89	5.00E-19	48	64	64	(AL049489) putative actin polymerisation complex protein [Schizosaccharomyces pombe]
22548	ENU06342	ANI61C5375: 1536..1	115-134	716-742	NAP	g3929399	896	153	2.00E-36	37	51	51	proline-specific permease (proline transport protein) [Emmericella nidulans]
22549	ENU06343	ANI61C7079: 2167..620			NAP	g549674	832	101	7.00E-42	39	56	56	hypothetical 49.6 KD protein in ELM1-PR12 intergenic region [Saccharomyces cerevisiae]
22550	ENU06344	ANI61C8750: 1..2178	29-54	790-809	NAP	g3021303	3668	554	e-157	99	12	12	(Y15996) acetyl-CoA carboxylase [Emmericella nidulans]
22551	ENU06345	ANI61C1034 9:5166..8019	22-44	644-663	NAP	g1209391	2070	254	4.00E-67	46	31	31	(D83659) TPR protein [Schizosaccharomyces pombe]
22552	ENU06346	ANI61C6562: 1021..1			NAP	g3282044	1037	377	e-104	70	19	19	(Y13967) alpha-aminoacidpate reductase large subunit [Penicillium chrysogenum]
22553	ENU06347	ANI61C9317: 1151..2158	22-45	803-829	NAP	g4581525	302	117	8.00E-26	34	47	47	(AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
22554	ENU06348	ANI61C888:4 328..3784	111-130	412-431	NAP	g3914142	36	38	0.052	25	50	50	Early nodulin 20 precursor (N-20) [Medicago truncatula]
22555	ENU06349	ANI61C2891: 1..1004			NAP	g2501152	660	222	2.00E-57	53	47	47	threonine synthase [Schizosaccharomyces pombe]
22556	ENU06350	ANI61C5514: 435..1353	23-42	805-829	NAP	g2956768	664	217	1.00E-55	51	63	63	(AL022103) transmembrane transporter hzl1p. [Schizosaccharomyces pombe]
22557	ENU06351	ANI61S3594: 561..156			NAP	g2258414	119	52	0.000000	38	54	54	(AF007873) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe]
22558	ENU06352	ANI61C234:1 575..1	22-42	612-635	NAP	g1077357	1063	124	1.00E-41	61	39	39	probable membrane protein YLR359w - yeast [Saccharomyces cerevisiae]
													[Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer 712-731	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22559	ENU06353	ANI61C8537:	40-59		712-731	NAP		g409547	239	86	3.00E-20	29	47	(L07492) sugar transport protein [Saccharomyces cerevisiae]
22560	ENU06354	ANI61C5810:				NAP		g544232	610	127	9.00E-29	50	59	elongation factor 1-gamma 2 (EF-1-gamma 2) [Saccharomyces cerevisiae]
22561	ENU06355	ANI61C8235:	22-49		786-813	NAP		g731465	818	267	9.00E-83	57	87	putative mitochondrial carrier YER053C [Saccharomyces cerevisiae]
22562	ENU06356	ANI61S1427:				NAP		g110849	161	52	0.000005	31	83	proline-rich protein - mouse [Mus musculus]
22563	ENU06357	ANI61C2541:	22-47		741-763	NAP		g2330704	727	249	3.00E-65	49	81	(Z98529) putative transcription initiation factor TFIIB subunit [Schizosaccharomyces pombe]
22564	ENU06358	ANI61C5404:	24-43		630-650	NAP		g3287946	1040	326	9.00E-89	64	25	putative helicase C6F12.16 in chromosome I [Schizosaccharomyces pombe]
22565	ENU06359	ANI61C8694:	27-50		639-658	NAP		g3978466	1587	275	2.00E-73	50	37	(AF086822) dihydroxyacetone synthase [Candida boidinii]
22566	ENU06360	ANI61C9257:	22-46		795-815	NAP		g2414649	827	198	6.00E-50	38	9	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
22567	ENU06361	ANI61C1087	22-45		800-819	NAP		g140474	576	76	4.00E-13			hypothetical 69.2 KD protein in HSP30-PMP1 intergenic region [Schizosaccharomyces cerevisiae]
22568	ENU06362	ANI61C669:1				NAP		g1722769	225	99	1.00E-20	38	20	Phosphatidylinositol 3-kinase VPS34 (PI3-kinase) (PTDINS-3-kinase) (PI3K) (vacuolar sorting protein 34) [Schizosaccharomyces pombe]
22569	ENU06363	ANI61C1138	38-64		477-503	NAP		g4106669	323	120	2.00E-31	56	33	(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
22570	ENU06364	ANI61C5198:	24-43		805-825	NAP		g129592	425	188	4.00E-47	45	35	Phenylalanine ammonia-lyase [Rhodotorula mucilaginosa]
22571	ENU06365	ANI61C445:1	44-63		722-740	NAP		g1708850	684	134	1.00E-49	48	33	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae]
22572	ENU06366	ANI61C7858:	23-44		566-585	NAP		g987116	126	52	0.000003	28	99	(X86780) cystathione synthase [Streptomyces hygroscopicus]
22573	ENU06367	ANI61C82:17	44-63		802-829	NAP		g3702638	416	127	1.00E-28	40	61	(AL031825) putative acetylornithine deacetylase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22574	ENU06368	ANT61C1781: 1..537	37-64	400-425	NAP		g1077382	275	133	7.00E-31	41	19	probable membrane protein YLR335w - yeast (Saccharomyces cerevisiae)
22575	ENU06369	ANT61C8774: 290..2421	35-54	802-829	NAP		g3885836	517	45	0.000002			[Saccharomyces cerevisiae]
22576	ENU06370	ANT61C5355: 391..1	40-67	441-468	NAP		g2828151	162	88	5.00E-17	39	41	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22577	ENU06371	ANT61C1843: 115..525	22-49	458-479	NAP		g3122326	348	163	8.00E-40	50	33	(AF042386) cyclophilin-33B [Homo sapiens]
22578	ENU06372	ANT61C1097 7:4250..5969	27-54	781-806	NAP		g3242972	1836	395	e-109	70	39	LEC14B protein [Lithospermum erythrorhizon]
22579	ENU06373	ANT61C1070 1:1..1037	48-67	791-814	NAP		g4521101	1136	289	e-121	79	75	(AF069523) heat shock protein Hsp88 [Neurospora crassa]
22580	ENU06374	ANT61C1096: 692..161	52-71	464-483	NAP		g1766062	285	125	2.00E-28	42	99	[Aspergillus niger]
22581	ENU06375	ANT61C9004: 3221..4026	22-41	684-705	NAP		g1077385	325	95	7.00E-19	47	66	(U82218) Ats1 [Schizosaccharomyces pombe]
22582	ENU06376	ANT61C4853: 1709..2856	43-63	782-801	NAP		g522302	1176	360	1.00E-98	63	23	hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae)
22583	ENU06377	ANT61C8573: 7384..7793	37-56	377-399	NAP		g1929333	186	90	1.00E-17	35	66	(L35053) endonuclease [Magnaporthe grisea]
22584	ENU06378	ANT61C9181: 7917..8414	32-51	433-460	NAP		g4115939	407	176	8.00E-44	66	46	(Z93767) ywrf [Bacillus subtilis]
22585	ENU06379	ANT61S1637: 154..690	95-114	296-319	NAP		g1351702	100	61	0.000000	33	31	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850)
22586	ENU06380	ANT61C2866: 491..1	64-82	447-470	NAP		g140371	224	104	4.00E-22	36	29	[Arabidopsis thaliana]
22587	ENU06381	ANT61C1059 9:1..477	22-44	431-452	NAP		g4263825	301	130	5.00E-30	42	12	hypothetical 61.1 KD protein C11D3.05 in chromosome I [Schizosaccharomyces pombe]
22588	ENU06382	ANT61C5967: 8462..9284	22-46	690-717	NAP		g585175	452	104	2.00E-43	47	60	hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region [Saccharomyces cerevisiae]
													(AC006067) hypothetical protein [Arabidopsis thaliana]
													guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha)
													[Neurospora crassa]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22589	ENU06383	ANI61C1050 1:1298..7124			NAP		g1491929	10043	316	e-126	98	13	"(U51272) 1,3-beta-D-glucan synthase catalytic subunit [Emericella nidulans]"
22590	ENU06384	ANI61C7768: 29-48 3164..3929		633-652	NAP		g3135013	507	136	1.00E-45	51	26	(AJ005963) 100 kDa protein [Ajellomyces capsulatus]
22591	ENU06385	ANI61C1085 3:4930..4464	40-64	422-445	NAP		g1834342	444	175	1.00E-43	60	9	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
22592	ENU06386	ANI61C2190: 62-81 2788..1		722-741	NAP		g1351615	1732	235	3.00E-61	41	23	hypothetical protein C23D3.15 in chromosome I [Schizosaccharomyces pombe]
22593	ENU06387	ANI61C5726: 22-48 1..959		728-749	NAP		g3298291	535	229	9.00E-61	46	52	(AB010389) ALK2 [Yarrowia lipolytica]
22594	ENU06388	ANI61C1262: 45-66 524..1		446-465	NAP		g2625138	275	122	2.00E-27	39	10	(AF032443) ABC1 transporter, ABC-type ATPase [Magnaporthe grisea]
22595	ENU06389	ANI61C8354: 22-44 1077..1		723-743	NAP		g3861449	420	108	7.00E-23	25	26	(Z98596) SMC-family protein [Schizosaccharomyces pombe]
22596	ENU06390	ANI61C5304: 22-49 1..1908		762-780	NAP		g2660670	680	135	4.00E-31	36	22	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
22597	ENU06391	ANI61C8656: 22-45 1944..2456		470-492	NAP		g4769004	415	74	5.00E-36			(AF140598) ring-box protein 1 [Homo sapiens]
22598	ENU06392	ANI61C3866: 87-105 497..962		439-458	NAP		g1352994	132	78	2.00E-16			hypothetical 30.6 KD protein in SCP160-SMC3 intergenic region precursor [Saccharomyces cerevisiae]
22599	ENU06393	ANI61C3152: 185..3464			NAP		g4539277	2340	127	1.00E-28	27	18	(AL049498) myosin II [Schizosaccharomyces pombe]
22600	ENU06394	ANI61C6685: 38-57 1..938		717-735	NAP		g3219947	566	244	5.00E-64	52	45	hypothetical 61.8 KD protein C1EF8.13 in chromosome I [Schizosaccharomyces pombe]
22601	ENU06395	ANI61C1464: 83-108 1183..1		735-762	NAP		g3219304	443	185	4.00E-46	40	30	(AB009461) MUS38 [Neurospora crassa]
22602	ENU06396	ANI61C8385: 26-45 1400..3387		771-790	NAP		g1351714	483	83	2.00E-15	33	44	putative transporter C11D3.18C [Schizosaccharomyces pombe]
22603	ENU06397	ANI61C1122 22-41 5:1..442		395-421	NAP		g2462931	228	100	5.00E-21	42	20	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
22604	ENU06398	ANI61C85:71 27-46 4..1		591-613	NAP		g136753	726	303	1.00E-81			"glycogen (starch) synthase, isoform 1 [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22605	ENU06399	ANI61C5996: 24-45		791-816	NAP		g4126481	196	100	1.00E-20	29	98	(AB015352) <i>Akt2</i> [<i>Alternaria alternata</i>]
22606	ENU06400	ANI61C1158: 63-82		802-829	NAP		g127277	841	254	1.00E-69			mitochondrial phosphate carrier protein (phosphate transport protein) (mitochondrial import receptor) (P32) [<i>Saccharomyces cerevisiae</i>] (Y14855) tropomyosin [<i>Helix aspersa</i>]
22607	ENU06401	ANI61C1029: 22-41		413-432	NAP		g4468224	84	48	0.00004	21	33	benzoate 4-monooxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) [<i>Aspergillus niger</i>]
22608	ENU06402	ANI61C8089: 31-53		767-784	NAP		g117178	147	86	3.00E-16	24	41	hypothetical 420.8 KD protein C1F5.11C in chromosome I [<i>Schizosaccharomyces pombe</i>]
22609	ENU06403	ANI61C5229: 22-42		725-744	NAP		g1351684	914	87	2.00E-16			hypothetical 21.1 KD protein in YMC2-CMD1 intergenic region [<i>Saccharomyces cerevisiae</i>] (AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [<i>Arabidopsis thaliana</i>]
22610	ENU06404	ANI61C1135: 53-72		596-615	NAP		g586531	379	140	1.00E-32	46	98	L-fucose permease [<i>Escherichia coli</i>]
22611	ENU06405	ANI61C100:1 22-48		802-829	NAP		g4388818	256	157	7.00E-38			hypothetical protein YPL226w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22612	ENU06406	ANI61C7675: 24-43		809-829	NAP		g120593	192	57	0.000000			hypothetical protein YPL226w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22613	ENU06407	ANI61C29:98 38-57		714-733	NAP		g2132238	370	151	7.00E-36	39	21	pyruvate dehydrogenase protein X component precursor [Saccharomyces cerevisiae] (X89442) peptidase synthetase [<i>Metarhizium anisopliae</i>]
22614	ENU06408	ANI61C7767: 22-46		694-712	NAP		g129072	68	49	0.00003	30	57	hypothetical 104.7 KD protein in PKC1-RTG3 intergenic region [Saccharomyces cerevisiae] (X92971) translocation elongation factor [Saccharomyces cerevisiae]
22615	ENU06409	ANI61C6108: 22-46		780-799	NAP		g2342601	656	100	2.00E-20	25	5	
22616	ENU06410	ANI61C4919: 59-86		628-648	NAP		g586461	272	112	3.00E-24	32	29	
22617	ENU06411	ANI61C1116: 22-48		793-820	NAP		g1279693	740	287	6.00E-77	70	19	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22618	ENU06412	ANI61C2633: 2627..2215	66-85	343-362	NAP		g1332941	348	151	3.00E-36	53	36	"branched-chain amino acid aminotransferase, cytosolic (BCAT) (TWT2 protein) [Saccharomyces cerevisiae]"
22619	ENU06413	ANI61C1352: 1761..1310	24-44	298-320	NAP		g1176707	81	52	0.000003	28	51	hypothetical 33.0 KD protein in PROB-PROA intergenic region [Corynebacterium glutamicum] "(U51118) Neurospora crassa NUC-2 (Nuc-2) gene, complete cds. [Neurospora crassa]"
22620	ENU06414	ANI61C8273: 303..3850	22-46	804-829	NAP		g1399532	2420	113	2.00E-42	41	24	(AB010442) PMR1 [Penicillium digitatum]
22621	ENU06415	ANI61C8911: 780..1	22-48	641-660	NAP		g3288709	506	193	1.00E-48	46	16	micronuclear linker histone polypeptide (MIC LH) [Tetrahymena thermophila]
22622	ENU06416	ANI61S1445: 1..1008			NAP		g730030	141	63	0.000000	16	44	ZRT1 protein [Saccharomyces cerevisiae]
22623	ENU06417	ANI61C7533: 990..1	22-42	800-827	NAP		g418391	823	328	2.00E-89	56	75	(Z81368) hlpK [Mycobacterium tuberculosis]
22624	ENU06418	ANI61C9971: 3979..3681	25-43	292-310	NAP		g1655675	73	67	7.00E-11	33	32	(AL035263) putative TFIIF subunit (transcription-repair fac tor) [Schizosaccharomyces pombe]
22625	ENU06419	ANI61C1064: 6:682..1	39-66	557-581	NAP		g4176535	417	122	2.00E-38	41	66	(Z68905) ATP-binding cassette multidrug transporter [Emmentella nidulans]
22626	ENU06420	ANI61C3805: 4037..3580	102-129	413-437	NAP		g1834342	447	186	7.00E-47	53	10	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
22627	ENU06421	ANI61C3317: 1261..1792	56-75	397-418	NAP		g3702646	59	41	0.0009	29	27	(U80846) No definition line found [Caenorhabditis elegans]
22628	ENU06422	ANI61C6551: 1999..1	22-46	723-749	NAP		g3834294	156	55	0.000000			(U68040) polyketide synthase [Cochliobolus heterostrophus]
22629	ENU06423	ANI61C9287: 473..4546	30-49	802-829	NAP		g1546072	1848	103	1.00E-21			(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22630	ENU06424	ANI61C8021: 3552..2294	51-70	805-829	NAP		g3885836	510	125	4.00E-28	30	43	hypothetical 126.6 KD protein in RPL39-VTT1 intergenic region [Saccharomyces cerevisiae]
22631	ENU06425	ANI61S2328: 555..1	33-52	505-527	NAP		g2497183	573	131	2.00E-60	57	17	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
22632	ENU06426	ANI61C566:3 597..2493	22-46	805-828	NAP		g3395556	131	43	0.000001	31	72	

Database Hit

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22633	ENU06427	ANT61C7197:	23-46	781-808	NAP		g1170186	1129	316	2.00E-85	53	36	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UF1) [Saccharomyces cerevisiae]
22634	ENU06428	ANT61C6444:	24-51	752-775	NAP		g3668171	894	313	1.00E-95	66	22	(AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]
22635	ENU06429	ANT61C362:1	22-44	801-828	NAP		g2330871	430	174	2.00E-48	41	29	(Z98603) hypothetical protein [Schizosaccharomyces pombe]
22636	ENU06430	ANT61C1027	67-88	727-746	NAP		g1711561	256	50	0.00002			sugar transporter STL1 [Saccharomyces cerevisiae]
22637	ENU06431	ANT61C7202:			NAP		g1709181	680	192	3.00E-48	47	46	high affinity methionine permease [Saccharomyces cerevisiae]
22638	ENU06432	ANT61C3971:	34-53	726-749	NAP		g3150253	605	178	6.00E-44	39	23	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
22639	ENU06433	ANT61C2161:	30-49	802-829	NAP		g3730	1119	197	3.00E-75	54	47	(X53424) glycolipid-anchored surface protein [Saccharomyces cerevisiae]
22640	ENU06434	ANT61C1116	27-46	728-747	NAP		g131768	541	136	2.00E-31	34	46	quinate permease (quinate transporter) [Emicella nidulans]
22641	ENU06435	ANT61C4297:			NAP		g553045	65	47	0.00009	32	64	(M28651) chloroperoxidase [Caldariomyces funago]
22642	ENU06436	ANT61C1263:	22-49	696-723	NAP		g3810839	375	150	1.00E-35	41	44	(AL032684) conserved hypothetical zinc-finger protein [Schizosaccharomyces pombe]
22643	ENU06437	ANT61C8233:	24-43	750-774	NAP		g3947877	540	91	1.00E-54	53	100	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]
22644	ENU06438	ANT61C3897:			NAP		g1799532	211	59	7.00E-17	30	66	(AB000564) salicylate hydroxylase [Sphingomonas sp.]
22645	ENU06439	ANT61C2901:	22-47	411-433	NAP		g3342802	197	87	5.00E-17	30	31	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]
22646	ENU06440	ANT61C8881:	22-49	725-749	NAP		g2494411	100	37	0.21	28	16	3-(3-hydroxy-phenyl)propionate hydroxylase [Escherichia coli]
22647	ENU06441	ANT61S4274:	35-62	494-519	NAP		g4733982	693	173	3.00E-61			(AC007268) hypothetical protein [Arabidopsis thaliana]
22648	ENU06442	ANT61C8550:	51-78	802-821	NAP		g1166378	743	132	2.00E-30	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22649	ENU06443	ANI61C9556: 7386..8061	36-55	632-651	NAP		g4106657	653	118	5.00E-61	79	50	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]
22650	ENU06444	ANI61C8783: 1.601	122-141	519-538	NAP		g1176982	71	59	0.000000	29	41	hypothetical metabolite transport protein in HTPG-IOLR intergenic region []
22651	ENU06445	ANI61C4477: 1..757	103-130	659-684	NAP		g3702635	288	135	3.00E-31	32	61	(AL031825) hypothetical protein [Schizosaccharomyces pombe]
22652	ENU06446	ANI61C1099 9:5329..6029	33-52	616-633	NAP		g78100	336	113	2.00E-24	33	37	cyclohexanone monooxygenase (EC 1.14.13.22) - Acinetobacter sp []
22653	ENU06447	ANI61C3891: 1..526	22-45	456-476	NAP		g3183364	236	94	6.00E-19	34	30	putative transporter C1B3.16C [Schizosaccharomyces pombe]
22654	ENU06448	ANI61S2827: 1..628			NAP		g3808062	134	57	0.000000	20	25	(AB019195) PV100 [Cucurbita maximal]
22655	ENU06449	ANI61C6432: 8274..9352	23-45	721-741	NAP		g3928166	346	149	3.00E-35	35	42	(AJ010317) Sand [Fugu rubripes]
22656	ENU06450	ANI61C6774: 1..1713	36-55	789-806	NAP		g461623	350	47	2.00E-10	36	21	beta-galactosidase precursor (lactase) [Aspergillus niger]
22657	ENU06451	ANI61S4263: 1..838			NAP		g4218005	300	45	0.0006	29	38	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22658	ENU06452	ANI61C1061 2:790..184	112-131	535-555	NAP		g4049341	99	35	0.52	38	34	(AL034567) putative protein [Arabidopsis thaliana]
22659	ENU06453	ANI61C3499: 2369..2795	22-41	460-479	NAP		g585899	97	56	0.000000	37	100	mitochondrial 60S ribosomal protein L37 precursor (YML37) [Saccharomyces cerevisiae]
22660	ENU06454	ANI61C4192: 4222..3816	153-178	360-386	NAP		g3913969	146	59	2.00E-11	37	28	kynureninase (L-kynurenine hydrolase) [Rattus norvegicus]
22661	ENU06455	ANI61C1912: 1325..348	30-49	785-804	NAP		g1723076	270	80	2.00E-21	35	48	hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C [Mycobacterium tuberculosis]
22662	ENU06456	ANI61S1424: 1..649			NAP		g228937	211	37	0.11	34	64	Hyp-rich glycoprotein [Zea mays]
22663	ENU06457	ANI61C3442: 740..2427	50-69	657-675	NAP		g400924	349	101	7.00E-21	24	26	DNA repair protein RAD3 [Schizosaccharomyces pombe]
22664	ENU06458	ANI61C9247: 1..1208	22-41	808-829	NAP		g3139137	592	111	8.00E-24	36	31	(AF063864) essential nuclear protein Mem3p [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22665	ENU06459	ANI61C1877:	31-51	716-738	NAP		g3288709	1663	267	8.00E-71	54	17	(AB010442) PMR1 [Penicillium digitatum]
22666	ENU06460	ANI61C1878:	59-82	314-341	NAP		g3041855	180	85	1.00E-16	34	29	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]
22667	ENU06461	ANI61C7121:	35-61	451-478	NAP		g1850540	183	56	0.000000	45	99	(U87806) ribosomal P2 phosphoprotein [Alternaria alternata]
22668	ENU06462	ANI61C1054:	28-49	700-719	NAP		g3183342	235	73	6.00E-28	38	54	hypothetical 44.5 KD protein C14C4.09 in chromosome I [Schizosaccharomyces pombe]
22669	ENU06463	ANI61C8705:			NAP		g2213552	369	163	1.00E-39	35	44	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
22670	ENU06464	ANI61C4350:			NAP		g1174862	141	52	4.00E-14	41	33	putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
22671	ENU06465	ANI61C7356:	22-48	803-828	NAP		g231993	2396	388	e-107			succinate dehydrogenase (ubiquinone) flavoprotein subunit precursor (FP) (flavoprotein subunit of complex II) [Saccharomyces cerevisiae]
22672	ENU06466	ANI61C2512:			NAP		g2492798	485	179	9.00E-47	48	62	aryl-alcohol dehydrogenase (NADP+) (AAD) [Phanerochaete chrysosporium]
22673	ENU06467	ANI61S1309:			NAP		g2959371	670	265	4.00E-72	64	38	(AL022117) asparagine synthetase [Schizosaccharomyces pombe]
22674	ENU06468	ANI61S3208:	120-141	284-304	NAP		g117820	515	132	4.00E-42	96	50	cytochrome B6 [Spinacia oleracea]
22675	ENU06469	ANI61S3578:			NAP		g1131489	72	45	0.0005	25	58	"(U42580) Pro-rich protein; PPAK (24X); similar to Triticum PK-rich protein, corresponds to GenBank Accession Number X52472 [Paramesicium bursaria Chlorella virus 1]"
22676	ENU06470	ANI61S1366:			NAP		g283032	153	60	0.000000	33	64	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]

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22677	ENU06471	ANI61C1037	22-48	549-576	NAP		g3914384	686	189	3.00E-71	84	100	probable peroxisomal membrane protein PMP20 (allergen ASP F 3)
		7:1768..1143											[Aspergillus fumigatus]
22678	ENU06472	ANI61C5116:	22-45	640-660	NAP		g117619	121	50	5.00E-10	27	28	choline transport protein
		780..1											[Saccharomyces cerevisiae]
22679	ENU06473	ANI61C1063	136-160	541-560	NAP		g3219959	290	87	1.00E-16	39	34	probable zinc metalloproteinase C17A5.04C precursor
		9:622..1											[Schizosaccharomyces pombe]
22680	ENU06474	ANI61C1118	89-108	730-749	NAP		g2146836	1134	270	7.00E-72	56	32	hypothetical protein YCL054w - yeast
		7:5234..6480											[Saccharomyces cerevisiae]
22681	ENU06475	ANI61C7956:	22-46	617-644	NAP		g3929357	223	87	2.00E-16	37	34	[Saccharomyces cerevisiae]
		752..1											O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase)
													(cytochrome P450 64)
22682	ENU06476	ANI61C8967:	22-48	802-829	NAP		g1168351	414	76	2.00E-13	38	71	[Aspergillus parasiticus]
		4367..3128											alcohol dehydrogenase (ADH)
22683	ENU06477	ANI61S4000:	214-231	401-420	NAP		g1723751	446	80	4.00E-28	72	42	[Bacillus stearothermophilus]
		472..1											hypothetical 34.9 KD protein in SMT1-PHO81 intergenic region
22684	ENU06478	ANI61C6670:	87-106	380-398	NAP		g4760344	167	49	0.00002			[Saccharomyces cerevisiae]
		1400..1791											(AL049769) mitochondrial 60s ribosomal protein 110 precursor
22685	ENU06479	ANI61C2264:	49-68	760-780	NAP		g409547	261	56	2.00E-16	29	47	[Schizosaccharomyces pombe]
		1412..43											(L07492) sugar transport protein
22686	ENU06480	ANI61C4164:	52-71	662-683	NAP		g1770212	175	81	1.00E-21	29	59	[Saccharomyces cerevisiae]
		1348..2131											(X99340) nucleic acid binding protein
22687	ENU06481	ANI61C1984:			NAP		g3776152	873	195	2.00E-84	62	55	[Drosophila melanogaster]
		1..1014											(AB018537) elongation factor 3
22688	ENU06482	ANI61C5698:	189-210	786-813	NAP		g3006179	436	139	2.00E-32	45	32	[Yarrowia lipolytica]
		925..1											(AL022304) putative long-chain-fatty-acid--coa ligase [Schizosaccharomyces pombe]
22689	ENU06483	ANI61C6002:	111-130	295-314	NAP		g118678	462	132	4.00E-46			dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae]
		1831..1443											(AC007369) Similar to RNA helicases
22690	ENU06484	ANI61S2737:			NAP		g4836896	198	63	0.000000			[Arabidopsis thaliana]
		1..928											molybdopterin biosynthesis MOEA
22691	ENU06485	ANI61S4388:	64-83	296-315	NAP		g2497956	114	71	4.00E-12	27	40	protein [Synecococcus sp.]
		470..1											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22692	ENU06486	ANT61C1404: 1463..496	22-48	629-647	NAP	g729296	180	76	2.00E-13	31	76	6	dihydropicolinate synthase (DHDPs) [Corynebacterium glutamicum]
22693	ENU06487	ANT61C4023: 1..1098	37-56	621-640	NAP	g1352956	1303	381	e-105	68	43	43	hypothetical 75.5 KD protein in CCT3-CCT8 intergenic region [Saccharomyces cerevisiae]
22694	ENU06488	ANT61S3272: 1..462	40-67	391-415	NAP	g2257528	597	209	4.00E-55	70	26	26	(AB004537) methionyl-tRNA synthetase [Schizosaccharomyces pombe]
22695	ENU06489	ANT61C6841: 2213..1178	22-46	803-829	NAP	g231361	910	308	4.00E-83	58	81	81	l-aminocyclopropane-l-carboxylate deaminase (ACC deaminase) [Pseudomonas sp.]
22696	ENU06490	ANT61S2126: 533..63	195-220	405-431	NAP	g1706695	96	34	0.48	26	31	31	phosphomevalonate kinase [Saccharomyces cerevisiae]
22697	ENU06491	ANT61C7863: 2642..1821	107-126	725-744	NAP	g1175491	570	129	4.00E-58	51	82	82	hypothetical 33.9 KD protein C16C9.02C in chromosome I [Schizosaccharomyces pombe]
22698	ENU06492	ANT61C1117: 8..1.497	22-43	360-379	NAP	g1546072	289	118	3.00E-26	40	6	6	(U68040) polyketide synthase [Cochliobolus heterotrophus]
22699	ENU06493	ANT61C9611: 1087..189	22-47	777-804	NAP	g2623175	982	226	2.00E-98	65	67	67	(AF030425) pyruvate dehydrogenase E1 component alpha subunit [Pichia stipitis]
22700	ENU06494	ANT61C4200: 632..1	22-45	508-531	NAP	g3560136	534	138	4.00E-53	54	32	32	(AL031534) 2-isopropylmalate synthase. [Schizosaccharomyces pombe]
22701	ENU06495	ANT61C8517: 541..1	89-108	412-432	NAP	g128862	354	154	4.00E-37	51	55	55	NADH-ubiquinone oxidoreductase 30.4 KD subunit precursor (complex I-30KD) (CI-31KD) []
22702	ENU06496	ANT61C2596: 1435..1	22-44	724-748	NAP	g2388993	693	129	3.00E-29	34	14	14	(Z98981) putative sodium channel [Schizosaccharomyces pombe]
22703	ENU06497	ANT61S3056: 1..536			NAP	g228937	164	53	0.000001	34	53	53	Hyp-rich glycoprotein [Zea mays]
22704	ENU06498	ANT61C2202: 1..1020	57-76	770-789	NAP	g3122099	1167	433	e-121	72	81	81	farnesyl pyrophosphate synthetase (FPP synthetase) (FPPs) (farnesyl diphosphate synthetase) (dimethylallyltransferase / geranyltransferase [Gibberella fujikuroi] (U73900) 2-hydroxybiphenyl-3-monooxygenase [Pseudomonas azelaica]
22705	ENU06499	ANT61C7060: 1..456	43-62	412-435	NAP	g2098616	210	100	7.00E-21	38	25	25	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22706	ENU06500	ANI61C6470:	40-64	801-824	NAP		g2497989	681	212	4.00E-54	49	65	putative mitochondrial carrier YMR166C [Saccharomyces cerevisiae]
22707	ENU06501	ANI61C4397:	45-66	799-818	NAP		g2408036	655	211	5.00E-54	43	67	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
22708	ENU06502	ANI61C7311:	31-52	795-822	NAP		g1345823	910	202	3.00E-51	47	52	nitrate transporter (nitrate permease) [Emericella nidulans]
22709	ENU06503	ANI61C294:4	28-48	808-827	NAP		g225924	273	51	7.00E-14			uracil transport protein [Saccharomyces cerevisiae]
22710	ENU06504	ANI61C7960:	22-45	780-799	LINAP		g728904	1577	261	3.00E-69	50	22	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
22711	ENU06505	ANI61C7336:	22-44	790-809	LINAP		g3915140	201	113	2.00E-24	32	45	isotrichoderm C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichoderm C-15 hydroxylase [Fusarium sporotrichoides]
22712	ENU06506	ANI61C3911:	42-61	750-770	LINAP		g464369	220	64	5.00E-16	31	37	phenol 2-monooxygenase (phenol hydroxylase) ; (L04488) phenol hydroxylase [Trichosporon cutaneum]
22713	ENU06507	ANI61C7950:	22-48	680-699	LINAP		g3925779	125	70	1.00E-11	22	41	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
22714	ENU06508	ANI61C9771:	24-45	451-471	LINAP		g549594	41	54	0.000000	33	15	hypothetical 102.5 KD protein in YPT52-DBP7 intergenic region ; hypothetical protein YKR021w - yeast (Saccharomyces cerevisiae) ; (Z28246) ORF YKR021w [Saccharomyces cerevisiae]
22715	ENU06509	ANI61C3160:	22-48	562-581	LINAP		g1582765	59	36	0.31	36	24	YFW1 gene [Saccharomyces cerevisiae]
22716	ENU06510	ANI61C6787:	23-42	671-690	LINAP		g3116145	494	208	3.00E-53	43	41	(AL023290) hypothetical protein [Schizosaccharomyces pombe]

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22717	ENU06511	ANI6IC7358: 1835..6555	30-49	705-730	LINAP	g124211	772	34	0.98				translation initiation factor IF-2; (M36878) translational initiation factor IF2 [Streptococcus faecium]
22718	ENU06512	ANI6IC801:8 60..1	22-47	752-773	LINAP	g4522004	367	164	5.00E-40	37	46		"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]"
22719	ENU06513	ANI6IC3916: 1..1021	22-46	776-795	LINAP	g2662028	577	166	2.00E-40	35	32		(Z99296) beta-transducin [Schizosaccharomyces pombe]
22720	ENU06514	ANI6IC6734: 855..482	23-45	439-458	LINAP	g4464201	120	66	2.00E-10	30	24		(AL031587) dJ1039K5.2 (similar to monocarboxylate transporter (MCT3)) [Homo sapiens]
22721	ENU06515	ANI6IC7353: 5597..3348	50-69	790-809	LINAP	g3184110	716	87	2.00E-16				(AL023780) putative mma stability protein [Schizosaccharomyces pombe]
22722	ENU06516	ANI6IC9768: 916..1	30-57	713-735	LINAP	g4249705	449	215	4.00E-55	38	48		(AF101074) step II splicing factor SLU7 [Homo sapiens]
22723	ENU06517	ANI6IC3176: 72..911	32-55	781-800	LINAP	g4107314	191	61	8.00E-18	29	52		(AL035075) conserved hypothetical SH3 domain-containing protein [Schizosaccharomyces pombe]
22724	ENU06518	ANI6IC7404: 1..1861	114-133	709-730	LINAP	g2388993	644	143	2.00E-33	29	15		(Z98981) putative sodium channel [Schizosaccharomyces pombe]
22725	ENU06519	ANI6IC3918: 1..1337	28-47	803-829	LINAP	g4033414	905	110	1.00E-23	31	24		putative importin beta-4 subunit (karyopherin beta-4 subunit); (AL023780) putative importin beta-4 subunit [Schizosaccharomyces pombe]
22726	ENU06520	ANI6IC6734: 4810..5529	22-48	632-654	LINAP	g284667	111	46	0.0002				neurofilament triplet H1 protein - rabbit (fragment); (M94315) neurofilament-H [Oryctolagus cuniculus]
22727	ENU06521	ANI6IC3180: 1499..2664	50-69	798-817	LINAP	g2262189	91	64	0.000000				(U56098) FacB [Aspergillus oryzae]
22728	ENU06522	ANI6IC6786: 1..361	22-45	314-340	LINAP	g2132273	99	59	0.000000				hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae); (U51033) P9513.3 gene product [Saccharomyces cerevisiae]
22729	ENU06523	ANI6IC7390: 313..1205	31-50	809-828	LINAP	g2388994	1466	235	2.00E-62	54	46		(Z98981) hypothetical gtp-binding protein associated [Schizosaccharomyces pombe]
22730	ENU06524	ANI6IC8005: 3207..1743	66-85	791-810	LINAP	g2465159	1080	231	6.00E-60	46	38		(Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22731	ENU06525	ANI61C378:4	22-46	550-569	LINAP		g2271503	90	57	0.000000	26	46	(AF009672) unknown [Acinetobacter sp. ADP1]
22732	ENU06526	ANI61C6790:567..5166			LINAP		g2688966	748	275	2.00E-73	51	46	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]
22733	ENU06527	ANI61C7416:1..979	38-57	805-829	LINAP		g728850	107	53	0.000003			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
22734	ENU06528	ANI61C7393:4538..3586	22-46	785-804	LINAP		g547769	561	177	7.00E-44	44	54	KES1 protein ; KES1 protein - yeast (Saccharomyces cerevisiae) ; (U03913) Kes1p [Saccharomyces cerevisiae] ; (U43703) Kes1p [Saccharomyces cerevisiae] ; (Z73501) ORF YPL145c [Saccharomyces cerevisiae] ; (X96770) P2614 product [Saccharomyces cerevisiae]
22735	ENU06529	ANI61C9798:2257..1	22-45	734-761	LINAP		g522302	1289	182	3.00E-45	40	23	(L35053) endonuclease [Magnaporthe grisea]
22736	ENU06530	ANI61C3204:1281..1	22-42	679-706	LINAP		g1169871	1040	120	4.00E-65	65	29	GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gen20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae]
22737	ENU06531	ANI61C6807:364..1149	22-45	727-748	LINAP		g4499840	209	93	2.00E-18	33	7	(AJ011964) d-lysergyl-peptide-synthetase [Claviceps purpurea]
22738	ENU06532	ANI61C9792:1991..1121	22-45	762-781	LINAP		g3738149	190	36	0.27			(AL031852) conserved protein-PHD-finger family [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score 68	Blast Score 51	Blast Prob 0.000007	% id	% cvrg	Description
22739	ENU06533	ANI61C6772:	54-73	627-647	LINAP		g3877858	68					(Z34801) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans]; (Z66514) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] (AB010810) phospholipase D [Candida albicans] (U89352) lysophospholipase I [Mus musculus]; (U97148) calcium-independent phospholipase A2 isoform 2 [Oryctolagus cuniculus] hypothetical 30.9 KD protein K07C11.7 in chromosome V; (U53336) coded for by C. elegans cDNA cm12g2; coded for by C. elegans cDNA yk56a6.5; coded for by C. elegans cDNA yk70a12.5; coded for by C. elegans cDNA cm11d9; coded for by C. elegans cDNA yk102d1.5; coded for by C. elegans cDNA yk102d1.3;...
22740	ENU06534	ANI61C8028:	113-132	569-588	LINAP		g3413518	711	291	4.00E-78	68	11	
22741	ENU06535	ANI61C8042:	23-42	775-794	LINAP		g1864159	214	85	7.00E-19	33	91	
22742	ENU06536	ANI61C3954:	102-128	421-440	LINAP		g3025256	118	67	1.00E-10	37	39	
22743	ENU06537	ANI61C8012:	48-67	456-479	LINAP		g3650394	77	52	0.000003	30	61	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe] (Z99165) protein kinase [Schizosaccharomyces pombe] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe] (U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans]
22744	ENU06538	ANI61C7420:	22-49	773-796	LINAP		g2408067	860	280	8.00E-75	50	44	(AL035076) putative allantoinase [Schizosaccharomyces pombe]
22745	ENU06539	ANI61C805:8	22-42	803-829	LINAP		g2462679	138	66	4.00E-10	24	26	
22746	ENU06540	ANI61C7418:	105-124	363-381	LINAP		g746510	310	144	3.00E-34	48	48	
22747	ENU06541	ANI61C3955:	27-46	519-538	LINAP		g4107287	320	85	5.00E-36	43	39	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22748	ENU06542	ANI61C7422:	25-44	486-508	LINAP		g731584	125	41	0.007			hypothetical 17.1 KD protein in PUR5 3region ; hypothetical protein YHR217c - yeast (Saccharomyces cerevisiae) ; (U00029) Yhr217cp [Saccharomyces cerevisiae] (Z95397) unknown
22749	ENU06543	ANI61C3946:	24-51	803-829	LINAP		g2104460	359	124	7.00E-28	34	25	[Schizosaccharomyces pombe] (U95159) gelsolin-related protein GRP125 [Dictyostelium discoideum] (AF091042) putative cercosporin transporter [Cercospora kikuchii] (U74380) cholinesterase 1 [Branchiostoma floridae] (U78523) histidine secretory acid phosphatase [Leishmania donovani] (AB010810) phospholipase D [Candida albicans]
22750	ENU06544	ANI61C9800:	41-68	648-669	LINAP		g4100186	110	43	0.002			probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
22751	ENU06545	ANI61C3970:	34-61	722-744	LINAP		g3885836	333	156	2.00E-37	36	45	spemr histone P2 precursor (protamine P2) ; protamine P2 - rhesus macaque ; (X71338) Protamine P2 [Macaca mulatta] (AF055904) acetylornithine deacetylase; ArgE [Myxococcus xanthus]
22752	ENU06546	ANI61C3143:	35-54	810-829	LINAP		g3435078	362	154	8.00E-43	40	46	amino-acid permease INDA1 ; INDA1 protein - fungus (Trichoderma harzianum) ; (Z22594) INDA1 [Trichoderma harzianum]
22753	ENU06547	ANI61C3210:	22-46	516-543	LINAP		g2058526	63	40	0.009			probable oxygenase - Streptomyces fradiae ; (X87093) putative oxygenase [Streptomyces fradiae]
22754	ENU06548	ANI61C8088:	108-127	801-820	LINAP		g3413518	467	94	2.00E-35	38	14	
22755	ENU06549	ANI61C7429:	31-49	465-485	LINAP		g2493391	303	145	2.00E-34	43	38	
22756	ENU06550	ANI61C397:1	22-48	739-758	LINAP		g462350	324	33	2.3			
22757	ENU06551	ANI61C3228:	50-69	492-512	LINAP		g3044087	217	94	1.00E-18			
22758	ENU06552	ANI61C9804:	41-60	417-438	LINAP		g462414	320	135	2.00E-31	52	23	
22759	ENU06553	ANI61C7396:	22-44	806-827	LINAP		g1076090	349	139	2.00E-32	33	54	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
22760	ENU06554	ANI61C3230:	69-87	625-649	LINAP		g1730591	132	76	2.00E-13			hypothetical 41.1 KD protein ON CDC91-PAU4 intergenic region ; hypothetical protein YLR460c - yeast (Saccharomyces cerevisiae) ; (U22383) Ylr460cp [Saccharomyces cerevisiae] hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
22761	ENU06555	ANI61C9803:	22-49	806-829	LINAP		g586486	328	71	2.00E-26	32	38	"(AL031540) internalin - related, Leucine rich repeat containing protein [Schizosaccharomyces pombe] " (AB010466) multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1) [Rattus norvegicus] ; (U73038) multidrug resistance-associated protein 6 [Rattus norvegicus]
22762	ENU06556	ANI61C3999:	122-141	264-289	LINAP		g3581887	70	48	0.00002			(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe] (AL031179) importin beta subunit [Schizosaccharomyces pombe]
22763	ENU06557	ANI61C3208:	22-47	794-813	LINAP		g3242458	382	111	2.00E-36	38	15	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]
22764	ENU06558	ANI61C9820:			LINAP		g4481949	149	63	7.00E-11	44	33	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
22765	ENU06559	ANI61C7446:	27-54	650-669	LINAP		g3395584	843	229	2.00E-59	42	25	
22766	ENU06560	ANI61C318.5	23-50	792-819	LINAP		g1706177	210	110	1.00E-23	26	28	
22767	ENU06561	ANI61C9777:	22-46	810-829	LINAP		g2507070	253	51	0.000009			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22768	ENU06562	ANI61C7436: 458..1	125-152	437-464	LINAP		g2499507	211	46	0.000000	32	28	"6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase liver isozyme (6PF-2-K/FRU-2,6-P2ASE) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) - chicken ; (S54076) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [chickens, liver, Peptide, 469 aa] [Gallus gallus] "
22769	ENU06563	ANI61C318:3 444..2978	50-77	454-479	LINAP		g2764632	651	233	8.00E-61	73	73	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
22770	ENU06564	ANI61C9796: 7361..6942	22-48	453-472	LINAP		g2149953	141	56	9.00E-18	39	10	(U97066) sulfonilylurea receptor 2B [Mus musculus]
22771	ENU06565	ANI61C3216: 1375..803	28-47	515-534	LINAP		g2894086	118	65	5.00E-10	38	36	(Y11395) seventransmembrane-domain protein [Homo sapiens]
22772	ENU06566	ANI61C4015: 1923..1370	64-83	494-513	LINAP		g2414599	74	52	0.000004	32	38	(Z99295) dihydrotoluate reductase [Schizosaccharomyces pombe]
22773	ENU06567	ANI61C7419: 2705..1866	22-44	783-810	LINAP		g133323	68	63	0.000000	003		DNA-directed RNA polymerase II largest subunit (RPB1) ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Chinese hamster (fragment) ; (M19538) RNA polymerase II largest subunit [Cricetus griseus]
22774	ENU06568	ANI61C7451: 1913..2465			LINAP		g2347100	423	136	3.00E-33	40	50	(U76846) ubiquitin-specific protease [Arabidopsis thaliana] ; (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana]
22775	ENU06569	ANI61C3238: 942..1	81-100	715-737	LINAP		g1077530	263	96	4.00E-24	32	48	hypothetical protein YDR132c - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae]
22776	ENU06570	ANI61C3257: 1104..339	53-72	715-734	LINAP		g3914096	214	116	2.00E-25	38	24	NA(+)/H(+) antiporter 2 : (AB010106) Zsod22p [Zygosaccharomyces rouxii]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22777	ENU06571	ANI61C7427: 5672..3569	41-60	769-788	LINAP	g549627	997	997	127	1.00E-28	39	37	hypothetical 83.6 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae) ; (Z28292) ORF YKR067w [Saccharomyces cerevisiae]
22778	ENU06572	ANI61C4052: 1755..251	26-46	802-829	LINAP	g1351681	479	141	5.00E-33	36	31	31	heat shock protein 70 homolog precursor ; (Z68136) unknown [Schizosaccharomyces pombe]
22779	ENU06573	ANI61C8108: 3842..3264	102-127	532-558	LINAP	g2924313	226	124	5.00E-28	35	18	18	"(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"
22780	ENU06574	ANI61C4051: 326..1	37-63	453-475	LINAP	g3915154	70	47	0.00007				trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
22781	ENU06575	ANI61C3252: 2449..1630	32-51	765-792	LINAP	g3093476	306	157	7.00E-38	33	31	31	(AF008915) EVI-5 homolog [Homo sapiens]
22782	ENU06576	ANI61C7454: 2674..2011	22-48	617-642	LINAP	g2981475	108	74	1.00E-15	31	60	60	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]
22783	ENU06577	ANI61C7447: 1052..2869	22-46	809-829	LINAP	g549738	610	158	4.00E-38	33	45	45	hypothetical amino-acid permease in STE3-GIN10 intergenic region ; probable transport protein YKL174c - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28174) ORF YKL174c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
22784	ENU06578	ANI61C4067: 17..1066	24-43	803-829	LINAP	g3116134	379	141	6.00E-33	36	10	10	(AL023288) hypothetical protein [Schizosaccharomyces pombe]
22785	ENU06579	ANI61C3274: 1629..2588	35-55	801-820	LINAP	g3006175	524	196	2.00E-49	39	53	53	(AL022305) putative transcription factor [Schizosaccharomyces pombe]
22786	ENU06580	ANI61C4055: 308..670	66-85	454-473	LINAP	g1073049	70	69	1.00E-11	28	36	36	salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida ; (X83926) salicylate 1-monoxygenase [Pseudomonas putida]
22787	ENU06581	ANI61C3287: 865..1187	22-48	459-478	LINAP	g4581773	111	62	0.000000	32	24	24	(AF110766) transcription factor AFLR [Aspergillus parasiticus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22788	ENU06582	AN161C815:1	22-49	776-802	LINAP	g2497523	820	260	1.00E-68	50	16	kinesin-like protein KIF1A (axonal transporter of synaptic vesicles) ; (X90840) axonal transporter of synaptic vesicles [Homo sapiens] (AB017641) polyketide synthase [Micromonospora griseorubida] (AL035161) putative secreted peptidase [Streptomyces coelicolor] probable phosphatidylinositol-4-phosphate 5-kinase FAB1 (1-phosphatidylinositol-4-phosphate kinase) (P1P5K) (PTDINS(4)P-5-kinase) (diphosphoinositide kinase) ; (U01017) Fab1p [Saccharomyces cerevisiae]
22789	ENU06583	AN161C4055: 25-48	724-747	LINAP	g4586928	757	263	9.00E-70	43	6		(AL033534) serine-rich protein [Schizosaccharomyces pombe] (U97191) similar to nucleoporins [Caenorhabditis elegans] "(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (M63836) beta-gluconidase [Mus musculus]
22790	ENU06584	AN161C8073: 32-58	552-572	LINAP	g4154074	76	56	0.000000	36	27		(U89492) arylsulfatase [Neurospora crassa] (AF033013) Notch homolog [Bombyx mori] (AF116463) unknown [Streptomyces lincolnensis] (AF027979) carnitine acetyl transferase [Magnaporthe grisea] (AL035075) putative transcription factor tftiib component [Schizosaccharomyces pombe] erythrocyte ankyrin [Homo sapiens]
22791	ENU06585	AN161C3281: 40-59	811-829	LINAP	g462047	759	225	4.00E-58	36	12		(AC006284) putative ankyrin [Arabidopsis thaliana]
22792	ENU06586	AN161C7469: 102-127	415-441	LINAP	g3873550	95	41	0.004				
22793	ENU06587	AN161C4090: 69-87	500-519	LINAP	g1943773	94	47	0.00008	34	22		
22794	ENU06588	AN161C814: 67-86	740-759	LINAP	g2246532	148	60	0.000000	20	24		
22795	ENU06589	AN161C329:1		LINAP	g193723	458	59	2.00E-21	33	41		
22796	ENU06590	AN161C7490: 27-54	729-749	LINAP	g2873363	841	237	8.00E-62	47	39		
22797	ENU06591	AN161C817:1	22-45	459-478	LINAP	g2654086	167	57	0.000000			
22798	ENU06592	AN161C409:4	117-135	517-536	LINAP	g4455041	77	33	1.4			
22799	ENU06593	AN161C8142: 22-41	463-485	LINAP	g2688966	449	130	8.00E-30	68	24		
22800	ENU06594	AN161C7484: 116-135	379-402	LINAP	g4107317	222	104	4.00E-22	38	27		
22801	ENU06595	AN161C814:1		LINAP	g226788	86	64	3.00E-10	41	5		
22802	ENU06596	AN161C411:6		LINAP	g4335756	99	65	3.00E-10	30	66		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat nchi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
22803	ENU06597	ANI61C814:5	23-50	796-823	LINAP	g2342601	805	100	3.00E-34	33	5	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22804	ENU06598	ANI61C4133: 1..502	92-111	456-479	LINAP	g557084	78	56	0.000000	32	10	10	(L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
22805	ENU06599	ANI61C7512: 1..828	48-74	770-789	LINAP	g3859678	398	185	3.00E-46	36	30	30	(AL033503) conserved hypothetical protein [Candida albicans]
22806	ENU06600	ANI61C3310: 1328..712	22-43	541-560	LINAP	g2791489	156	70	1.00E-14	38	36	36	(AL021246) hypothetical protein Rv2449c [Mycobacterium tuberculosis]
22807	ENU06601	ANI61C3306: 1895..310	22-48	806-829	LINAP	g1546072	714	129	2.00E-50	45	10	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22808	ENU06602	ANI61C4133: 2028..1713			LINAP	g730197	54	43	0.0005	31	18	18	protein N-terminal amidase (NT-amidase) ; amino-terminal amidase NTA1 - yeast (Saccharomyces cerevisiae) ; (L35564) N-terminal amidase [Saccharomyces cerevisiae] ; (Z49562) ORF YJR062c [Saccharomyces cerevisiae] ; (L47993) ORF YJR062c [Saccharomyces cerevisiae]
22809	ENU06603	ANI61C8187: 409..1	29-48	460-479	LINAP	g2497685	51	55	0.000000	2			platelet-activating factor acetylhydrolase precursor (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetylgllyceroph... ; (U34246) plasma PAF acetylhydrolase [Canis familiaris] ; platelet-activating factor acetylhydrolase [Canis familiaris]
22810	ENU06604	ANI61C413:1 205..1889	49-68	612-631	LINAP	g3153851	236	94	1.00E-27	41	38	38	(AF064524) carboxylesterase [Anisopteromalus calandrae]
22811	ENU06605	ANI61C8185: 1..715	107-126	672-693	LINAP	g1352321	561	137	9.00E-32	45	57	57	ubiquitin-like protein DSK2 ; (L40587) ubiquitin-like protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22812	ENU06606	ANT61C8180:	25-51	805-827	LINAP		g4522026	74	40	0.018			"(AC004886) C-terminus matches KIAA0559, N-terminus similar to Basoon protein; match to P1D:g3043642; similar to P1D:g3413810 [Homo sapiens]" unknown ; (AF072250) methyl-CpG binding protein MBD4 [Homo sapiens] ; (AF114784) methyl-CpG binding endonuclease [Homo sapiens] probable membrane protein YPR022c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] putative polypeptide hydroxylase
22813	ENU06607	ANT61C7516:	24-51	427-447	LINAP		g4505121	160	78	1.00E-15	39	22	
22814	ENU06608	ANT61C4132:	37-56	671-690	LINAP		g1084945	282	99	1.00E-28	35	19	(AL031907) putative cystine-rich transcriptional regulator [Schizosaccharomyces pombe] (AL035592) hypothetical protein [Schizosaccharomyces pombe] hypothetical 78.3 KD protein in R1P1-URA3 intergenic region ; hypothetical protein YEL023c - yeast (Saccharomyces cerevisiae) ; (U18530) Yel023cp [Saccharomyces cerevisiae] sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
22815	ENU06609	ANT61C7536:	43-62	380-399	LINAP		g729786	170	89	2.00E-17	31	28	homolog of yeast Rael (Bharathi) mRNA-associated protein of 41 kDa (Kraemer) ; MRNA-associated protein MRNP41 (RAE1 protein homolog) ; (U84720) mRNA export protein [Homo sapiens]
22816	ENU06610	ANT61C8186:	22-47	589-614	LINAP		g3766365	454	212	3.00E-54	44	20	
22817	ENU06611	ANT61C7535:	44-62	566-591	LINAP		g4538674	132	70	2.00E-13	34	81	
22818	ENU06612	ANT61C4134:	51-70	790-815	LINAP		g731409	264	124	6.00E-28	39	36	
22819	ENU06613	ANT61C8218:	34-53	447-466	LINAP		g729862	120	64	3.00E-10	32	27	
22820	ENU06614	ANT61C4168:	38-58	429-449	LINAP		g4506399	222	32	3.4			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22821	ENU06615	ANI61C7519:	23-44	802-829	LINAP		g2132156	336	150	2.00E-35	36	45	hypothetical protein YPL030w - yeast (Saccharomyces cerevisiae) ; (U36624)
		6109..4986											Lpb1p [Saccharomyces cerevisiae] (AJ005273) Kin17 [Homo sapiens]
22822	ENU06616	ANI61C4155:	22-47	804-829	LINAP		g3850704	443	94	1.00E-40	44	59	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) A066 ankyrin [Caenorhabditis elegans]
22823	ENU06617	ANI61C7554:	102-128	458-477	LINAP		g1208874	66	57	0.000000	33	8	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) A066 ankyrin [Caenorhabditis elegans]
		1674..2564											(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) A066 ankyrin [Caenorhabditis elegans]
		53..499							08				(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) A066 ankyrin [Caenorhabditis elegans]
22824	ENU06618	ANI61C8221:	33-53	426-445	LINAP		g3451460	72	48	0.000002	26	25	(AL031349) zinc-finger protein [Schizosaccharomyces pombe]
		291..644											(AL031349) zinc-finger protein [Schizosaccharomyces pombe]
22825	ENU06619	ANI61C8238:	22-48	809-829	LINAP		g4115619	254	32	5.3			(AB014768) chitinase [Aeromonas sp. 10S-24]
		1..1254											(AB014768) chitinase [Aeromonas sp. 10S-24]
22826	ENU06620	ANI61C412:5	24-48	808-828	LINAP		g586455	784	73	3.00E-12	37	15	hypothetical 83.0 KD protein in ATP1-ROX3 intergenic region ; hypothetical protein YBL097w - yeast (Saccharomyces cerevisiae) ; (X79489) C-728 protein [Saccharomyces cerevisiae] ; (Z35858) ORF YBL097w [Saccharomyces cerevisiae] (AJ011964) d-lysergyl-peptide-synthetase [Claviceps purpurea] (U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]
		746..3420											(AJ011964) d-lysergyl-peptide-synthetase [Claviceps purpurea] (U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]
22827	ENU06621	ANI61C4161:	29-48	799-823	LINAP		g4499840	1058	109	3.00E-23	35	8	(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
		1..2181											(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
22828	ENU06622	ANI61C8239:	22-44	745-765	LINAP		g1086900	178	86	2.00E-21	37	72	"(AL031525) RNA binding protein, punilio-family [Schizosaccharomyces pombe]"
		1534..748											(AL031525) RNA binding protein, punilio-family [Schizosaccharomyces pombe]"
22829	ENU06623	ANI61C4153:	24-51	441-460	LINAP		g3551484	107	38	0.046			(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
		1988..2361											(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
22830	ENU06624	ANI61C4153:	56-75	765-784	LINAP		g4539278	117	82	5.00E-15	24	20	(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
		3043..4469											(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
22831	ENU06625	ANI61C825:1	22-47	726-745	LINAP		g3560162	674	276	1.00E-73	54	34	(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
		714..2502											(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
22832	ENU06626	ANI61C8266:	59-78	795-814	LINAP		g2842702	544	228	4.00E-59	44	45	probable chitin biosynthesis protein C6G9.12 (CHS5 homolog) ; (Z81317) yeast chs5 homolog [Schizosaccharomyces pombe]
		10..898											probable chitin biosynthesis protein C6G9.12 (CHS5 homolog) ; (Z81317) yeast chs5 homolog [Schizosaccharomyces pombe]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22833	ENU006627	ANI61C4186:	119-138	452-473	LINAP		g1175456	119	78	3.00E-14	34	29	hypothetical 60.5 KD protein C13G6.08 in chromosome I;
		448..1											hypothetical protein SPAC13G6.08 - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative cdc protein [Schizosaccharomyces pombe] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum] "
22834	ENU006628	ANI61C4107:	25-46	796-817	LINAP		g2924313	956	107	1.00E-29	49	18	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22835	ENU006629	ANI61C8222:	22-46	805-829	LINAP		g1723918	178	62	1.00E-10	30	20	(L42758) proteinase [Streptomyces lividans] ; (AL035636) proteinase [Streptomyces coelicolor] (Z83857) ppsc [Mycobacterium tuberculosis]
22836	ENU006630	ANI61C8252:	23-44	661-680	LINAP		g940303	309	111	5.00E-24	29	51	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium] (AB018274) KIAA0731 protein [Homo sapiens]
22837	ENU006631	ANI61C4198:	50-71	457-476	LINAP		g3242253	218	106	8.00E-23	38	7	(U97407) strong similarity to the ATP-binding transport protein family (ABC transporters) [Caenorhabditis elegans] (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
22838	ENU006632	ANI61C8234:	23-48	794-813	LINAP		g2147662	2178	97	1.00E-19	25	11	suppressor of RNA polymerase B SRB4 ; RNA polymerase II suppressor protein SRB4 - yeast (Saccharomyces cerevisiae) ; (L12026) SRB4 [Saccharomyces cerevisiae] ; (U18778) Srb4p: transcription factor [Saccharomyces cerevisiae]
22839	ENU006633	ANI61C8283:	68-87	231-250	LINAP		g3882183	89	66	1.00E-10	35	9	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
22840	ENU006634	ANI61C4234:	122-147	308-330	LINAP		g1943844	201	101	3.00E-21	50	8	
		1..351											
22841	ENU006635	ANI61C4240:	72-91	423-441	LINAP		g3980387	59	57	0.000000			
		2166..1839								1			
22842	ENU006636	ANI61C4216:	22-42	484-509	LINAP		g417806	107	66	2.00E-10	28	22	
		4493..5022											
22843	ENU006637	ANI61C8298:			LINAP		g2408014	288	68	3.00E-11	40	22	
		941..481											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22844	ENU06638	ANI61C4252:	26-53	416-443	LINAP		g3688380	379	147	5.00E-35	51	26	(AJ006267) ClpX-like protein [Homo sapiens]
22845	ENU06639	ANI61C8280:	26-45	603-622	LINAP		g3953466	201	73	3.00E-27	34	28	(AC002328) F20N2.11 [Arabidopsis thaliana]
22846	ENU06640	ANI61C4233:	47-66	803-829	LINAP		g3004489	351	100	1.00E-34	43	75	(AJ223304) geranylgeranyl transferase type I [Schizosaccharomyces pombe]
22847	ENU06641	ANI61C4220:	22-42	806-829	LINAP		g1351690	216	104	8.00E-22	24	47	hypothetical 63.5 KD protein C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
22848	ENU06642	ANI61C8282:	67-86	772-795	LINAP		g3451312	1627	126	3.00E-42	45	17	(AL031324) membrane atpase [Schizosaccharomyces pombe]
22849	ENU06643	ANI61C8303:	41-60	414-438	LINAP		g3879389	147	78	3.00E-14	50	9	(Z83123) Similarity to S.pombe ATP-dependent DNA helicase (SW:Q09811); cDNA EST EMBL:DJ27628 comes from this gene; cDNA EST CEMSC83FB comes from this gene; cDNA EST EMBL:D35012 comes from this gene; cDNA EST yk398a1.3 comes from...
22850	ENU06644	ANI61C4272:	36-55	796-813	LINAP		g4007734	256	44	0.001			(AL034447) putative transmembrane protein [Streptomyces coelicolor]
22851	ENU06645	ANI61C8296:			LINAP		g88462	162	37	0.00001	31	70	"proline-rich phosphoprotein (gene PRH1, Db allele) - human "
22852	ENU06646	ANI61C4276:	46-65	414-433	LINAP		g4505829	108	76	2.00E-13	32	21	gene from NF2/meningioma region of 22q12 ; gene anonymous protein - human ; (L18972) anonymous [Homo sapiens]
22853	ENU06647	ANI61C8291:	23-42	457-479	LINAP		g116415	147	79	2.00E-14	37	8	Cubitus interruptus dominant protein ; DNA-binding protein ci (D) - fruit fly (Drosophila melanogaster) ; (X54360) cld product [Drosophila melanogaster]
22854	ENU06648	ANI61C4283:	37-56	454-473	LINAP		g4507069	143	42	0.000000			"SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ; SNF2alpha protein - human ; (D26155) hSNF2a [Homo sapiens] "

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22855	ENU06649	ANT61C8302: 24-43	2038..668	810-829	LINAP		g2342601	375	95	5.00E-19	27	5	(X89442) peptide synthetase [Methanizium anisopliae]
22856	ENU06650	ANT61C8316: 23-44	932..1611	627-646	LINAP		g1730692	54	49	0.00003			putative transcriptional regulatory protein in BIO3-HXT17 intergenic region ; probable membrane protein YNR063w - yeast (Saccharomyces cerevisiae) ; (Z71678) ORF YNR063w [Saccharomyces cerevisiae]
22857	ENU06651	ANT61C4300: 42-69	1208..773	460-479	LINAP		g4008551	647	144	4.00E-40	52	28	(AL034490) pseudouridyate synthase [Schizosaccharomyces pombe]
22858	ENU06652	ANT61C8320: 24-51	2159..1676	422-449	LINAP		g729298	231	107	6.00E-23			RHO-type GTPase activating protein RGA1/DBM1 ; DBM1 protein - yeast (Saccharomyces cerevisiae) ; (U07421) Dbm1p [Saccharomyces cerevisiae] ; (X90518) ORF O3290 [Saccharomyces cerevisiae] ; (X94335) YOR3290w [Saccharomyces cerevisiae] ; (Z75035) ORF YOR127w [Saccharomyces cerevisiae] ; GTPase-activating protein [Saccharomyces cerevisiae]
22859	ENU06653	ANT61C8338: 22-43	335..752	404-428	LINAP		g1706094	122	76	9.00E-15	34	31	cytochrome P450 4F5 (CYP1F5) ; cytochrome P450 4F5 protein - rat ; (U39207) cytochrome P450 4F5 [Rattus norvegicus]
22860	ENU06654	ANT61C8332: 22-48	2196..1878	271-290	LINAP		g1082604	106	42	0.002			mucin 5AC (clone JER58) - human (fragment) ; (Z34278) mucin [Homo sapiens]
22861	ENU06655	ANT61C8344: 48-70	1..905	787-814	LINAP		g135969	619	274	6.00E-73			TRNA nucleotidyltransferase precursor (TRNA adenylyltransferase) (TRNA CCA-pyrophosphorylase) (CCA-adding enzyme) ; tRNA nucleotidyltransferase - yeast (Saccharomyces cerevisiae) ; (M59870) transfer RNA nucleotidyltransferase [Saccharomyces cerevisiae] ; (U18922) Ccalp: tRNA nucleotidyltransferase(tRNA CCA-pyrophosphorylase) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat nchi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
22862	ENU06656	ANI61C8337: 1..1325	22-46	807-826	LINAP	g3810845	686	243	1.00E-63	46	53		(AL032684) possible ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
22863	ENU06657	ANI61C8362: 962..260	31-53	480-499	LINAP	g3746895	258	98	8.00E-20	36	30		(AF088906) clock-controlled gene-9 protein [Neurospora crassa]
22864	ENU06658	ANI61C8308: 4900..4412	22-48	452-479	LINAP	g729853	62	45	0.0003	29	50		protein-tyrosine-phosphatase precursor ; dual specificity phosphatase (EC 3.1.3.-) IphP - Nostoc commune ; (L11392) protein tyrosine/serine phosphatase [Nostoc commune]
22865	ENU06659	ANI61C8356: 2099..837	50-69	785-804	LINAP	g728850	78	54	0.000001				"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylhydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
22866	ENU06660	ANI61C1000 3:978..1837	22-48	803-822	LINAP	g2132941	157	57	3.00E-18	29	57		probable membrane protein YOR301w - yeast (Saccharomyces cerevisiae) ; (Z75209) ORF YOR301w [Saccharomyces cerevisiae]
22867	ENU06661	ANI61C1002 2:2945..2086	22-49	802-829	LINAP	g2497214	508	114	5.00E-45	44	27		hypothetical 107.7 KD protein in TSP3-IPP2 intergenic region ; probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae]
22868	ENU06662	ANI61C1000 4:2709..669	24-43	792-811	LINAP	g2498597	699	206	1.00E-52	42	27		MRNA transport regulator MTR10 ; MTR10 protein - yeast (Saccharomyces cerevisiae) ; (U55020) Mtr10p [Saccharomyces cerevisiae] ; (Z75068) ORF YOR160w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22869	ENU06663	AN161C1004	22-41	805-829	LINAP		g731872	777	99	3.00E-20	34	26	"putative 108.8 KD transcriptional regulatory protein in FKH1-STH1 intergenic region ; probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae) ; (Z38059)orf, len: 964, CAI: 0.15, possible regulatory protein [Saccharomyces cerevisiae] "
22870	ENU06664	AN161C1006	24-45	713-737	LINAP		g2924771	181	64	0.000000			(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]
22871	ENU06665	AN161C1005	39-58	449-476	LINAP		g1723454	219	55	0.000000	33	25	hypothetical 43.9 KD protein C13G7.10 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69729) hypothetical protein [Schizosaccharomyces pombe] (AC006248) putative copia polyprotein [Arabidopsis thaliana]
22872	ENU06666	AN161C1008	208-229	388-411	LINAP		g4335736	44	64	5.00E-10			hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synecocystis sp.]
22873	ENU06667	AN161C1009	22-48	777-800	LINAP		g1723513	250	64	0.000000	31	49	hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synecocystis sp.]
22874	ENU06668	AN161C1010	22-44	456-479	LINAP		g1652216	93	68	3.00E-11			(AC006248) putative copia polyprotein [Arabidopsis thaliana]
22875	ENU06669	AN161C1008	28-55	502-521	LINAP		g4335736	166	85	1.00E-18	32	14	proline transport protein - Emericella nidulans
22876	ENU06670	AN161C1012	102-121	449-476	LINAP		g630383	178	85	3.00E-16	40	25	"putative 40S ribosomal protein YJR113C ; probable ribosomal protein S7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49613) ORF YJR113c [Saccharomyces cerevisiae] "
22877	ENU06671	AN161C1010	112-139	450-477	LINAP		g1352914	132	63	0.000000	37	40	(AF079900) tetracycline efflux protein [Streptomyces rimosus]
22878	ENU06672	AN161C1015	22-42	279-299	LINAP		g3617954	105	65	4.00E-10			(AF076848) trihydroxyolene oxygenase [Burkholderia cepacia]
22879	ENU06673	AN161C1016	54-77	328-350	LINAP		g3746666	91	57	0.000000	42	30	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description	
22880	ENU06674	ANI61C1011	26-53	457-477	LINAP	g4107286	50	59	0.000000	03		(AL035076) putative zinc-finger protein [Schizosaccharomyces pombe]	
22881	ENU06675	ANI61C1017	66-85	456-478	LINAP	g1877327	162	96	1.00E-19			(Z92771) hypothetical protein Rv3272 [Mycobacterium tuberculosis]	
22882	ENU06676	ANI61C1018	22-41	452-472	LINAP	g47149	90	62	0.000000	003		(X67953) carboxyphosphonoenolpyruvate mutase [Streptomyces hygroscopicus]	
22883	ENU06677	ANI61C1020	42-61	311-332	LINAP	g1942321	69	59	0.000000	01	29	13	"Bacterial Chitinase Complexed With Chitinobiose (Dinag) ; Bacterial Chitinobiose, Glycosyl Hydrolase Family 20"
22884	ENU06678	ANI61C1019	122-149	635-658	LINAP	g2498702	138	55	9.00E-14	35	35		sterigmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
22885	ENU06679	ANI61C1022	36-61	802-829	LINAP	g1709181	283	78	6.00E-14	28	46		"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
22886	ENU06680	ANI61C1023	64-83	461-480	LINAP	g2501427	152	66	9.00E-19	45	24		tyrosinase (monophenol monooxygenase) ; (U66807) tyrosinase [Podospora anserinal] ; (U66808) tyrosinase [Podospora anserinal] (AL033388) leucine-rich repeat protein - weak similarity to adenylate cyclase [Schizosaccharomyces pombe]
22887	ENU06681	ANI61C1062	41-60	576-594	LINAP	g3850105	179	65	3.00E-15	38	17		

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22888	ENU06682	ANI61C1024	22-49	367-386	LINAP		g1172542	267	88	3.00E-27	60	14	dolichyl-phosphate-mannose--protein mannosyltransferase 4 ; dolichyl-phosphate-mannose--protein mannosyltransferase (EC 2.4.1.109)
		0:1709..2074											PMT4 - yeast (Saccharomyces cerevisiae) ; (X83798) PMT4 [Saccharomyces cerevisiae] ; (Z49643) ORF YJR143c [Saccharomyces cerevisiae]
22889	ENU06683	ANI61C1065	41-62	619-639	LINAP		g4584202	123	42	0.000000	29	45	(AJ000394) chromate transport protein [Bacillus cereus]
		1:812..1496								06			(AL023594) protein complex assembly protein [Schizosaccharomyces pombe]
22890	ENU06684	ANI61C1058	22-47	805-829	LINAP		g3150136	460	90	1.00E-18	33	38	regulatory protein algr3 - Pseudomonas aeruginosa
22891	ENU06685	ANI61C1058	22-44	503-528	LINAP		g94816	98	42	0.002			(U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
		9:9595..10143											(AL023518) hypothetical protein [Schizosaccharomyces pombe]
22892	ENU06686	ANI61C1024	23-46	657-681	LINAP		g2673951	324	140	8.00E-33	36	17	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]
		3:722..1											(Z99168) putative heat shock transcription factor [Schizosaccharomyces pombe]
22893	ENU06687	ANI61C1058	100-119	713-732	LINAP		g3130045	203	89	3.00E-17	31	17	(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
		9:10697..1163											(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
22894	ENU06688	ANI61C4949	22-48	756-780	LINAP		g3080393	1399	118	1.00E-34	39	50	glutathione-dependent formaldehyde dehydrogenase (FALDH) ; (L33464) alcohol dehydrogenase 3 [Methylobacter marinus]
		640..2097								0.000000			(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
22895	ENU06689	ANI61C4971	22-46	421-442	LINAP		g3327019	80	63	0.000000			
		681..319								001			
22896	ENU06690	ANI61C4972	22-49	614-633	LINAP		g3184059	536	96	4.00E-48	65	39	
		739..1406											
22897	ENU06691	ANI61C4990	119-144	486-505	LINAP		g1345955	106	46	3.00E-12	31	40	
		809..255											
22898	ENU06692	ANI61C1067	51-70	767-786	LINAP		g3282044	216	99	3.00E-20	35	17	
		2:1359..546											

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22899	ENU06693	ANI61C4929: 2226..1582	52-71	585-603	LINAP		g125727	291	76	5.00E-29			killer toxin alpha and beta subunits precursor (RF2 protein) (endothitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URF2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
22900	ENU06694	ANI61C4929: 5034..5547	25-44	469-493	LINAP		g584748	53	52	0.000004			autolysin (N'-acetylmuramoyl-L-alanine amidase) ; autolysin - Enterococcus faecalis ; (M58002) bacterial cell wall hydrolase [Streptococcus faecalis]
22901	ENU06695	ANI61C1068 1:1252..1586	79-98	360-380	LINAP		g113517	95	72	3.00E-12			alpha-glucosidase precursor (maltase) ; alpha-glucosidase (EC 3.2.1.20) - yeast (Candida tsukubaensis) ; (XS6024) alpha-glucosidase [Pseudozyma tsukubaensis]
22902	ENU06696	ANI61C5004: 495..903	58-77	455-476	LINAP		g1077401	477	151	3.00E-36	49	18	probable membrane protein YLR277c - yeast (Saccharomyces cerevisiae) ; (U17245) Ysh1p: subunit of polyadenylation factor I (PF1) [Saccharomyces cerevisiae]
22903	ENU06697	ANI61C1069 8:1..499	36-59	442-461	LINAP		g2507475	87	57	0.000000	27	9	paired amphipathic helix protein ; regulatory protein SIN3 - yeast (Saccharomyces cerevisiae) ; (Z74746) ORF YOL004w [Saccharomyces cerevisiae]
22904	ENU06698	ANI61C1068 7:2970..2166	22-48	758-784	LINAP		g2618766	327	153	7.00E-38	39	46	(U94362) glycoengin-2 alpha [Homo sapiens]
22905	ENU06699	ANI61C5009: 1519..964	61-80	515-534	LINAP		g1469400	50	34	0.6			(U44088) TDA G51 [Mus musculus]
22906	ENU06700	ANI61C1025 1:1382..3059	22-45	802-829	LINAP		g125935	418	118	6.00E-26	29	44	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]

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22907	ENU06701	ANI61C1027	22-48	804-824	LINAP		g3559970	656	66	8.00E-24	37	28	(AL031514) putative beta-mannosidase [Streptomyces coelicolor]
22908	ENU06702	ANI61C8537: 3561..4370	52-71	765-789	LINAP		g121087	162	56	3.00E-18			GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228) GCY protein (AA 1-312) [Saccharomyces cerevisiae] ; (X90518) ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w [Saccharomyces cerevisiae] ; (X96740) GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w [Saccharomyces cerevisiae] (AL031155) putative amidase [Streptomyces coelicolor]
22909	ENU06703	ANI61C5049: 1594..928	102-121	539-558	LINAP		g3367750	322	81	2.00E-28	46	34	hypothetical 36.9 KD protein C21E11.07 in chromosome 1 ; hypothetical protein SPAC21E11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67999) hypothetical protein [Schizosaccharomyces pombe] (AJ000482) Hormone-sensitive lipase [Sus scrofa] ; (AJ000483) hormone-sensitive lipase [Sus scrofa] (Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22912	ENU06706	ANI61C1070	25-44	726-753	LINAP		g2104438	429	138	2.00E-43	50	22	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22913	ENU06707	ANI61C1027	44-71	472-499	LINAP		g2494132	74	70	9.00E-12			(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22914	ENU06708	ANI61C8658: 1172..303	41-68	802-829	LINAP		g2239203	431	89	2.00E-36	39	92	(Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22915	ENU06709	ANI61C5032: 1..1205	22-49	809-828	LINAP		g2134102	564	198	6.00E-50	48	19	kinesin-like protein 1 - African clawed frog ; (X82012) kinesin-like protein 1 [Xenopus laevis]
22916	ENU06710	ANI61C1024	48-67	537-555	LINAP		g168849	114	77	6.00E-15	33	13	(M80368) pathway-specific regulatory protein [Neurospora crassa] (U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]
22917	ENU06711	ANI61C1024	22-43	803-825	LINAP		g2731377	988	175	3.00E-43	32	29	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22918	ENU06712	ANI61C507.2	89-116	453-479	LINAP		g3080535	391	177	4.00E-44	57	7	(AL022600) RNA helicase [Schizosaccharomyces pombe]
22919	ENU06713	ANI61C1024	22-42	453-479	LINAP		g2495215	184	94	8.00E-19	39	67	hypothetical 20.9 KD protein in ROX1-SPE3 intergenic region ; hypothetical protein YPR067w - yeast (Saccharomyces cerevisiae) ; (Z49219) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
22920	ENU06714	ANI61C1073	42-61	644-671	LINAP		g1351612	256	90	3.00E-29	39	64	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe) PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens] ATP-dependent DNA helicase HUS2 ; hypothetical protein SPAC2G11.12 - fission yeast (Schizosaccharomyces pombe) ; (Z54354) atp-dependent dna helicase hus2 [Schizosaccharomyces pombe] ; (Y09426) DNA-helicase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] hypothetical protein YDR051c - yeast (Saccharomyces cerevisiae) ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74347) ORF YDR051c [Saccharomyces cerevisiae] (D88734) membrane glycoprotein [Equine herpesvirus 1] cell division control protein 2 cognate ; protein kinase (EC 2.7.1.37) cdc2 homolog C - fruit fly (Drosophila sp.) ; (X57486) p34-cdc2 homologue [Drosophila melanogaster]
22921	ENU06715	ANI61C507.3	32-52	481-502	LINAP		g2135950	122	39	0.017			
22922	ENU06716	ANI61C1028	23-46	678-700	LINAP		g1175484	276	110	2.00E-28	41	15	
22923	ENU06717	ANI61C5107	22-46	455-479	LINAP		g1077552	286	135	2.00E-31	40	49	
22924	ENU06718	ANI61C505.1	34-53	810-828	LINAP		g2114323	106	41	0.011	21	32	
22925	ENU06719	ANI61C1028	47-66	365-388	LINAP		g115918	128	63	1.00E-17			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22926	ENU06720	ANI61C1074	22-45	773-790	LINAP		g1351636	860	292	2.00E-78	49	22	hypothetical 143.3 KD TRP-ASP repeats containing protein
		7:1714..362											C12G12.13C in chromosome I ; hypothetical protein SPAC12G12.13c - fission yeast (Schizosaccharomyces pombe)
22927	ENU06721	ANI61C1028	35-58	785-812	LINAP		g112713	184	63	0.000000			"1-aminocyclopropane-1-carboxylate synthase CMW33 (ACC synthase) (S-adenosyl-L-methionine
		8:1152..1											methyllithioadenosine-lyase) ; 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14), wound-induced - winter squash ; (D01032) 1-aminocyclopropane-1-carboxylate synthase [Cucurbita maxima] ; aminocyclopropane carboxylate synthase [Cucurbita maxima] ; aminocyclopropane carboxylate synthase:ISOtype=wound-induced [Cucurbita maxima] "
22928	ENU06722	ANI61C1027	31-50	419-438	LINAP		g586486	90	57	0.000000			hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
		0:612..1042											UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase) ; UDPglucose 4-epimerase (EC 5.1.3.2) - yeast (Pachysolen tannophilus) ; (X68593) UDP-galactose-4-epimerase [Pachysolen tannophilus]
22929	ENU06723	ANI61C8691:	69-87	492-516	LINAP		g729562	442	160	2.00E-44	60	23	phosphate transporter - Glomus versiforme ; (U38650) phosphate transporter [Glomus versiforme] ; phosphate transporter [Glomus versiforme]
		1089..553											
22930	ENU06724	ANI61C8668:	22-45	520-539	LINAP		g2147899	275	77	2.00E-21	40	32	
		600..1											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22931	ENU06725	ANI61C8674:	32-51	673-692	LINAP		g1730741	143	51	0.000000			hypothetical 65.3 KD protein in SUN4-MASS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141)
		2419..1690								0.002			
22932	ENU06726	ANI61C5139:	211-230	628-647	LINAP		g500628	280	120	1.00E-26	37	37	[Saccharomyces cerevisiae] (U05211) Ttp1p [Saccharomyces cerevisiae]
22933	ENU06727	ANI61C1070	22-44	638-657	LINAP		g3219924	276	112	2.00E-24	36	43	hypothetical 57.6 KD protein C30D10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (AL035216) probable involvement in ergosterol biosynthesis [Schizosaccharomyces pombe] (AF038585) pyruvate dehydrogenase kinase isoform 1; [PDK1 [Zea mays] (X97119) pectate lyase [Erwinia chrysanthemi] cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum] putative 89.3 KD transcriptional regulatory protein C1F7.11C ; (AL021837) histone promoter control 2 protein [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae] (S58126) Unknown [Saccharomyces cerevisiae] (AL049497) hypothetical protein [Streptomyces coelicolor] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum] "
		6:6562..5865											
22934	ENU06728	ANI61C8669:	46-65	542-561	LINAP		g4160344	171	88	6.00E-17	51	23	
		627..1											
22935	ENU06729	ANI61C5129:	24-50	446-471	LINAP		g3746431	244	62	0.000000	44	24	
		1253..1604								0.002			
22936	ENU06730	ANI61C1027	22-41	748-775	LINAP		g1765918	190	61	0.000000	34	57	
		8:4789..5584								0.008			
22937	ENU06731	ANI61C1067	22-41	719-743	LINAP		g1083855	388	131	9.00E-30	35	1	
		7:1299..1											
22938	ENU06732	ANI61C5136:	22-44	457-476	LINAP		g1351672	63	38	0.061	21	20	
		1914..1594											
22939	ENU06733	ANI61C1030	22-44	458-479	LINAP		g2894295	162	90	6.00E-18	40	39	
		5:277..769											
22940	ENU06734	ANI61C1067	36-55	805-828	LINAP		g2342601	571	140	1.00E-32	32	5	
		7:3220..1716											
22941	ENU06735	ANI61C8697:	46-70	295-314	LINAP		g4261597	79	55	0.000000	30	11	
		1460..1832								2			
22942	ENU06736	ANI61C5133:	39-58	807-829	LINAP		g4539214	817	177	1.00E-43	52	64	
		2148..974											
22943	ENU06737	ANI61C1077	22-43	454-473	LINAP		g2924313	109	64	6.00E-10	27	15	
		0:1696..2012											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22944	ENU06738	ANT61C8696:	43-63	628-647	LINAP		g2499841	1691	315	3.00E-85	54	31	26S proteasome regulatory subunit MTS4 (19S regulatory CAP region of 26S protease subunit 2) ; (Y09819) 19S regulatory cap region of 26S protease subunit 2 [Schizosaccharomyces pombe]
		2694..628											(AB010740) OsS5a [Oryza sativa]
22945	ENU06739	ANT61C506:1	121-140	307-326	LINAP		g3550985	194	63	8.00E-10	35	34	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
		..420											(AJ007590) XRP2 protein [Homo sapiens]
22946	ENU06740	ANT61C8681:			LINAP		g1293655	407	107	1.00E-22	35	35	DNA-directed RNA polymerase II largest subunit ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Caenorhabditis elegans ; (M29235) RNA polymerase II [Caenorhabditis elegans]
		1356..1											(U58946) transposase [Aspergillus awamori]
22947	ENU06741	ANT61C1079:	26-46	452-479	LINAP		g3550283	80	55	0.000000	31	40	probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
		295..726											(AB002369) KIAA0371 [Homo sapiens]
22948	ENU06742	ANT61C5149:	109-129	571-590	LINAP		g1333322	78	49	0.00003			novel nuclear protein 1 ; NNP-1 protein (D21S2056E) ; (U79775) NNP-1 [Homo sapiens]
		1..620											(AL022071) hypothetical protein [Schizosaccharomyces pombe]
22949	ENU06743	ANT61C1032			LINAP		g1805251	275	92	6.00E-18	30	51	(AL023592) betaine-aldehyde dehydrogenase precursor [Schizosaccharomyces pombe]
		3:115..1300											(U68040) polyketide synthase [Cochliobolus heterostrophus]
22950	ENU06744	ANT61C1077	41-59	262-285	LINAP		g479395	77	51	0.000005	34	6	
		7:2749..3110											
22951	ENU06745	ANT61C1031	29-48	459-479	LINAP		g2224683	121	68	6.00E-11	28	10	
		7:1497..1193											
22952	ENU06746	ANT61C1078	25-46	536-558	LINAP		g4503247	126	55	0.000000	33	29	
		7:109..687											
22953	ENU06747	ANT61C1032	34-53	459-479	LINAP		g2950464	185	75	4.00E-17	55	17	
		1:1452..1008											
22954	ENU06748	ANT61C1032	24-51	453-479	LINAP		g3136055	76	57	0.000000	24	27	
		0:2635..2956											
22955	ENU06749	ANT61C8702:	32-51	710-730	LINAP		g1546072	925	108	7.00E-23	32	10	
		2218..1											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22956	ENU06750	ANI61C8694:	53-72	803-821	LINAP		g481230	566	104	4.00E-30	41	63	L-idiol 2-dehydrogenase (EC 1.1.1.14) precursor - rat ; (X74593) L-idiol 2-dehydrogenase [Rattus norvegicus] (X75561) GTPase activating protein [Saccharomyces cerevisiae] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]
22957	ENU06751	ANI61C5154:	22-49	782-802	LINAP		g414689	329	146	1.00E-34	30	30	
22958	ENU06752	ANI61C1078	27-46	653-674	LINAP		g3600039	103	59	1.00E-10	25	31	
22959	ENU06753	ANI61C8703:	27-46	459-478	LINAP		g2132846	139	73	2.00E-12			probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae] (Z99295) phosphatidyl synthase [Schizosaccharomyces pombe] putative transporter C1B3.16C ; (Z98598) putative transporter [Schizosaccharomyces pombe] (AL023634) hypothetical protein [Schizosaccharomyces pombe] "hypothetical 32.9 KD protein in NFO-FRUA intergenic region ; (U00007) yeiN [Escherichia coli] ; (AE000306) orf, hypothetical protein [Escherichia coli] ; yeiN gene [Escherichia coli] " exocyst complex component SEC3 (PSL1 protein) ; PSL1 protein - yeast (Saccharomyces cerevisiae) ; (L22204) PsiIp [Saccharomyces cerevisiae] ; (U18778) Sec3p [Saccharomyces cerevisiae] (AL031107) putative secreted glucosidase [Streptomyces coelicolor]
22960	ENU06754	ANI61C1079	22-43	804-829	LINAP		g2414601	414	149	3.00E-35	39	43	
22961	ENU06755	ANI61C8703:	66-93	572-591	LINAP		g3183364	178	100	1.00E-20	33	30	
22962	ENU06756	ANI61C1033	116-143	450-473	LINAP		g3150252	62	50	0.00001	38	6	
22963	ENU06757	ANI61C1145	34-54	754-780	LINAP		g465602	389	70	2.00E-11			
22964	ENU06758	ANI61C5147:	22-42	598-625	LINAP		g464482	235	100	1.00E-20	42	11	
22965	ENU06759	ANI61C1081	22-47	804-823	LINAP		g3334796	373	154	1.00E-45	41	55	

Sequence Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22966	ENU06760	ANI61C1147	22-44	452-479	LINAP		g127992	117	31	6			"beta(1-->2)glucan export ATP-binding protein NDVA ; beta-1,2-glucan export protein ndvA - Rhizobium meliloti ; (M20726) ndvA peptide (put.); putative [Rhizobium meliloti]"
22967	ENU06761	ANI61C8695:	22-44	460-479	LINAP		g1799532	77	59	0.000000	33	38	(AB000564) salicylate hydroxylase [Sphingomonas sp.]
22968	ENU06762	ANI61C5176:	40-59	572-591	LINAP		g2193933	66	46	0.0002			(Z96800) hypothetical protein Rv0312 [Mycobacterium tuberculosis]
22969	ENU06763	ANI61C1079	27-46	767-786	LINAP		g1020413	464	143	2.00E-33	34	50	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
22970	ENU06764	ANI61C1032	22-49	807-829	LINAP		g3023956	787	256	2.00E-67	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
22971	ENU06765	ANI61C8710:			LINAP		g3367797	472	208	2.00E-53	55	22	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
22972	ENU06766	ANI61C5177:	108-127	454-477	LINAP		g4191793	71	40	0.000000			(AC005917) putative zinc finger protein [Arabidopsis thaliana]
22973	ENU06767	ANI61C1079	22-43	732-751	LINAP		g4455664	347	166	2.00E-40	37	13	(AL035480) putative polyketide synthase [Mycobacterium leprae]
22974	ENU06768	ANI61C1032	40-59	490-508	LINAP		g2582351	370	164	4.00E-40	43	40	(AF018639) unknown [Dictyostelium discoideum]
22975	ENU06769	ANI61C5177:	22-49	456-479	LINAP		g1703534	68	67	7.00E-11	43	29	(U80030) short region of weak similarity to rat dihydroxypolyprenylbenzoate methyltransferase (GI:457372) [Caenorhabditis elegans]
22976	ENU06770	ANI61C1082	36-55	648-669	LINAP		g3023956	801	243	6.00E-69	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
22977	ENU06771	ANI61C1034	25-44	802-829	LINAP		g1352911	983	112	2.00E-35	41	38	hypothetical 80.2 KD protein in CPA2-NNF1 intergenic region ; hypothetical protein YJR110w - yeast (Saccharomyces cerevisiae) ; (Z49610) ORF YJR110w [Saccharomyces cerevisiae]

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22978	ENU06772	ANI61C1147	22-47	809-829	LINAP		g1708195	190	66	5.00E-11			HFM1 protein ; (U22156) Hfm1p [Saccharomyces cerevisiae]
22979	ENU06773	6:3430..2272	22-47	805-829	LINAP		g538067	461	141	6.00E-33	34	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
22980	ENU06774	9:2123..721	22-46	805-824	LINAP		g1723769	247	55	0.000000			putative transporter YGR260W ; probable membrane protein YGR260w - yeast [Saccharomyces cerevisiae] ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
22981	ENU06775	ANI61C1081	22-41	495-518	LINAP		g127060	184	77	4.00E-24	40	92	zinc finger protein MFG-1 (zinc finger protein 58) ; finger protein mfg1 - mouse (fragment) ; (M28513) zinc finger protein mfg1 mRNA (put.) ; putative [Mus musculus] elongation factor 3B (EF-3B) ; probable membrane protein YNL014w - yeast [Saccharomyces cerevisiae] ; (Z71290) ORF YNL014w [Saccharomyces cerevisiae]
22982	ENU06776	ANI61C1034	22-46	779-806	LINAP		g1706591	412	175	3.00E-43	48	23	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) alpha chain - yeast (Candida albicans) ; (L29063) fatty acid synthase alpha subunit [Candida albicans] " (AJ011849) fengycin synthetase [Bacillus subtilis]
22983	ENU06777	ANI61C1030	43-62	807-826	LINAP		g1169645	227	32	5.3			(AF000149) ATP-binding cassette transporter [Mus musculus] (AL033389) putative antioxidant protein [Schizosaccharomyces pombe]
22984	ENU06778	ANI61C5932:	22-41	771-791	LINAP		g3724089	212	58	4.00E-16	35	8	sepB protein - Emericella nidulans ; sepB protein - Emericella nidulans ; (X86399) sepB [Emericella nidulans]
22985	ENU06779	9680..11615	22-46	798-825	LINAP		g2547314	466	192	3.00E-48	40	12	
22986	ENU06780	ANI61C5187:	22-44	454-477	LINAP		g3850080	120	58	3.00E-14			
22987	ENU06781	ANI61C1148	25-46	737-755	LINAP		g1078634	2239	323	e-127	97	35	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score 413	Blast Score 171	Blast Prob 4.00E-43	% id 57	% cvrg 90	Description
22988	ENU06782	ANI61C6060: 1366..2025	58-83	482-501	LINAP		g549628	413	171	4.00E-43	57	90	hypothetical 22.1 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YKRO68c - yeast (Saccharomyces cerevisiae) ; (Z28293) ORF YKRO68c [Saccharomyces cerevisiae]
22989	ENU06783	ANI61C1080: 7:3996..5261	53-72	807-829	LINAP		g125727	533	90	8.00E-35			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URF2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
22990	ENU06784	ANI61C6076: 359..1325	27-46	802-829	LINAP		g3560253	470	139	7.00E-37	50	39	(AL031532) sap2 family putative cell cycle dependent phosphatase associated protein [Schizosaccharomyces pombe] (AJ224865) IgE-binding protein [Aspergillus fumigatus]
22991	ENU06785	ANI61C1148: 4:3284..3668	22-47	423-448	LINAP		g2980819	135	88	5.00E-17			alpha-glucosidase precursor (malase) ; (D45356) alpha-glucosidase [Aspergillus niger] (Y12527) HMWP1 protein [Yersinia enterocolical] (AF030886) telomere-associated recQ-like helicase [Ustilago maydis]
22992	ENU06786	ANI61C8728: 1012..2089	29-51	805-827	LINAP		g3023267	950	209	8.00E-58	45	26	HST1 protein (homologous TO SIR2 protein 1) ; HST1 protein - yeast (Saccharomyces cerevisiae) ; (L47120) homolog of SIR2; transcribed ORF flanked by NUF2 (X72225) and RTG1 (M97690) [Saccharomyces cerevisiae] ; (U39041) Hst1p [Saccharomyces cerevisiae] ; (Z74810) ORF YOL068c [Saccharomyces cerevisiae]
22993	ENU06787	ANI61C6090: 1..364	63-80	308-327	LINAP		g2765195	79	58	0.000000			
22994	ENU06788	ANI61C1163: 1..518	72-92	469-488	LINAP		g2642224	61	57	0.000000	26	16	
22995	ENU06789	ANI61C1084: 6:668..1854	49-67	766-785	LINAP		g1708325	638	137	9.00E-32	45	46	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22996	ENU06790	ANI61C8729: 5126..5536			LINAP		g1731071	66	72	2.00E-12	30	35	hypothetical 47.0 KD protein in GLNQ-ANSR intergenic region ; (D84432) Y qjH [Bacillus subtilis] ; (Z99116) similar to DNA-damage repair protein [Bacillus subtilis] (AF024496) contains similarity to Plasmodium falciparum glycophorin-binding protein homolog 2 (GB:X69769) [Caenorhabditis elegans] (AB002377) KIAA0379 [Homo sapiens]
22997	ENU06791	ANI61C5223: 23-44 2348..825		805-827	LINAP		g2394451	212	59	0.000000	31	18	(M74066) Major body wall myosin [Onchocerca volvulus] (AP000003) 348aa long hypothetical dehydrogenase [Pyrococcus horikoshii] regulatory protein CYS-3 ; regulatory protein cys-3 - Neurospora crassa ; (M26008) cys-3 [Neurospora crassa] (AL034563) putative yeast CF Ib (RNA3' Cleavage factor Ib) homolog; ribonucleoprotein [Schizosaccharomyces pombe]
22998	ENU06792	ANI61C1086 1:302..1	97-117	432-451	LINAP		g2224699	117	80	1.00E-14	31	18	cell cycle protein kinase CDC5/MSD2 ; protein kinase CDC5 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (M84220) PKX2 protein kinase [Saccharomyces cerevisiae] ; (Z48613) Cdc5p [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
22999	ENU06793	ANI61C1036 5:1658..1991	30-49	364-385	LINAP		g159893	80	52	0.000004			(AL049559) protein kinase cek1 [Schizosaccharomyces pombe]
23000	ENU06794	ANI61C5213: 1108..1539			LINAP		g3257063	123	45	1.00E-10			Leucine rich repeat containing protein [Schizosaccharomyces pombe] " (AE001017) conserved hypothetical protein [Archaeoglobus fulgidus]
23001	ENU06795	ANI61C1085 6:2845..2191	22-48	593-620	LINAP		g118126	226	71	9.00E-12	33	91	UV-endonuclease - Neurospora crassa
23002	ENU06796	ANI61C1034 9:3166..4194	44-64	797-816	LINAP		g4049514	642	153	2.00E-45	49	53	
23003	ENU06797	ANI61C1178: 1625..2522	22-49	772-799	LINAP		g416768	438	203	1.00E-51	41	36	
23004	ENU06798	ANI61C8746: 619..1315	39-58	639-658	LINAP		g4499843	203	74	9.00E-13	37	40	
23005	ENU06799	ANI61C5230: 2738..464	25-52	806-829	LINAP		g4581521	696	240	7.00E-63	68	12	
23006	ENU06800	ANI61C1085 8:3973..4384	22-45	263-289	LINAP		g3581887	234	92	2.00E-18	34	15	
23007	ENU06801	ANI61C1086 0:2530..2876	22-45	437-458	LINAP		g2649315	98	63	0.000000	29	65	
23008	ENU06802	ANI61C1037 8:900..1809	22-48	803-827	LINAP		g1362529	1047	391	e-108	69	40	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23009	ENU06803	ANT61C1037	22-49	805-824	LINAP		g2655202	1286	206	3.00E-70	56	32	(AF026402) U5 snRNP 100 kD protein [Homo sapiens]
23010	ENU06804	ANT61C9209: 6:2137..433	22-44	522-541	LINAP		g3914934	129	99	2.00E-20			probable RNA 3'-terminal phosphate cyclase (RNA-3'-phosphate cyclase) (RNA cyclase) ; (AP000006) 369aa long hypothetical phosphate cyclase [Pyrococcus horikoshii]
		8281..7674											(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
23011	ENU06805	ANT61C9263: 1380..883	22-43	441-460	LINAP		g2414601	235	106	8.00E-23	43	28	zinc finger protein 183 ; (X98253) ZNF183 [Homo sapiens] ; (AC002477) zinc-finger protein [Homo sapiens] (AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
23012	ENU06806	ANT61C5998: 10102..10727	135-158	484-503	LINAP		g3123165	372	167	7.00E-41	42	57	regulatory protein GAL4 ; regulatory protein GAL4 - yeast (Saccharomyces cerevisiae) ; (K01486) GAL4 protein [Saccharomyces cerevisiae] ; (Z67751) GAL4 [Saccharomyces cerevisiae] ; (Z73604) ORF YPL248c [Saccharomyces cerevisiae]
23013	ENU06807	ANT61C9250: 3162..4281	37-56	798-825	LINAP		g2257514	480	182	2.00E-45	39	49	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] "succinyl-CoA ligase (GDP-forming), beta-chain precursor (succinyl-CoA synthetase, beta chain) (SCS-beta) ; beta-succinyl CoA synthetase - rumen fungus (Neocallimastix frontalis) ; (X84222) beta-succinyl CoA synthetase [Neocallimastix frontalis] " (U58946) transposase [Aspergillus awamori]
23014	ENU06808	ANT61C8731: 4890..3869	59-78	807-829	LINAP		g1169823	219	109	2.00E-23	28	28	(AL031764) putative FAD synthetase [Schizosaccharomyces pombe] (AL033534) serine-rich protein [Schizosaccharomyces pombe]
23015	ENU06809	ANT61C5930: 388..933	175-195	499-518	LINAP		g125935	56	45	0.0004	24	24	[Schizosaccharomyces pombe]
23016	ENU06810	ANT61C120:1 015..1	30-57	797-824	LINAP		g1711577	697	222	2.00E-68	53	61	
23017	ENU06811	ANT61C5930: 3180..1803	24-43	803-822	LINAP		g1805251	1122	289	1.00E-77	50	50	
23018	ENU06812	ANT61C5245: 452..1	104-127	451-477	LINAP		g3668151	111	59	0.000000	32	52	
23019	ENU06813	ANT61C9251: 295..851	23-47	513-536	LINAP		g3873550	105	50	0.00002	28	34	

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23020	ENU06814	ANI61C8754:	23-48	783-810	LINAP		g138350	121	57	0.000000	1		glycoprotein X precursor ; glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p) ; (M86664) membrane glycoprotein [Equine herpesvirus 1] "(AJ223012) rifamycin polypeptide synthase, type 1 [Amycolatopsis mediterranei] ; (AF040570) polypeptide synthase [Amycolatopsis mediterranei]
23021	ENU06815	ANI61C6099:	22-46	575-602	LINAP		g2764761	51	34	0.0006			hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...
23022	ENU06816	ANI61C1086	22-46	780-806	LINAP		g1353088	176	89	4.00E-17	32	69	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...
23023	ENU06817	ANI61C1159:	27-46	616-640	LINAP		g1703266	249	109	2.00E-23	41	43	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...
23024	ENU06818	ANI61C6067:			LINAP		g3879121	265	128	4.00E-29			hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...
23025	ENU06819	ANI61C5243:	109-132	364-391	LINAP		g1711534	261	112	1.00E-24	47	37	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...

Sequence Overview

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23026	ENU06820	ANI61C1160:	22-45	663-690	LINAP		g119164	271	134	5.00E-31	40	48	elongation factor 1-gamma (EF-1-gamma) ; translation elongation factor eEF-1 gamma chain - brine shrimp ; (M28020) elongation factor 1-gamma [Artemia sp.]
23027	ENU06821	ANI61C9253:			LINAP		g2494878	828	319	1.00E-89	90	55	guanine nucleotide-binding protein alpha subunit ; (U49917) Fada [Emeticella nidulans]
23028	ENU06822	ANI61C8748:	22-45	654-679	LINAP		g1172741	337	111	1.00E-37	40	36	peptide transporter PTR2 ; (U09781) peptide transporter [Candida albicans]
23029	ENU06823	ANI61C9281:	48-67	769-789	LINAP		g4164426	403	159	2.00E-38	42	29	(AL035247) putative spindle pole body-associating protein [Schizosaccharomyces pombe]
23030	ENU06824	ANI61C8743:	23-50	570-589	LINAP		g1729825	101	47	6.00E-10	31	57	transaldolase ; transaldolase (EC 2.2.1.2) - yeast (Saccharomyces cerevisiae) ; (U19102) Tal1p: Transaldolase [Saccharomyces cerevisiae]
23031	ENU06825	ANI61C5255:	22-46	451-478	LINAP		g1176486	114	80	1.00E-14	34	25	hypothetical 63.9 KD protein in IME2-MEF2 intergenic region ; protein YKR029c homolog YJL105w - yeast (Saccharomyces cerevisiae) ; (X85021) YKR029c homologue [Saccharomyces cerevisiae] ; (Z49380) ORF YJL105w [Saccharomyces cerevisiae]
23032	ENU06826	ANI61C1084	22-45	572-592	LINAP		g2493399	74	77	1.00E-13			putative cytochrome P450 T10B9.5 in chromosome II ; (Z48717) similar to cytochrome P450 [Caenorhabditis elegans]
23033	ENU06827	ANI61C9282:	22-43	449-468	LINAP		g731628	436	167	2.00E-44	59	44	putative mitochondrial carrier YHR002W ; hypothetical protein YHR002w - yeast (Saccharomyces cerevisiae) ; (U10555) Yhr002wp [Saccharomyces cerevisiae]

Sequence Alignment

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23034	ENU06828	ANI6IC8744:	39-58	803-822	LINAP		g1175977	738	185	3.00E-58	47	48	hypothetical 61.8 KD peptidase in MPRI-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae]
23035	ENU06829	ANI6IC6078:	23-43	446-473	LINAP		g284667	100	36	0.13			neurofilament triplet H1 protein - rabbit (fragment) ; (M94315) neurofilament-H [Oryctolagus cuniculus]
23036	ENU06830	ANI6IC5244:	26-46	562-584	LINAP		g586937	171	34	0.66			zinc-finger protein 2 (zinc-finger homeodomain protein 2) ; homeotic protein zfh-2 - fruit fly (Drosophila melanogaster) ; (M63450) zinc-finger homeodomain protein 2 [Drosophila melanogaster]
23037	ENU06831	ANI6IC1088	22-47	656-675	LINAP		g2492758	123	38	2.00E-10	34	66	probable short-chain type dehydrogenase/reductase VDLC
23038	ENU06832	ANI6IC8753:	52-71	807-829	LINAP		g114967	244	71	2.00E-17	35	30	beta-glucosidase (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) - Agrobacterium tumefaciens ; (M59852) beta-D-glucosidase [Agrobacterium tumefaciens]
23039	ENU06833	ANI6IC527:1	25-44	306-325	LINAP		g4587324	142	39	0.011			(AB025420) Family 19 chitinase (PRYA1 ORF) [Aeromonas sp. 10S-24]
23040	ENU06834	ANI6IC1187:	54-73	459-478	LINAP		g1652749	201	117	4.00E-26	45	65	(D90908) hypothetical protein [Synechocystis sp.]
23041	ENU06835	ANI6IC1089	38-59	781-800	LINAP		g4107289	654	94	2.00E-18	32	47	(AL035076) putative carboxylesterase-lipase family member [Schizosaccharomyces pombe]
23042	ENU06836	ANI6IC1090	22-47	464-483	LINAP		g1945094	145	48	0.00004	31	51	(D88802) ydhJ [Bacillus subtilis] ; (Z99107) similar to hypothetical proteins [Bacillus subtilis]
23043	ENU06837	ANI6IC6147:	45-64	801-820	LINAP		g1346290	423	137	1.00E-31	33	45	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]

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23044	ENU06838	ANI61C9285: 1551..941	58-77	568-590	LINAP	g1082283	125	34	0.78				protein kinase (EC 2.7.1.37) cdc2-related PITS/LRE alpha 2-1 - human (X91243) XrpFbeta1 [Xenopus laevis]
23045	ENU06839	ANI61C8762: 2587..2010	25-52	530-557	LINAP	g992626	64	49	0.00003	29	35		(AF026032) ATRX protein [Mus musculus]
23046	ENU06840	ANI61C6148: 536..1492			LINAP	g3002558	72	57	0.000000	26	9		hypothetical 73.8 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL125c - yeast (Saccharomyces cerevisiae) ; (Z46843) orf23 [Saccharomyces cerevisiae] ; (Z69382) Identical to putative protein ESBP6 [Saccharomyces cerevisiae] ; (Z71401) ORF YNL125c [Saccharomyces cerevisiae]
23047	ENU06841	ANI61C1210: 4317..3508	47-73	740-759	LINAP	g1730773	211	103	2.00E-21				(D89164) unnamed protein product [Schizosaccharomyces pombe]
23048	ENU06842	ANI61C9292: 2016..1490	23-50	480-506	LINAP	g1749536	235	103	8.00E-22	45	44		"epoxide hydrolase (microsomal epoxide hydrolase) (epoxide hydratase) ; epoxide hydrolase (EC 3.3.2.3), microsomal - rabbit ; (M21496) microsomal epoxide hydrolase (EC 3.3.2.3) [Oryctolagus cuniculus]" (AC002294) Similar to transcription factor gblZ46606 1658307 and others [Arabidopsis thaliana]
23049	ENU06843	ANI61C8740: 2899..2451	64-83	459-478	LINAP	g123927	84	54	1.00E-12				"(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]" (AF052435) odd-paired-like [Danio rerio]
23050	ENU06844	ANI61C6153: 1472..1033			LINAP	g2443887	166	61	0.000000	29	11		(M77661) putative pol polypeptide [Magnaporthe grisea]
23051	ENU06845	ANI61C5274: 1181..611	53-74	528-549	LINAP	g3850821	247	33	1.8	45	26		(U58946) transposase [Aspergillus awamori]
23052	ENU06846	ANI61C1214: 3821..4206	22-44	364-391	LINAP	g3283028	182	53	8.00E-17	40	30		
23053	ENU06847	ANI61C9286: 2977..4449	22-45	775-795	LINAP	g538067	718	270	7.00E-72	47	20		
23054	ENU06848	ANI61C876: 037..324			LINAP	g1805251	475	190	8.00E-48	42	42		

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23055	ENU06849	ANI61C526:1	25-45	662-689	LINAP		g3219917	167	89	3.00E-17	31	85	hypothetical 27.4 KD protein C30D10.14 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
23056	ENU06850	ANI61C1092			LINAP		g493955	223	71	1.00E-11	35	38	Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase) ; Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase) (AB002377) KIAA0379 [Homo sapiens]
23057	ENU06851	ANI61C9299:1..642	105-124	597-616	LINAP		g2224699	133	49	2.00E-13	32	23	hypothetical 55.5 KD GTP-binding protein in CDC23-DBP8 intergenic region ; probable purine nucleotide-binding protein YHR168w - yeast (Saccharomyces cerevisiae) ; (U00027) Yhr168wp [Saccharomyces cerevisiae]
23058	ENU06852	ANI61C122:3	22-49	278-304	LINAP		g731739	188	92	1.00E-18	50	19	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
23059	ENU06853	ANI61C8758:2220..998	22-47	807-827	LINAP		g3367789	530	109	2.00E-23	48	50	(U13646) homeotic region most like HMPB_DROME: homeotic proboscipedia protein [Caenorhabditis elegans]
23060	ENU06854	ANI61C6155:917..201	22-41	629-647	LINAP		g532113	77	41	0.01			probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae) ; (U28371) P9584.4 gene product [Saccharomyces cerevisiae]
23061	ENU06855	ANI61C5259:3275..2159	33-54	809-828	LINAP		g2133035	226	82	8.00E-30	36	51	(X89442) peptide synthetase [Metarhizium anisopliae]
23062	ENU06856	ANI61C9288:2693..896	27-53	801-828	LINAP		g2342601	408	101	9.00E-21	29	5	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
23063	ENU06857	ANI61C8774:3868..3465	22-48	272-291	LINAP		g1729996	69	54	0.000000	29	51	(AL021428) hypothetical protein Rv0063 [Mycobacterium tuberculosis]
23064	ENU06858	ANI61C6159:2762..3303	54-73	477-494	LINAP		g2808720	152	55	0.000000	32	27	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti]
23065	ENU06859	ANI61C5247:1364..936	30-50	454-476	LINAP		g1353088	151	75	3.00E-13	34	37	

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23066	ENU06860	ANT61C1092	22-42	529-552	LINAP		g3023677	67	50	0.00001			probable translation initiation factor EIF-2B gamma subunit (EIF-2B GDP-GTP exchange factor) ; (Z98602) translation initiation factor eif-2b gamma subunit [Schizosaccharomyces pombe]
23067	ENU06861	ANT61C8761: 4912..402			LINAP		g3080535	4244	395	e-109	67	14	(AL022600) RNA helicase [Schizosaccharomyces pombe]
23068	ENU06862	ANT61C6176: 800..1	45-63	753-779	LINAP		g3122874	354	105	2.00E-35	37	50	D-3-phosphoglycerate dehydrogenase (PGDH) ; phosphoglycerate dehydrogenase (EC 1.1.1.95) - Methanococcus jannaschii ; (U67544) phosphoglycerate dehydrogenase (serA) [Methanococcus jannaschii]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23070	ENU06864	AN161C9267: 7363..7704	22-47	416-435	LINAP		g1706177	147	48	0.00004	38	15	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisil]
23071	ENU06865	AN161C8784: 2558..1722	28-53	762-781	LINAP		g2781417	162	109	3.00E-23	25	15	(AF081920) polyketide synthase type I; PtC [Pseudomonas fluorescens]
23072	ENU06866	AN161C6188: 1002..282	93-113	678-700	LINAP		g4102999	440	168	3.00E-41	46	64	(AF019630) pathogenicity protein [Magnaporthe grisea]
23073	ENU06867	AN161C5275: 1687..3309	40-59	756-783	LINAP		g1176583	924	162	3.00E-61	49	28	hypothetical 102.5 KD protein in KRE1-HXT14 intergenic region ; probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae) ; (Z46259) NO339 [Saccharomyces cerevisiae] ; (Z71597) ORF YNL321w [Saccharomyces cerevisiae] (Z99163) similar to nitrogen permease regulator. [Schizosaccharomyces pombe]
23074	ENU06868	AN161C1191: 11557..10509	45-68	784-808	LINAP		g2832742	576	199	3.00E-50	42	59	(AF111179) G-septin alpha [Rattus norvegicus]
23075	ENU06869	AN161C8791: 1038..702	22-48	331-352	LINAP		g4455009	91	60	0.000000	01		(AB010442) PMR1 [Penicillium digitatum]
23076	ENU06870	AN161C6183: 1..1296	45-72	742-767	LINAP		g3288709	997	139	2.00E-62	50	18	hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRP127 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018 [Saccharomyces cerevisiae]
23077	ENU06871	AN161C1191: 11790..13388	22-48	730-749	LINAP		g586394	369	100	9.00E-23			(U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]
23078	ENU06872	AN161C8759: 5302..4296	52-71	779-798	LINAP		g1173638	301	144	7.00E-34	30	75	

Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23079	ENU06873	ANI61C5284:	82-101	712-732	LINAP		g1168817	847	136	1.00E-48	52	20	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7 [Schizosaccharomyces pombe] (U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA yk184h5.3; coded for by C. elegans cDNA yk184h5.5; coded for by C. elegans cDNA yk13d7.3; coded for by C. elegans cDNA yk13d7.5; coded for by C. elegans cDNA yk31e1.5; co... ; (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans] proline utilization trans-activator ; transcription activator PUT3 - yeast (Saccharomyces cerevisiae) ; (X55384) proline utilization trans-activator [Saccharomyces cerevisiae] ; (X74152) orf5; homologous to S.cerevisiae PUT3 gene [Saccharomyces cerevisiae] ; (Z28015) ORF YKL015w [Saccharomyces cerevisiae] PIM1 protein ; pim1 hypothetical protein - fission yeast (Schizosaccharomyces pombe) (AF041382) microtubule binding protein D-CLIP-190 [Drosophila melanogaster] (AL049608) putative protein [Arabidopsis thaliana] cell-cycle nuclear autoantigen SG2NA (S/G2 nuclear antigen) ; nuclear autoantigen - human ; (U17989) GS2NA [Homo sapiens]
23080	ENU06874	ANI61C1093:	61-87	587-614	LINAP		g1397341	85	44	7.00E-10	35	23	
23081	ENU06875	ANI61C1212:	22-48	503-528	LINAP		g131653	62	45	0.000008			
23082	ENU06876	ANI61C5251:	49-68	433-452	LINAP		g132172	108	63	0.000000	26	28	
23083	ENU06877	ANI61C1095	22-47	565-584	LINAP		g2773363	85	52	0.000002	26	11	
23084	ENU06878	ANI61C6137:	22-45	599-618	LINAP		g4584545	125	84	7.00E-16	35	55	
23085	ENU06879	ANI61C2185:	71-90	455-476	LINAP		g3122872	177	65	3.00E-11	31	20	

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23086	ENU06880	ANI61C1239:	98-118	456-474	LINAP		g547902	89	35	0.37			putative nucin core protein precursor 24 (multi-glycosylated core protein 24) (MGC-24) (MUC-24) (CD164 antigen) ; core protein MGC-24 - human ; (D14043) MGC-24 precursor [Homo sapiens]
23087	ENU06881	ANI61C2134:	24-51	506-529	LINAP		g559044	160	68	4.00E-11	26	27	(L29296) alpha-adducin [Homo sapiens]
23088	ENU06882	ANI61C8786:	22-48	609-629	LINAP		g559964	145	52	4.00E-15	40	68	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
23089	ENU06883	ANI61C6181:	22-49	803-828	LINAP		g2842510	423	96	2.00E-19	26	30	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
23090	ENU06884	ANI61C5251:	24-45	741-765	LINAP		g1076802	106	64	0.000000	34	11	extensin-like protein - maize ; (Z34465) extensin-like protein [Zea mays] ; extensin-like domain [Zea mays]
23091	ENU06885	ANI61C1216:	22-48	806-829	LINAP		g538067	2006	169	2.00E-41	38	19	(M77661) putative pol polypeptide [Magnaporthe grisea]
23092	ENU06886	ANI61C8786:	22-49	675-693	LINAP		g1709181	249	42	0.000000	36	40	"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
23093	ENU06887	ANI61C1216:	28-47	804-829	LINAP		g2132868	160	34	1.4			probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae) ; (Z74961) ORF YOR053w [Saccharomyces cerevisiae] ; (Z70678) YOR29-04 [Saccharomyces cerevisiae] (AF074951) cellulose dehydrogenase [Thielavia heterothallica]
23094	ENU06888	ANI61C1096	22-47	586-605	LINAP		g3319315	340	150	1.00E-35	38	26	cytochrome P450 3A2 (CYP3A2) (P450-PCN2) ; cytochrome P450 3A2 - rat ; (M13646) cytochrome P450 [Rattus norvegicus]
23095	ENU06889	ANI61C2160:	102-126	447-474	LINAP		g117154	113	66	1.00E-10	34	23	cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum]
23096	ENU06890	ANI61C9256:	23-42	805-829	LINAP		g1083855	340	96	2.00E-19	25	1	

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23097	ENU06891	ANT61C8777: 22-48		804-829	LINAP		g1491795	672	248	4.00E-65	47	28	"(U39812) beta-1,4-mannanase [Caldicellulosiuptor saccharolyticus]"
23098	ENU06892	2603..1599 ANT61C6218: 37-57		809-828	LINAP		g4522004	160	94	9.00E-19	31	38	"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]"
23099	ENU06893	ANT61C5291: 22-44		615-638	LINAP		g3850084	85	83	1.00E-15	37	62	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
23100	ENU06894	1929..1250 ANT61C9272: 83-102		603-625	LINAP		g2773203	545	224	8.00E-61	51	43	(AF039713) Similar to phosphoglycerate mutase, coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f9; coded for by C. elegans cDNA cm18g...
23101	ENU06895	ANT61C8802: 22-46		793-812	LINAP		g3395351	350	79	3.00E-14	29	25	(AB012696) DNA polymerase V [Schizosaccharomyces pombe]; (AL022305) DNA polymerase V [Schizosaccharomyces pombe]
23102	ENU06896	ANT61C5300: 22-41		453-473	LINAP		g2120949	87	77	9.00E-14	37	28	lipase-like enzyme - Alcaligenes eutrophus; (L36817) lipase-like enzyme [Alcaligenes eutrophus]; ORF 8 [Ralstonia eutropha]
23103	ENU06897	ANT61C1095 0:1..423		376-400	LINAP		g1181493	97	61	0.000000	33	21	"(U42580) 4 ankyrin repeats; similar to Drosophila melanogaster ankyrin, encoded by GenBank Accession Number L35601 [Paramecium bursaria Chlorella virus 1]"
23104	ENU06898	ANT61C219:1 22-48		595-615	LINAP		g3757521	302	121	4.00E-27	40	17	(AC005167) unknown protein [Arabidopsis thaliana]
23105	ENU06899	677..2320 ANT61C9301: 23-46		414-432	LINAP		g2673951	172	50	4.00E-14	31	11	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
23106	ENU06900	ANT61C8766: 34-53		802-821	LINAP		g2494692	999	118	6.00E-26	36	22	(X94300) wc-1 protein (WC1); (AL049495) hypothetical protein [Schizosaccharomyces pombe]
23107	ENU06901	ANT61C219:3 22-47		781-800	LINAP		g4539260	123	53	0.000003			

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23108	ENU06902	ANI61C8806: 1480..1947	29-50	444-463	LINAP		g1723291	489	150	6.00E-36	47	69	hypothetical 26.3 KD protein C13D6.03C in chromosome I ; (Z69725) unknown [Schizosaccharomyces pombe]
23109	ENU06903	ANI61C625: 70..1414	39-58	626-643	LINAP		g464347	135	82	3.00E-15	29	17	peroxisome biosynthesis protein PASS (peroxin-6) ; (Z22556) PASS [Pichia pastoris]
23110	ENU06904	ANI61C5296: 1627..3637	53-80	724-746	LINAP		g2094857	599	108	5.00E-23	42	32	(Z95334) unknown [Schizosaccharomyces pombe]
23111	ENU06905	ANI61C1098: 2023..2692	22-44	627-649	LINAP		g3980042	135	85	6.00E-16			(AL033514) similar to ABC transporters ; ABC transporter transmembrane region. [Caenorhabditis elegans]
23112	ENU06906	ANI61C8822: 2014..319	31-50	778-804	LINAP		g4262148	772	190	1.00E-47	40	35	(AC005275) predicted protein of unknown function [Arabidopsis thaliana]
23113	ENU06907	ANI61C6255: 642..1	143-170	592-612	LINAP		g2388993	392	98	1.00E-35	49	10	(Z98981) putative sodium channel [Schizosaccharomyces pombe]
23114	ENU06908	ANI61C5309: 1418..1978	52-71	489-510	LINAP		g2498971	131	64	0.000000	37	26	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
23115	ENU06909	ANI61C8764: 920..4304	23-48	809-828	LINAP		g1175466	1302	215	2.00E-55	43	23	hypothetical 126.9 KD protein C22G7.04 in chromosome I ; hypothetical protein SPAC22G7.04 - fission yeast (Schizosaccharomyces pombe) ; (Z54328) putative poly(a)-specific ribonuclease subunit [Schizosaccharomyces pombe]
23116	ENU06910	ANI61C6247: 1889..2799	65-84	803-829	LINAP		g119857	1026	309	2.00E-83	72	80	fibritarin (nucleolar protein 1) ; nucleolar protein NOP1 - yeast (Saccharomyces cerevisiae) ; (J05230) fibrillarlin [Saccharomyces cerevisiae] ; (Z48432) nucleolar protein NOP1 (J05230) [Saccharomyces cerevisiae] ; (Z74062) ORF YDL014w [Saccharomyces cerevisiae] (D85895) diacylglycerol lipase [Aspergillus oryzae]
23117	ENU06911	ANI61C5311: 797..89			LINAP		g1772352	181	106	1.00E-22	34	52	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23118	ENU06912	ANI61C1099	107-132	254-273	LINAP		g3122326	90	59	0.000000	43	17	LEC14B protein ; (D83074) LEC14B protein [Lithospermum erythrorhizon]
23119	ENU06913	ANI61C817	41-60	454-473	LINAP			85		008	29		
23120	ENU06914	ANI61C1099	34-53	731-755	LINAP		g1175399	288	89	4.00E-17			hypothetical 180.2 KD protein C31A2.05C in chromosome I ; hypothetical protein SPAC31A2.05c - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] ; (AB016866) Mis4 [Schizosaccharomyces pombe]
23121	ENU06915	ANI61C930	1 29-51	796-815	LINAP		g4154078	472	98	9.00E-30	37	29	[Schizosaccharomyces pombe] (AL035161) putative efflux protein [Streptomyces coelicolor]
23122	ENU06916	ANI61C6811	122-142	427-446	LINAP		g1171755	279	82	3.00E-23	54	36	"neutral protease II precursor (deuterolysin) (NPII) ; neutral proteinase II - Aspergillus oryzae ; (S53810) neutral protease II, NPII [Aspergillus oryzae, Peptide, 352 aa] [Aspergillus oryzae] ; neutral protease II [Aspergillus oryzae] "
23123	ENU06917	ANI61C2244	22-41	460-479	LINAP		g549706	183	68	4.00E-11	38	35	KTII2 protein ; KTII2 protein - yeast (Saccharomyces cerevisiae) ; (Z28110) ORF YKL110c [Saccharomyces cerevisiae] ; (X77511) KTII2 [Saccharomyces cerevisiae] (AL031515) hypothetical protein SC5C7.08 [Streptomyces coelicolor] (AF016585) polyketide synthase module 3 [Streptomyces caelestis]
23124	ENU06918	ANI61C6808	22-45	613-633	LINAP		g3559998	312	116	2.00E-27	37	62	hypothetical 84.5 KD protein C24H6.09 in chromosome I ; hypothetical protein SPAC24H6.09 - fission yeast (Schizosaccharomyces pombe) ; (Z54142) putative guanine nucleotide exchange factor [Schizosaccharomyces pombe]
23125	ENU06919	ANI61C8823	43-63	808-829	LINAP		g2558839	204	118	5.00E-26	34	14	
23126	ENU06920	ANI61C6788	108-127	749-766	LINAP		g1175438	223	100	2.00E-20	27	34	

Sequence Information

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23127	ENU06921	ANI61C6265: 909..1657	50-69	693-712	LINAP		g2275336	263	44	0.001			(AF001978) differentially expressed in relation to the extent of cell elongation [Candida albicans]
23128	ENU06922	ANI61C931:1 ..598	102-125	552-573	LINAP		g4490644	155	66	2.00E-10	36	18	"(Z98762) SPAC4A8.06c, unknown, len:578aa, some similarity eg. to BAH_STRHY, Q01109, acetyl-hydrolase, (Z99aa), fasta sco res, opt:259, E0:8.2e-17, (35.6% identity in 118 aa over lap) [Schizosaccharomyces pombe]"
23129	ENU06923	ANI61C8833: 1833..609	22-42	810-829	LINAP		g4096660	376	104	1.00E-27			(U34807) extracellular lipase [Candida albicans]
23130	ENU06924	ANI61C6788: 3962..4460	22-49	451-478	LINAP		g2257504	171	90	1.00E-17	37	39	(AB004535) similar to S.pombe unknown protein : DDBJ ACC# D89156 [Schizosaccharomyces pombe] (U72998) ErpM [Borrelia burgdorferi]
23131	ENU06925	ANI61C6269: 1..1100	35-54	810-829	LINAP		g2627268	71	36	0.35	28	57	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
23132	ENU06926	ANI61C1209: 7140..6797	23-47	428-455	LINAP		g3367791	149	65	4.00E-10	31	26	(Y10491) putative cytochrome P450 [Glycine max]
23133	ENU06927	ANI61C9291: 1094..432	48-67	608-627	LINAP		g3334663	59	38	0.000003	31	21	(AF069442) putative polypeptide of LTR transposon [Arabidopsis thaliana]
23134	ENU06928	ANI61C6814: 1..341	67-86	299-320	LINAP		g3924609	91	34	0.38			(AF016449) Similar to cytochrome P450 [Caenorhabditis elegans]
23135	ENU06929	ANI61C6274: 607..1048	22-44	420-439	LINAP		g2315475	59	52	0.000002			regulatory protein MSR1 - yeast (Saccharomyces cerevisiae) ; (Z70202) unknown [Saccharomyces cerevisiae]
23136	ENU06930	ANI61C1259: 967..385			LINAP		g2133082	128	79	3.00E-14	38	29	(AF009672) unknown [Acinetobacter sp. ADP1]
23137	ENU06931	ANI61C1098 1:5200..5803	22-49	559-580	LINAP		g2271503	156	45	0.0006	26	51	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
23138	ENU06932	ANI61C9265: 11512..10812	122-144	657-680	LINAP		g3650376	283	122	3.00E-27	37	24	(U88309) T23B3.5 gene product [Caenorhabditis elegans]
23139	ENU06933	ANI61C8847: 740..1109	22-47	452-479	LINAP		g1825739	123	39	0.016	24	59	

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23140	ENU06934	ANI61C5355: 105-124	648-666		LINAP		g2257531	155	68	4.00E-19	34	15	[Schizosaccharomyces pombe] ; (AB004537) WEB1 protein
		1074..1826											[Schizosaccharomyces pombe] ; (AL022072) web1 homolog: protein transport protein: WD-repeat protein [Schizosaccharomyces pombe]
23141	ENU06935	ANI61C1208: 25-43	452-472		LINAP		g3123302	150	81	6.00E-15	31	24	hypothetical 75.1 KD protein C22E12.19 in chromosome I
23142	ENU06936	ANI61C6833: 22-48	433-452		LINAP		g1351664	310	78	9.00E-24	43	28	hypothetical 59.0 KD protein C30D11.14 in chromosome I ; hypothetical protein SPAC30D11.14 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe]
23143	ENU06937	ANI61C6224: 22-48	802-829		LINAP		g1168457	782	130	1.00E-29	29	15	Ankyrin ; ankyrin - mouse ; (M84756) ankyrin [Mus musculus]
23144	ENU06938	ANI61C2250: 315..754			LINAP		g1172906	165	60	7.00E-11	31	24	cell division cycle related-protein RES2/PCT1 ; cell cycle regulator res2 - fission yeast (Schizosaccharomyces pombe) ; RES2 protein - fission yeast (Schizosaccharomyces pombe) ; (D17761) cell cycle regulator Res2 [Schizosaccharomyces pombe] ; (Z54285) Res2 [Schizosaccharomyces pombe]
23145	ENU06939	ANI61C932: 8 09..1	44-63	682-701	LINAP		g731024	711	259	2.00E-68	62	59	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) ; TWT1 protein - yeast (Saccharomyces cerevisiae) ; (U00029) Bat1p: Branched-Chain Amino Acid Transaminase [Saccharomyces cerevisiae] ; (X78961) TWT1 [Saccharomyces cerevisiae] "
23146	ENU06940	ANI61C628: 3 84..1	106-128	444-471	LINAP		g2117302	710	173	7.00E-43	49	48	(Z95620) putative ribose-phosphate pyrophosphokinase [Schizosaccharomyces pombe]
23147	ENU06941	ANI61C5335: 22-46	799-818		LINAP		g1749560	134	41	0.00003			(D89176) unnamed protein product [Schizosaccharomyces pombe]

Sequence Alignment

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23148	ENU06942	ANI61C1273:	69-88	260-282	LINAP		g547991	62	57	0.000000	25	35	NA(+)/H(+) antiporter ; Na+/H+-exchanging protein - fission yeast (Schizosaccharomyces pombe) ; (Z11736) putative sodium/proton antiporter [Schizosaccharomyces pombe]
		1086..712								1			
23149	ENU06943	ANI61C1100:	22-48	481-500	LINAP		g2497628	114	65	4.00E-10	38	62	microsomal SIGNAL peptidase 21.3 KD subunit ; probable membrane protein YLR066w - yeast (Saccharomyces cerevisiae) ; (X94607) L2186 [Saccharomyces cerevisiae] ; (Z73238) ORF YLR066w [Saccharomyces cerevisiae] ; (U92975) signal peptidase subunit [Saccharomyces cerevisiae] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
23150	ENU06944	ANI61C2231:	22-40	502-521	LINAP		g2462679	56	58	0.000000	25	22	
		637..1								07			
23151	ENU06945	ANI61C932:1	33-52	762-783	LINAP		g1711351	585	83	2.00E-15			SCY1 protein ; SCY1 protein - yeast (Saccharomyces cerevisiae) ; (X97305) suppressor of GTPase mutant [Saccharomyces cerevisiae] ; (Z72605) ORF YGL083w [Saccharomyces cerevisiae]
		682..3727											
23152	ENU06946	ANI61C6847:	23-42	767-793	LINAP		g1175418	1174	229	2.00E-59	43	21	hypothetical 147.4 KD protein C12C2.02C in chromosome II ; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe] ; (AJ223984) Ste20 protein [Schizosaccharomyces pombe]
		1662..4157											
23153	ENU06947	ANI61C6256:	28-47	590-609	LINAP		g548757	202	106	2.00E-22	33	83	50S ribosomal protein L1 ; (M94319) ribosomal protein L1 [Citrus greening disease-associated bacterium-like organism] ; ribosomal protein L1 [Citrus greening disease-associated bacterium]
		4907..4259											
23154	ENU06948	ANI61C1100	22-45	773-800	LINAP		g1946288	442	200	9.00E-51	46	55	(Y11520) vanillin dehydrogenase [Pseudomonas sp.]
		7:1209..2066											

Genomic Data

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23155	ENU06949	ANI61C2241: 1732..719	33-51	808-827	LINAP	g131777	746	247	2.00E-77	53	25		DNA repair protein RAD13 ; excision repair protein - fission yeast (Schizosaccharomyces pombe) ; (X66795) excision repair protein [Schizosaccharomyces pombe]
23156	ENU06950	ANI61C9340: 1050..1515	30-57	446-473	LINAP	g117090	259	80	9.00E-25				cytochrome C oxidase polypeptide IV precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - yeast (Saccharomyces cerevisiae) ; (X01418) cytochrome c oxidase subunit IV precursor [Saccharomyces cerevisiae] ; (X91489) cytochrome C oxidase chain IV precursor [Saccharomyces cerevisiae] ; (Z72709) ORF YGL187c [Saccharomyces cerevisiae]
23157	ENU06951	ANI61C8861: 2192..2787	22-45	548-575	LINAP	g417762	227	114	5.00E-25	30	18		exocyst complex component SEC8 ; SEC8 protein - yeast (Saccharomyces cerevisiae) ; (X64693) SEC8 [Saccharomyces cerevisiae] ; (Z49219) Sec8p [Saccharomyces cerevisiae] ; (Z71255) Sec8p [Saccharomyces cerevisiae]
23158	ENU06952	ANI61C1098: 2..1262	56-75	780-799	LINAP	g4107287	474	83	6.00E-24				(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
23159	ENU06953	ANI61C2241: 1676..2069	40-59	429-448	LINAP	g2606019	84	38	0.061				(AF030027) 71 [Equine herpesvirus 4]
23160	ENU06954	ANI61C1098: 2..2486..3656	44-63	771-790	LINAP	g128340	262	120	1.00E-26	30	29		nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nira - Emericella nidulans ; (M68900) NIRA protein [Emericella nidulans]
23161	ENU06955	ANI61C8867: 2737..2018	22-41	675-694	LINAP	g448109	160	82	6.00E-15	33	34		6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
23162	ENU06956	ANI61C1230: 7214..8025	32-51	636-655	LINAP	g2132661	378	180	1.00E-44	42	45		probable membrane protein YLR020c - yeast (Saccharomyces cerevisiae) ; (Z73192) ORF YLR020c [Saccharomyces cerevisiae]

Sequence Summary

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23163	ENU06957	ANI61C6860:	31-50	720-746	LINAP		g464912	1190	256	1.00E-68	47	19	helicase SGS1 (helicase TPS1) ; DNA helicase TPS1 - yeast (Saccharomyces cerevisiae) ; (L07870) bps. 390..881 = homology to E.coli recQ; bps. 414..430 = ATP binding site [Saccharomyces cerevisiae] ; (Z47815) Tps1p [Saccharomyces cerevisiae] ; (U22341) Sgs1p [Saccharomyces cerevisiae] (AF042799) suppressor of white apricot homolog 2 [Mus musculus] (AL031013) putative secreted protein [Streptomyces coelicolor] hypothetical 37.6 KD protein in GNTR-HTPG intergenic region ; (AB005554) see SWISS_PROT ACC#: P42106 [Bacillus subtilis] ; (Z99124) yxaG [Bacillus subtilis] (Z99113) polyketide synthase [Bacillus subtilis]
23164	ENU06958	ANI61C9827:	41-60	810-829	LINAP		g3941324	65	38	0.092		4	cutinase transcription factor I beta ; (U51672) cutinase transcription factor I [Fusarium solani f. sp. pisi] interleukin enhancer-binding factor 1 (cellular transcription factor ILF-1) ; (U58196) interleukin enhancer binding factor 1 [Homo sapiens] hypothetical 44.8 KD protein C57A10.01 in chromosome I
23165	ENU06959	ANI61C9347:	33-54	633-659	LINAP		g3288616	100	53	0.000001		16	GAM1 gene [Saccharomyces cerevisiae]
23166	ENU06960	ANI61C6815:	22-48	448-475	LINAP		g1176967	105	42	0.000000	30	43	probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) ; (Z48758) unknown [Saccharomyces cerevisiae] (D64006) Ap-4-A phosphorylase II [Synechocystis sp.]
		1517..838											
		3666..3211							2				
23167	ENU06961	ANI61C9346:			LINAP		g2634103	157	80	1.00E-14	29	4	cutinase transcription factor I beta ; (U51672) cutinase transcription factor I [Fusarium solani f. sp. pisi] interleukin enhancer-binding factor 1 (cellular transcription factor ILF-1) ; (U58196) interleukin enhancer binding factor 1 [Homo sapiens] hypothetical 44.8 KD protein C57A10.01 in chromosome I
		1850..1301											
23168	ENU06962	ANI61C2233:	22-46	767-790	LINAP		g1706177	322	109	3.00E-23	32	27	GAM1 gene [Saccharomyces cerevisiae]
		2373..3739											
23169	ENU06963	ANI61C8870:	22-42	455-479	LINAP		g3183529	60	64	6.00E-10			probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) ; (Z48758) unknown [Saccharomyces cerevisiae] (D64006) Ap-4-A phosphorylase II [Synechocystis sp.]
		2181..2534											
23170	ENU06964	ANI61C6839:	22-43	378-398	LINAP		g3287948	152	82	2.00E-15	34	32	cutinase transcription factor I beta ; (U51672) cutinase transcription factor I [Fusarium solani f. sp. pisi] interleukin enhancer-binding factor 1 (cellular transcription factor ILF-1) ; (U58196) interleukin enhancer binding factor 1 [Homo sapiens] hypothetical 44.8 KD protein C57A10.01 in chromosome I
		6118..6445											
23171	ENU06965	ANI61C6278:	41-60	781-800	LINAP		g228213	2404	265	4.00E-70	56	16	GAM1 gene [Saccharomyces cerevisiae]
		4317..1706											
23172	ENU06966	ANI61C2238:	29-54	767-786	LINAP		g1077569	996	255	2.00E-67	47	39	probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) ; (Z48758) unknown [Saccharomyces cerevisiae] (D64006) Ap-4-A phosphorylase II [Synechocystis sp.]
		1..1351											
23173	ENU06967	ANI61C9335:	24-47	437-456	LINAP		g1001338	62	63	0.000000			cutinase transcription factor I beta ; (U51672) cutinase transcription factor I [Fusarium solani f. sp. pisi] interleukin enhancer-binding factor 1 (cellular transcription factor ILF-1) ; (U58196) interleukin enhancer binding factor 1 [Homo sapiens] hypothetical 44.8 KD protein C57A10.01 in chromosome I
		2550..2129											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23174	ENU06968	ANI61C6798:	23-42	802-829	LINAP		g1708909	356	62	1.00E-19	27	56	malic acid transport protein (malate permease) ; C4-dicarboxylate transport protein mae1 - fission yeast (Schizosaccharomyces pombe) ; (U21002) malic acid transport protein [Schizosaccharomyces pombe]
23175	ENU06969	ANI61C1229:	50-69	460-479	LINAP		g2146829	173	91	5.00E-18	43	54	"hypothetical protein YCL010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL010c, len:146 [Saccharomyces cerevisiae] "
23176	ENU06970	ANI61C9328:	28-47	776-794	LINAP		g2342601	1390	166	1.00E-40	35	5	(X89442) peptide synthetase [Metarhizium anisopliae]
23177	ENU06971	ANI61C6798:	22-44	453-479	LINAP		g4160354	125	69	1.00E-11	47	28	(Z64354) unknown [Schizosaccharomyces pombe]
23178	ENU06972	ANI61C2212:			LINAP		g3549891	170	75	7.00E-17	33	34	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
23179	ENU06973	ANI61C9349:	24-51	787-809	LINAP		g2144467	1068	159	1.00E-54	44	42	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae)
23180	ENU06974	ANI61C6835:	158-179	476-499	LINAP		g3395590	193	90	1.00E-17	37	56	(AL031179) hypothetical protein [Schizosaccharomyces pombe]
23181	ENU06975	ANI61C6308:	48-67	527-549	LINAP		g3702642	398	98	7.00E-42	56	41	(AL031825) ma binding protein - putative pre mna splicing factor [Schizosaccharomyces pombe]
23182	ENU06976	ANI61C1322:	22-42	777-797	LINAP		g125731	162	75	1.00E-16	30	32	"ATP-dependent DNA helicase II, 86 KD subunit (Iupus KU autoantigen protein P86) (86 KD subunit of KU antigen) (thyroid-lupus autoantigen) (TLAA) (CTC BOX binding factor 85 KD subunit) (CTCBF) (CTC85) (nuclear factor IV) (...; Ku antigen 80K chain - human ; (J04977) Ku antigen [Homo sapiens] ; (M30938) Ku (p70/p80) subunit [Homo sapiens] "
23183	ENU06977	ANI61C2259:	36-55	442-467	LINAP		g3123282	98	56	0.000000	20	7	TRNA-splicing endonuclease positive effector ; SEN1 protein - yeast (Saccharomyces cerevisiae) ; (U20939) Sen1p [Saccharomyces cerevisiae] (AB023145) KIAA0928 protein [Homo sapiens]
23184	ENU06978	ANI61C9795:	22-49	804-829	LINAP		g4589488	54	75	9.00E-13	24	11	

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23185	ENU06979	ANI61C8832:	22-46	795-822	LINAP		g3122656	1264	161	2.00E-61	57	50	amidophosphoribosyltransferase (glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) ; (U32992) glutamine phosphoribosylpyrophosphate amidotransferase [Saccharomyces kluyveri]
23186	ENU06980	ANI61C5401:	22-48	380-398	LINAP		g1438949	60	53	0.000001			(U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi]
23187	ENU06981	ANI61C227:1	22-48	806-825	LINAP		g2764761	171	104	6.00E-22	30	5	"(AJ223012) rifamycin polyketide synthase, type 1 [Amycolatopsis mediterranei] ; (AF040570) polyketide synthase [Amycolatopsis mediterranei]"
23188	ENU06982	ANI61C8882:	22-43	736-761	LINAP		g2497111	304	123	2.00E-27	30	35	hypothetical 84.6 KD protein in GLO1-YPT7 intergenic region ; probable membrane protein YML002w - yeast (Saccharomyces cerevisiae)
23189	ENU06983	ANI61C5382:	22-45	476-495	LINAP		g2494239	241	100	3.00E-24	37	52	probable peroxisomal enoyl-CoA hydratase ; peroxisomal enoyl hydratase-like protein - rat ; (U08976) peroxisomal enoyl hydratase-like protein [Rattus norvegicus]
23190	ENU06984	ANI61C2257:	22-43	434-453	LINAP		g4581525	170	75	4.00E-13	34	27	(AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
23191	ENU06985	ANI61C8894:	22-44	794-817	LINAP		g1168817	418	143	6.00E-35	37	24	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7
23192	ENU06986	ANI61C6882:	36-60	587-610	LINAP		g4507075	250	122	2.00E-27	40	17	[Schizosaccharomyces pombe] "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 ; (AB010882) hSNF2H [Homo sapiens]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23193	ENU06987	ANI61C5397: 22-46	2937..2595	414-434	LINAP		g2499778	176	41	0.007			cell binding factor 2 precursor (antigen PEB4A) ; cell binding factor 2 - Campylobacter jejuni ; (X84703) cell binding factor 2 [Campylobacter jejuni]
23194	ENU06988	ANI61C1337: 24-43	405..1105	566-585	LINAP		g3122986	160	110	1.00E-23	33	42	beta-TRCP (beta-transducin repeat-containing protein) (BTRCP) ; beta-transducin repeat-containing protein - African clawed frog ; (M98268) beta-TRCP [Xenopus laevis]
23195	ENU06989	ANI61C5418: 24-45	929..1313	443-466	LINAP		g1788578	90	63	0.000000			"(AE000314) orf, hypothetical protein [Escherichia coli]"
23196	ENU06990	ANI61C1329: 34-53	1267..2834	810-829	LINAP		g2499839	331	94	2.00E-18			thyroid receptor interacting protein 12 (TRIP12) (KIAA0045) ; (D28476)
23197	ENU06991	ANI61C2215: 31-50	2977..4211	777-796	LINAP		g3183326	351	151	5.00E-36	31	31	KIAA0045 [Homo sapiens] hypothetical 93.2 KD TRP-ASP repeats containing protein C4F8.11 in chromosome I ; (Z98530) beta-transducin [Schizosaccharomyces pombe]
23198	ENU06992	ANI61C1330: 22-45	1244..274	782-801	LINAP		g2656001	294	109	2.00E-23	35	31	(Z98977) hypothetical protein [Schizosaccharomyces pombe]
23199	ENU06993	ANI61C8878: 25-45	4372..5020	559-586	LINAP		g2132218	263	139	2.00E-32	42	32	hypothetical protein YPL169c - yeast (Saccharomyces cerevisiae) ; (Z73525) ORF YPL169c [Saccharomyces cerevisiae] ; (X96770) P2520 protein [Saccharomyces cerevisiae]
23200	ENU06994	ANI61C539:2 64-83	021..1434	542-567	LINAP		g3915438	151	89	2.00E-17	31	62	hypothetical protein C10D6.08 in chromosome I ; (Z98951) hypothetical protein [Schizosaccharomyces pombe]
23201	ENU06995	ANI61C1360: 66-93	1..889	776-795	LINAP		g2244866	215	80	6.00E-23	35	13	(Z97337) hypothetical protein [Arabidopsis thaliana]
23202	ENU06996	ANI61C538:8 22-45	038..5666	758-781	LINAP		g1354473	2931	180	2.00E-90	67	21	(U53189) Os-1p [Neurospora crassa]
23203	ENU06997	ANI61C9831: 24-43	6221..5845	446-465	LINAP		g2132165	413	60	3.00E-17	54	51	hypothetical protein YPL051w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe21p [Saccharomyces cerevisiae] ; (AF017142) ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]